

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:28:39 ; Search time 21.53 Seconds
(without alignments)
969.093 Million cell updates/sec

Title: US-08-887-977-10
Perfect score: 365
Sequence: 1 MFSTPVKILQCSILHITOL.....NISRTSETADNDNASFTM 365

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0
Searched: 390729 seqs, 57163235 residues
Word size : 10

Total number of hits satisfying chosen parameters: 7

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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14: /SID56/gcgdata/geneseq/geneseq/AA1993.DAT.*
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16: /SID56/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SID56/gcgdata/geneseq/geneseq/AA1996.DAT.*
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21: /SID56/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID56/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	365	100.0	365	19	W48086 Human dendritic ce
2	264	72.3	365	21	Y97077 Primate (human) ch
3	10	2.7	360	17	R99274 Chemokine receptor
4	10	2.7	360	21	B07498 A human CCR4 chemo
5	10	2.7	469	21	Y92934 Human G-protein co
6	10	2.7	476	21	Y92932 Rat G-protein coup
7	10	2.7	476	21	Y92933 Rat G-protein coup

ALIGNMENTS

RESULT 1

W48086
ID W48086 standard; Protein; 365 AA.
XX
AC W48086;
XX
DT 11-JUN-1998 (first entry)
XX
DE Human dendritic cell chemokine receptor.
XX
KW Human; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta;
KW receptor; dendritic cell; macrophage; inflammation; asthma.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 193 /note= "encoded by CAN"
FT
XX
PN W09801557-A2.
PD 15-JAN-1998.
XX
PF 02-JUL-1997; 97WO-US10819.
XX
PR 04-JUN-1997; 97US-0048593.
PR 05-JUL-1996; 96US-0675814.
PR 11-OCT-1996; 96US-0028329.
XX
(SCHE) SCHERING CORP.
XX
PI Gish KC, Schall TJ, Vicari A, Wang W, Zlotnik A;
XX
DR WPI; 1998-101054/09.
DR N-PSDB; V15418.
XX
PT Novel chemokines, e.g. thymus expressed chemokine - used for
PT treating inflammatory conditions including asthma.
XX
PS Claim 3; Page 94-95; 202pp; English.
XX
CC The present sequence represents human dendritic cell chemokine receptor.
CC Antibodies which bind to the protein can be used in detecting or
CC diagnosing various immunological conditions related to expression
CC of the protein. The nucleic acid can be used for screening and
CC isolating DNA clones for the chemokines, especially from other
CC species. The chemokine can be used in the treatment of conditions
CC associated with abnormal physiology or development, including
CC inflammatory conditions such as asthma.
XX
SQ Sequence 365 AA;

Query Match 100.0%; Score 365; DB 19; Length 365;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFSTPVKILQCSILHITQLILRCYCPCRRSSGSPGYLYRIAYSLICVLGLNLIWVI 60
DB 1 mfstpvkllcqsilhitqlilrcycpcrrsgsgpylyriaysllcvgllgnllvvi 60
QY 61 TFAFYKKARSMTDVYLLNMAIADILFVLTLPFWAVSHATGAWVPSNATCKLLKGIYAINF 120
DB 61 tfafykkarsmtdvyllynmaiadilfvtlpfwavshatgawvpsnatckllkgiyainf 120
QY 121 NCGMLLLTCLISMDRYTAIVQATKSFRLSRTLPRSKITICLVWGLSVIISSTVFVNOKY 180
DB 121 ncgmllltclismdrytaivqatksfrlrsrtlprskitiiclvwglsviisstvfvnqky 180
QY 181 NTQGSVCEPKYQTVSEPIRWKLMGLLELFGFFIFLPMFMIFCYTFIVKTLVQAQNSKR 240
DB 181 ntqgsdvcepkvqtvsepiwrwklmgllelfgffiflpmfmifcytfivktlvqaqnskr 240

QY 241 HKAIRVIAVVLVFLACQIPHNMLLVTAANLGMNRSCQSEKLGTYTKTVEVLAFLHC 300
 Db 241 HKAIRVIAVVLVFLACQIPHNMLLVTAANLGMNRSCQSEKLGTYTKTVEVLAFLHC 300
 QY 301 CLNPVLYAFIGQFRNYFLKILKDLWCVRKRYKSSGFCAGRYSENISROTSETADNDNA 360
 Db 301 CLNPVLYAFIGQFRNYFLKILKDLWCVRKRYKSSGFCAGRYSENISROTSETADNDNA 360
 QY 361 SSFTM 365
 Db 361 ssftm 365

RESULT 2
 Y97077
 ID Y97077 standard; Protein; 365 AA.
 XX
 AC Y97077;
 XX
 DT 04-DEC-2000 (first entry)
 XX
 DE Primate (human) chemokine receptor CCR6.
 XX
 KW MIP-3-alpha; chemokine; CCR6 receptor; ligand; cytostatic; agonist;
 KW antagonist; anti-psoriatic; dermatological; immunosuppressive;
 KW anti-inflammatory.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 193
 FT /note= "Encoded by CAN#"
 XX
 PN WO200046248-A1.
 XX
 PD 10-AUG-2000.
 XX
 PF 02-FEB-2000; 2000WO-US00511.
 XX
 PR 03-FEB-1999; 99US-0244281.
 XX
 FA (SCHE) SCHERING CORP.
 XX
 PI Oldham ER, Homey B, Dieu-Nosjean M, Caux C, Zlotnik A;
 XX
 DR WPI: 2000-543477/49.
 DR N-PSDB; A51971.
 XX
 PT Novel methods for modulating the migration of cells within or to the
 PT skin using MIP-3-alpha or CCR6 agonists or antagonists, useful for
 PT treating skin disorders, e.g. cancer
 XX
 PS Disclosure; Page 53-54; 61pp; English.
 XX
 CC The MIP-3-alpha chemokine is expressed in inflamed skin cells. This
 CC chemokine is the ligand for the CCR6 receptor. MIP-3-alpha or CCR6
 CC agonists or antagonists can be used to modulate the migration of a cell
 CC within or to the skin of a mammal. MIP-3-alpha can be used to purify a
 CC population of cells expressing a MIP-3-alpha receptor. The methods are
 CC useful for treating a mammalian subject with a skin disease or condition,
 CC e.g. cancer, metastasis, psoriasis, atopic or contact dermatitis,
 CC systemic lupus erythematosus and lichen ruber planus, or for treating
 CC skin transplants or grafts.
 XX
 SQ Sequence 365 AA;

Query Match 72.3%; Score 264; DB 21; Length 365;
 Best Local Similarity 99.7%; Pred. No. 1.4e-251;
 Matches 364; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFSTPVKILQCSILHITQLIRCYCAPCRSGSPGYLYRIAYSLICVLGLNLIYVI 60
 Db 1 MFSTPVKILQCSILHITQLIRCYCAPCRSGSPGYLYRIAYSLICVLGLNLIYVI 60
 QY 61 TFAYYKARSMTDYLNLNMTADILFVLTPFWAVSHATGAWFNSNATCKLLKGIYAINF 120
 Db 61 TFAYYKARSMTDYLNLNMTADILFVLTPFWAVSHATGAWFNSNATCKLLKGIYAINF 120
 QY 121 NCGMLLTCISMDRYIAIVQATKSFRLRSRTPRLSKIIICLVVWGLSVIISSTFVFNQY 180
 Db 121 NCGMLLTCISMDRYIAIVQATKSFRLRSRTPRLSKIIICLVVWGLSVIISSTFVFNQY 180
 QY 181 NTQGSVCEPKYQTVSEPIRWKLLMLGLELFGFPIPLMFIFCYTFVTKVLVQONSKR 240
 Db 181 NTQGSVCEPKYQTVSEPIRWKLLMLGLELFGFPIPLMFIFCYTFVTKVLVQONSKR 240
 QY 241 HKAIRVIAVVLVFLACQIPHNMLLVTAANLGMNRSCQSEKLGTYTKTVEVLAFLHC 300
 Db 241 HKAIRVIAVVLVFLACQIPHNMLLVTAANLGMNRSCQSEKLGTYTKTVEVLAFLHC 300
 QY 301 CLNPVLYAFIGQFRNYFLKILKDLWCVRKRYKSSGFCAGRYSENISROTSETADNDNA 360
 Db 301 CLNPVLYAFIGQFRNYFLKILKDLWCVRKRYKSSGFCAGRYSENISROTSETADNDNA 360
 QY 361 SSFTM 365
 Db 361 ssftm 365

RESULT 3
 R99274
 ID R99274 standard; Protein; 360 AA.
 XX
 AC R99274;
 XX
 DT 09-DEC-1996 (first entry)
 XX
 DE Chemokine receptor K5.5.
 XX
 KW Chemokine receptor K5.5; MIP-1-alpha; RANTES; MCP-1; allergy;
 KW atheroma; HIV; AIDS; graft rejection; stem cell.
 XX
 OS Homo sapiens.
 XX
 PN WO9623068-A1.
 XX
 PD 01-AUG-1996.
 XX
 PF 24-JAN-1996; 96WO-GB00143.
 XX
 PR 27-JAN-1995; 95GB-0001683.
 XX
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Power CA, Wells TNC;
 XX
 DR WPI: 1996-362692/36.
 DR N-PSDB; T35277.
 XX
 PT Chemokine receptor which binds MIP-1-alpha, RANTES and/or MCP-1 -
 PT useful in screening for agents to treat asthma, hay fever, eczema,
 PT allergies, atopic dermatitis, rhinitis or conjunctivitis.
 XX
 PS Claim 1; Fig 3; 47pp; English.
 XX
 CC Human chemokine receptor K5.5 (R99274) binds MIP-1-alpha, RANTES
 CC and/or MCP-1. Its amino acid sequence was deduced from a cDNA
 CC clone (T35277) obt'd. from a human spleen lambda gt11 cDNA
 CC library. Recombinant chemokine receptor K5.5 can be expressed
 CC in transfected host cells. It can be used to screen for agents
 CC which act as antagonists to MCP-1, MIP-1-alpha and/or RANTES.
 CC Such agents may be useful in treating allergies, atheromas and
 CC diseases mediated by viruses, such as AIDS. They can also be
 CC used to prevent graft rejection or to protect stem cells from

CC the effects of chemotherapy.
XX
SQ Sequence 360 AA;

Query Match 2.7%; Score 10; DB 17; Length 360;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 RSMSTDVYLLN 78
 |||||
Db 71 rsmtdvyl n 80

RESULT 4
B07498
ID B07498 standard; Protein; 360 AA.
XX
AC B07498;
DT 20-OCT-2000 (first entry)
DE A human CCR4 chemokine receptor polypeptide.
XX
KW Systemic memory T cell; CCR4; TARC; integrin dependent arrest;
KW thymus and activation-regulated chemokine; vascular receptor;
KW MDC; monokine derived chemokine; adhesion trigger; inflammation.
XX
OS Homo sapiens.
XX
PN WO200041724-A1.
XX
PD 20-JUL-2000.
XX
PF 14-JAN-2000; 2000WO-US00953.
XX
PR 15-JAN-1999; 99US-0232878.
XX
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PA (LEUK-) LEUKOSITE INC.
XX
PI Butcher EC, Campbell JJ, Wu L, Rottman JB;
XX
DR WPI: 2000-475957/41.
DR N-PSDB: A58872.

XX Modulating the trafficking of systemic memory T cells in mammals by
PT administering a CCR4 modulating agent, useful for the treatment of
PT inflammation -
XX
XX Disclosure; Page 35-36; 39pp; English.
XX
CC The specification describes a method of modulating the trafficking of
CC systemic memory T cells in a mammalian host. The method comprises
CC administering a CCR4 modulating agent. It has been found that systemic
CC T cells such as express high levels of CCR4. Ligands of CCR4 such as
CC TARC (thymus and activation-regulated chemokine) and MDC (monokine
CC derived chemokine) act as an adhesion trigger and, upon CCR4 binding,
CC these cells undergo integrin dependent arrest to the appropriate
CC vascular receptors. This arrest acts to localize the cells at the
CC target site. The method modulates this triggering and CCR4 mediated
CC chemotaxis to affect the localization of T cells in targeted tissues.
CC The active agent may be a CCR4 agonist that acts to enhance T cell
CC localization. Alternatively, it may be an antagonist that blocks CCR4
CC biological activity. A CCR4 antagonist may be administered for the
CC treatment of inflammation. The present sequence represents a human CCR4.
XX
SQ Sequence 360 AA;

Query Match 2.7%; Score 10; DB 21; Length 360;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 RSMSTDVYLLN 78
 |||||
Db 71 rsmtdvyl n 80

RESULT 5
Y92934
ID Y92934 standard; Protein; 469 AA.
XX
AC Y92934;
DT 25-OCT-2000 (first entry)
DE Human G-protein coupled receptor clone hOT7T009 protein.
XX
KW Hypotensive; G-protein coupled receptor protein; brain stem region;
KW antibody; hypertension; ligand; human.
XX
OS Homo sapiens.
XX
PN WO200024891-A1.
XX
PD 04-MAY-2000.
XX
PF 27-OCT-1999; 99WO-JP05938.
XX
PR 28-OCT-1998; 98JP-0306543.
PR 28-JAN-1999; 99JP-0020356.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Watanabe T, Matsumoto Y, Terao Y, Shintani Y;
XX
DR WPI: 2000-350733/30.
DR N-PSDB: A11249.

XX G protein coupled receptor protein, antibodies to it and a method of
PT screening compounds which alter the binding of the receptor to its
PT ligands for treatment of disorders such as hypertension -
XX
XX Example 2; Fig 10-12; 120pp; Japanese.
XX
CC This sequence represents a novel human G-protein coupled receptor protein
CC (GCPR) designated clone hOT7T009. The coding sequence was isolated from
CC a foetal cDNA library. The protein and antibodies raised against it are
CC useful in the diagnosis, treatment and prevention of disorders associated
CC with the GCPR, such as hypertension. The protein is also used to identify
CC ligands of GCPR and compounds which affect the binding of GCPR to its
CC ligands.
XX
SQ Sequence 469 AA;

Query Match 2.7%; Score 10; DB 21; Length 469;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 FVLTLPFWAV 95
 |||||
Db 131 fvltpfwav 140

RESULT 6
Y92932
ID Y92932 standard; Protein; 476 AA.
XX
AC Y92932;
XX
DT 25-OCT-2000 (first entry)
XX
DE Rat G-protein coupled receptor clone rOT7T009C protein.
XX

KW Hypotensive; rat; G-protein coupled receptor protein; brain stem region;
 KW antibody; hypertension; ligand.
 XX
 OS Rattus sp.
 XX

PN WO200024891-A1.

XX
 PD 04-MAY-2000.

XX
 PF 27-OCT-1999; 99WO-JP05938.

XX
 PR 28-OCT-1998; 98JP-0306543.

PR 28-JAN-1999; 99JP-0020356.

XX
 PA (TAKE) TAKEDA CHEM IND LTD.

XX
 PI Watanabe T, Matsumoto Y, Terao Y, Shintani Y;

XX
 DR WPI; 2000-350733/30.

DR
 N-PSDB; A11247.

XX
 PT G protein coupled receptor protein, antibodies to it and a method of
 PT screening compounds which alter the binding of the receptor to its
 PT ligands for treatment of disorders such as hypertension -

XX
 PS Claim 1; Fig 1-4; 120pp; Japanese.

XX
 CC This sequence represents a novel rat G-protein coupled receptor protein
 CC (GPR) designated clone rOT7T009C. The coding sequence was isolated from
 CC a brain stem region library. The protein and antibodies raised against
 CC it are useful in the diagnosis, treatment and prevention of disorders
 CC associated with the GPR, such as hypertension. The protein is also used
 CC to identify ligands of GPR and compounds which affect the binding of
 CC GPR to its ligands.

XX
 SQ Sequence 476 AA;

Query Match 2.7%; Score 10; DB 21; Length 476;
 Best Local Similarity 100.0%; Pred. No. 0.16;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 86 FVLTLPFWAV 95

Db 138 fvltpfwav 147

RESULT 7

Y92933

ID Y92933 standard; Protein; 476 AA.

XX

AC Y92933;

XX
 DT 25-OCT-2000 (first entry)

DE Rat G-protein coupled receptor clone rOT7T009T protein.

XX
 KW Hypotensive; rat; G-protein coupled receptor protein; brain stem region;

XX
 KW antibody; hypertension; ligand.

XX
 OS Rattus sp.

XX
 PN WO200024891-A1.

XX
 PD 04-MAY-2000.

XX
 PF 27-OCT-1999; 99WO-JP05938.

XX
 PR 28-OCT-1998; 98JP-0306543.

XX
 PR 28-JAN-1999; 99JP-0020356.

XX
 PA (TAKE) TAKEDA CHEM IND LTD.

XX

PI Watanabe T, Matsumoto Y, Terao Y, Shintani Y;

XX
 DR WPI; 2000-350733/30.

DR
 N-PSDB; A11248.

XX
 PT G protein coupled receptor protein, antibodies to it and a method of
 PT screening compounds which alter the binding of the receptor to its
 PT ligands for treatment of disorders such as hypertension -

XX
 PS Claim 2; Fig 5-8; 120pp; Japanese.

XX
 CC This sequence represents a novel rat G-protein coupled receptor protein
 CC (GPR) designated clone rOT7T009T. The coding sequence was isolated from
 CC a brain stem region library. The protein and antibodies raised against
 CC it are useful in the diagnosis, treatment and prevention of disorders
 CC associated with the GPR, such as hypertension. The protein is also used
 CC to identify ligands of GPR and compounds which affect the binding of
 CC GPR to its ligands.

XX
 SQ Sequence 476 AA;

Query Match 2.7%; Score 10; DB 21; Length 476;
 Best Local Similarity 100.0%; Pred. No. 0.16;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 86 FVLTLPFWAV 95

Db 138 fvltpfwav 147

Search completed: May 23, 2001, 15:36:41
 Job time: 482 sec

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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:30:14 ; Search time 13 Seconds
(without alignments)
539.382 Million cell updates/sec

Title: US-08-887-977-10
Perfect score: 365
Sequence: 1 MFSTPVKILCOSILHITOL.....NISQTSADNDNASSFTM 365

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 185757 seqs, 19210857 residues

Word size : 10

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents_AA.*

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- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	2.7	360	4	US-08-875-573-20 Sequence 20, Appl

ALIGNMENTS

RESULT 1

US-08-875-573-20
Sequence 20, Application US/08875573
Patent No. 6150132

GENERAL INFORMATION:

APPLICANT: Wells, Timothy N.C.

APPLICANT: Power, Christine A.

TITLE OF INVENTION: A CHEMOKINE RECEPTOR ABLE TO BIND TO

TITLE OF INVENTION: MCP-1, MIP-1 ALPHA AND/OR RANTES. ITS USES

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHUYE P.C.

STREET: 1100 No. 6150132th Glebe Rd. 8th floor

CITY: Arlington

STATE: VA

COUNTRY: USA

ZIP: 22201-4741

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/875,573

FILING DATE: 31-OCT-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB96/00143

FILING DATE: 24-JAN-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9501683.8

FILING DATE: 27-JAN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Wilson, Mary J.

REGISTRATION NUMBER: 32,955

REFERENCE/DOCKET NUMBER: 1430-172

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-816-4000

TELEFAX: 703-816-4100

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 360 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-875-573-20

Query Match 2.7%; Score 10; DB 4; Length 360;

Best Local Similarity 100.0%; Pred. No. 0.065;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 RSMTDVYLLN 78

Db 71 RSMTDVYLLN 80

Search completed: May 23, 2001, 15:36:57

Job time: 403 sec

1

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:32:09 ; Search time 18.5 Seconds
(without alignments)
1355.885 Million cell updates/sec

Title: US-08-887-977-10
Perfect score: 365
Sequence: 1 MFSTPVKIIILCQSLIHITQL.....NISROTSETADNDNASFTM 365

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 198801 seqs, 68722935 residues

Word size : 10

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR_67:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	315	86.3	369	2 JC5068	G protein-coupled
2	11	3.0	353	2 S28787	neuropeptide Y/pep
3	10	2.7	360	2 A57160	chemokine (C-C) re
4	10	2.7	383	2 S55594	G protein-coupled

ALIGNMENTS

RESULT 1
JC5068
G protein-coupled receptor CKR-L3 - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
C:Accession: JC5068
R:Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
Biochem. Biophys. Res. Commun. 227, 846-853, 1996
A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-like
A:Reference number: JC5067; MUID:97040707
A:Accession: JC5068
A:Molecule type: DNA
A:Residues: 1-369 <ZAB>
A:Cross-references: EMBL:Z79784; NID:g1668737; PIDN:CAB02144.1; PID:g1668738
C:Comment: This protein belongs to the family of alpha chemokine receptors.
C:Genetics:
A:Gene: GDB:CMKBR6; STR:22; GPR29; CCR6; CKR-L3; GPR-CX4
A:Cross-references: GDB:5370639; OMIM:601835
A:Map position: 6q27-6q27
C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein
F:42-68/Domain: transmembrane #status predicted <TM1>
F:79-99/Domain: transmembrane #status predicted <TM2>
F:115-136/Domain: transmembrane #status predicted <TM3>
F:160-180/Domain: transmembrane #status predicted <TM4>
F:212-233/Domain: transmembrane #status predicted <TM5>
F:250-271/Domain: transmembrane #status predicted <TM6>
F:292-315/Domain: transmembrane #status predicted <TM7>

Query Match 86.3%; Score 315; DB 2; Length 369;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GLGNILVVTFAFYKKARSMTDVYLLNMAADILFVLTLPFWAVSHATGAWFSNATCK 110
DB 55 GLGNILVVTFAFYKKARSMTDVYLLNMAADILFVLTLPFWAVSHATGAWFSNATCK 114
QY 111 LLKGIYAINFNCGMLLTCTISMDRYIAIVQATKSFRLRSRTLPRSKIIICLVVWGLSVIS 170
DB 115 LLKGIYAINFNCGMLLTCTISMDRYIAIVQATKSFRLRSRTLPRSKIIICLVVWGLSVIS 174
QY 171 SSTFVFNQYNTQGSVDCEPKYQTVSEPIRWKLLMLGLELLFGFFIPLMFICYTFIVK 230
DB 175 SSTFVFNQYNTQGSVDCEPKYQTVSEPIRWKLLMLGLELLFGFFIPLMFICYTFIVK 234
QY 231 TLVQAQNSKRHKAIIRVIAVVLFLACQIPHNVLLVTAANLGMNRSCQSEKLIYTKT 290
DB 235 TLVQAQNSKRHKAIIRVIAVVLFLACQIPHNVLLVTAANLGMNRSCQSEKLIYTKT 294
QY 291 VTEVLAFHCLNPVLYAFIGOKERNYFLKILKDLWCVRKYKSGFSCAGRYSENISRQ 350
DB 295 VTEVLAFHCLNPVLYAFIGOKERNYFLKILKDLWCVRKYKSGFSCAGRYSENISRQ 354
QY 351 TSETADNDNASFTM 365
DB 355 TSETADNDNASFTM 369

RESULT 2

S28787
neuropeptide Y/peptide YY receptor Y3 - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 26-Aug-1999
C:Accession: S28787
R:Rimland, J.; Xin, W.; Sweetnam, P.; Saijoh, K.; Nestler, E.J.; Duman, R.S.
Mol. Pharmacol. 40, 869-875, 1991
A:Title: Sequence and expression of a neuropeptide Y receptor cDNA.
A:Reference number: S28787; MUID:92100053
A:Accession: S28787
A:Molecule type: mRNA
A:Residues: 1-353 <RIM>
A:Cross-references: EMBL:M86739
C:Superfamily: vertebrate rhodopsin
C:Keywords: appetite; G protein-coupled receptor; transmembrane protein

Query Match 3.0%; Score 11; DB 2; Length 353;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 LFVLTLPFWAV 95
DB 87 LFVLTLPFWAV 97

RESULT 3

A57160
chemokine (C-C) receptor 4 - human
N:Alternate names: C-C CKR-4
C:Species: Homo sapiens (man)
C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C:Accession: A57160

R:Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.; W
J. Biol. Chem. 270, 19495-19500, 1995
A:Title: Molecular cloning and functional expression of a novel CC chemokine receptor c
A:Reference number: A57160; MUID:95370289
A:Accession: A57160
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-360 <POM>
A:Cross-references: GB:X85740; NID:g1370103; PIDN:CAA59743.1; PID:g971452
A:Note: source clone K5-5
C:Genetics:
A:Gene: GDB:CMKBR4
A:Cross-references: GDB:677463
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot
F:40-65/Domain: transmembrane #status predicted <TM1>
F:76-97/Domain: transmembrane #status predicted <TM2>
F:112-133/Domain: transmembrane #status predicted <TM3>
F:151-175/Domain: transmembrane #status predicted <TM4>
F:208-226/Domain: transmembrane #status predicted <TM5>
F:243-264/Domain: transmembrane #status predicted <TM6>
F:291-308/Domain: transmembrane #status predicted <TM7>
F:29-276, 110-187/Disulfide bonds: #status predicted
F:72,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 2.7%; Score 10; DB 2; Length 360;

Best Local Similarity 100.0%; Pred. No. 0.023;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 69 RSMYDVLN 78

Db 71 RSMYDVLN 80

RESULT 4

S55594

G protein-coupled receptor E1 - equine herpesvirus 2

C:Species: equine herpesvirus 2

C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 13-Aug-1999

C:Accession: S55594

R:Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.

J. Mol. Biol. 249, 520-528, 1995

A:Title: The DNA sequence of equine herpesvirus 2.

A:Reference number: S55594; MUID:95302501

A:Accession: S55594

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-383 <TEL>

A:Cross-references: GB:U20824; NID:g695172; PIDN:AAC13788.1; PID:g695173

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor

Query Match

Best Local Similarity 2.7%; Score 10; DB 2; Length 383;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 GLGNILVVI 60

Db 86 GLGNILVVI 95

Search completed: May 23, 2001, 15:37:19

Job time: 310 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:36:24 ; Search time 11.88 seconds
(without alignments)
1052.462 Million cell updates/sec

Title: US-08-887-977-10
Perfect score: 365
Sequence: 1 MFSTPVKIIICOSILHITQL.....NISROTSETADNDNASSFTM 365

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 93435 seqs, 34255486 residues

Word size : 10

Total number of hits satisfying chosen parameters: 6

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	315	86.3	374	1 CRR6_HUMAN	P51684 homo sapien
2	26	7.1	367	1 CRR6_MOUSE	O54689 mus musculu
3	11	3.0	192	1 CCR4_SHEEP	Q28553 ovis aries
4	11	3.0	353	1 CCR4_BOVIN	P25930 bos taurus
5	11	3.0	353	1 CCR4_FELCA	P56498 felis silve
6	10	2.7	360	1 CRR4_HUMAN	P51679 homo sapien

ALIGNMENTS

RESULT 1
ID CRR6_HUMAN STANDARD; PRT; 374 AA.
AC P51684; Q92846; P78553;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CRR-6) (CC-CRR-6) (CCR-6) (LARC
DE RECEPTOR) (GPR-CY4) (GPCY4) (CHEMOKINE RECEPTOR-LIKE 3) (CRR-L3)
DE (DRY6).
GN CCR6 OR CCR6 OR STRL22 OR GPR29 OR CCR6L3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND FUNCTION.
RX MEDLINE=97313465; PubMed=9169459;
RA Baba M., Imai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K.,
RA Nomiya H., Yoshie O.,
RT "Identification of CCR6, the specific receptor for a novel
RT lymphocyte-directed CC chemokine LARC.";

RL J. Biol. Chem. 272:14893-14898(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Lautens L.L., Modi W., Bonner T.I.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97040707; PubMed=8886020;
RA Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G.;
RT "Molecular cloning and RNA expression of two new human chemokine
RT receptor-like genes.";
RL Biochem. Biophys. Res. Commun. 227:846-853(1996).
RN [4]
RP SEQUENCE FROM N.A.
RA McCoy R., Perlmutter D.H.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=97224503; PubMed=9070937;
RA Liao F., Lee H.-H., Farber J.M.;
RT "Cloning of STRL22, a new human gene encoding a G-protein-coupled
RT receptor related to chemokine receptors and located on chromosome
RT 6q27.";
RL Genomics 40:175-180(1997).
CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-
CC ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE
CC INTRACELLULAR CALCIUM IONS LEVEL.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: SPLEEN, LYMPH NODES, APPENDIX, AND FETAL
CC LIVER. EXPRESSED IN LYMPHOCYTES, T CELLS AND B CELLS BUT NOT IN
CC NATURAL KILLER CELLS, MONOCYTES, OR GRANULOCYTES.
CC -1- INDUCTION: INTERLEUKIN-2.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-6 IS THE INITIATOR.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U45984; AAB62714.1; -
CC EMBL; Z79784; CAB02144.1; ALT_INIT.
CC EMBL; U60000; AAB05949.1; -
CC EMBL; U68030; AAC51124.1; -
CC EMBL; U68032; AAC51125.1; -
CC HSSP; P34996; IDDD.
CC GCRDB; GCR_1037; -
CC GCRDB; GCR_1075; -
CC GCRDB; GCR_1906; -
CC GCRDB; GCR_1919; -
CC GCRDB; GCR_1941; -
CC GCRDB; GCR_2110; -
CC MIM; 601835; -
CC InterPro; IPR000276; -
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PROSITE; PS00237; G-PROTEIN_RECP_FL_1; 1.
CC PROSITE; PS50262; G-PROTEIN_RECP_FL_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
KW DOMAIN 1 47 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 48 74 1 (POTENTIAL).
FT DOMAIN 75 83 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 84 104 2 (POTENTIAL).
FT DOMAIN 105 119 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 120 141 3 (POTENTIAL).
FT DOMAIN 142 159 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 160 180 4 (POTENTIAL).
FT DOMAIN 181 211 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 212 238 5 (POTENTIAL).
FT DOMAIN 239 254 CYTOPLASMIC (POTENTIAL).

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FT TRANSMEM 255 279 6 (POTENTIAL).
FT DOMAIN 280 301 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 304 321 7 (POTENTIAL).
FT DOMAIN 322 374 CYTOPLASMIC (POTENTIAL).
FT DISULFID 118 197 BY SIMILARITY.
FT CARBOHYD 7 7 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 23 23 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 60 60 G -> A (IN REF. 4).
FT CONFLICT 74 74 Y -> N (IN REF. 4).
FT CONFLICT 86 86 L -> V (IN REF. 4).
FT CONFLICT 164 164 S -> T (IN REF. 5).
FT CONFLICT 182 182 T -> S (IN REF. 4).
FT CONFLICT 192 192 Q -> L (IN REF. 4).
FT CONFLICT 206 206 E -> V (IN REF. 4).
FT CONFLICT 225 225 I -> F (IN REF. 4).
FT CONFLICT 370 374 SSFTM -> VLVHVIES (IN REF. 4).
FT SEQUENCE 374 AA; 42494 MW; D7F963534E990BC4 CRC64;

Query Match 86.3%; Score 315; DB 1; Length 374;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GLLGNILVITFAFYKARSMTDVILLNMAIADILVLTLPFWAVSHATGAWFSNATCK 110
Db 60 GLLGNILVITFAFYKARSMTDVILLNMAIADILVLTLPFWAVSHATGAWFSNATCK 119

QY 111 LLKGIYAINFCNGMLLTICISMDRYTAIVQATKSFRLSRTLPKSIICLVWGLSVIIS 170
Db 120 LLKGIYAINFCNGMLLTICISMDRYTAIVQATKSFRLSRTLPKSIICLVWGLSVIIS 179

QY 171 SFTFVNQYNTQGSVDCEPKYQTVSEPIRWKLLMLGLLELFGFFIPLMFMICYTFIVK 230
Db 180 SFTFVNQYNTQGSVDCEPKYQTVSEPIRWKLLMLGLLELFGFFIPLMFMICYTFIVK 239

QY 231 TLVQAQNSKRHRKAIRVIAVILVFLACQIPHNNVLLVTAANLGMNRSKSEKLIYTKT 290
Db 240 TLVQAQNSKRHRKAIRVIAVILVFLACQIPHNNVLLVTAANLGMNRSKSEKLIYTKT 299

QY 291 VTEVLAFHCLLPVLYAFYIGQKFRNYFLKLDLVCVRKRYKSSGFSAGRYSENISRQ 350
Db 300 VTEVLAFHCLLPVLYAFYIGQKFRNYFLKLDLVCVRKRYKSSGFSAGRYSENISRQ 359

QY 351 TSETADNDNASFTM 365
Db 360 TSETADNDNASFTM 374

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RESULT 2
ID CKR6_MOUSE STANDARD; PRT; 367 AA.
AC 054689;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CC-CKR-6) (KY411).
GN CKR6 OR CMKBR6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Yanagihara S., Komura E., Yamaguchi Y.;
RT "Mouse G protein-coupled receptor KY411.";
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95077268; PubMed=9862452;
RA Varona R., Zaballos A., Gutierrez J., Martin P., Roncal F.,
RA Albar J.P., Ardavin C., Marquez G.;
RT "Molecular cloning, functional characterization and mRNA expression
analysis of the murine chemokine receptor CKR6 and its specific ligand

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RT MIP-3alpha.";
RL FEBS Lett. 440:188-194(1998).
CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-
CC ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE
CC INTRACELLULAR CALCIUM IONS LEVEL.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL; AB009369; BAA23776.1; -
CC EMBL; AJ222714; CAAL0956.1; -
CC MGD; MGI:1333797; Cmkbr6.
CC InterPro: IPR000276; -
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS: PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G-PROTEIN_RECP_F1_1; 1.
CC PROSITE; PS00262; G-PROTEIN_RECP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
CC DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 40 66 1 (POTENTIAL).
CC DOMAIN 67 75 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 76 96 2 (POTENTIAL).
CC DOMAIN 97 111 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 112 133 3 (POTENTIAL).
CC DOMAIN 134 151 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 152 172 4 (POTENTIAL).
CC DOMAIN 173 203 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 204 230 5 (POTENTIAL).
CC DOMAIN 231 246 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 247 271 6 (POTENTIAL).
CC DOMAIN 272 295 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 296 313 7 (POTENTIAL).
CC DOMAIN 314 367 CYTOPLASMIC (POTENTIAL).
CC DISULFID 110 189 BY SIMILARITY.
CC CARBOHYD 2 2 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 35 35 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 367 AA; 42102 MW; 6A309AF833B1117E CRC64;

Query Match 7.1%; Score 26; DB 1; Length 367;
Best Local Similarity 100.0%; Pred. No. 5e-18;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 293 EVLAFHCLLPVLYAFYIGQKFRNYF 318
Db 294 EVLAFHCLLPVLYAFYIGQKFRNYF 319

RESULT 3
CCR4_SHEEP STANDARD; PRT; 192 AA.
ID CCR4_SHEEP AC Q28553;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXC-R4) (CCR-4) (SDF-1 RECEPTOR)
DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LEUKOCYTE-DERIVED
DE SEVEN TRANSMEMBRANE DOMAIN RECEPTOR) (LESTR) (FRAGMENT).
GN CXCR4 OR LESTR.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.

```

RC TISSUE-Hypothalamus;
RA Dyer C.J., Matteri R.L., Keisler D.H.;
RT "Development of an ovine Y3 cDNA and expression of the Y3 receptor
RL mRNA in the ovine hypothalamus and pituitary.";
RL Abstr. Soc. Neurosci. 21:1890-1890(1995)
CC CC
CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -1- CAUTION: WAS ORIGINALLY THOUGHT TO BE A RECEPTOR FOR NEUROPEPTIDE
CC Y, TYPE 3 (NPY3-R).
CC
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CC -----
CC EMBL; U38942; AAA81347.1;
CC GCRDB; GCR_1581;
CC InterPro; IPR000276;
CC Pfam; PF00001; 7tm.1; 1.
CC PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.
CC PROSITE; PS50262; G_PROTEIN_RECEP_FL_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
CC FT NON_TER 1 1
CC FT DOMAIN 1 29 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 30 53 1 (POTENTIAL).
CC FT DOMAIN 54 69 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 70 89 2 (POTENTIAL).
CC FT DOMAIN 90 100 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 101 122 3 (POTENTIAL).
CC FT DOMAIN 123 144 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 145 165 4 (POTENTIAL).
CC FT DOMAIN 166 190 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 191 >192 5 (POTENTIAL).
CC FT DISULFID 99 176 BY SIMILARITY.
CC FT NON_TER 192 192
CC SEQUENCE 192 AA; 22178 MW; ABBCE303C52BD98 CRC64;

Query Match 3.0%; Score 11; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 LFVLTLPFWAV 95
|||||
Db 76 LFVLTLPFWAV 86

RESULT 4
CCR4_BOVIN STANDARD; PRT; 353 AA.
AC P25930;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (CXCR-4) (SDF-1 RECEPTOR)
DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LEUKOCYTE-DERIVED
DE SEVEN TRANSMEMBRANE DOMAIN RECEPTOR) (LESTR) (LCR1).
GN CXCR4.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Locus coeruleus;
RX MEDLINE=92100053; PubMed=1661837;
RA Rimland J., Xin W., Sweetnam P., Saijoh K., Nestler E.J., Duman R.S.;

RT "Sequence and expression of a neuropeptide Y receptor cDNA.";
RL Mol. Pharmacol. 40:869-875(1991).
RN [2]
RP SHOWS THAT IT IS NOT A NPY3-R.
RX MEDLINE=94052833; PubMed=8234909;
RA Jazin E.E., Yoo H., Blomqvist G., Yee F., Weng G., Walker M.W.,
RA Salon J., Larhammar D., Wahlestedt C.R.;
RT "A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its
RT human homologue, confers neither NPY binding sites nor NPY
RT responsiveness on transfected cells.";
RL Regul. Pept. 47:247-258(1993).
CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: BRAIN, HEART, KIDNEY, LUNG AND LIVER.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -1- CAUTION: WAS ORIGINALLY THOUGHT TO BE A RECEPTOR FOR
CC NEUROPEPTIDE Y, TYPE 3 (NPY3-R).
CC
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CC -----
CC EMBL; M86739; -; NOT_ANNOTATED_CDS.
CC PIR; S28787; S28787.
CC GCRDB; GCR_0180;
CC InterPro; IPR000276;
CC InterPro; IPR001277;
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PRINTS; PR00645; LCRIORPHANR.
CC PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.
CC PROSITE; PS50262; G_PROTEIN_RECEP_FL_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
CC KW DOMAIN 1 40 EXTRACELLULAR (POTENTIAL).
CC FT NON_TER 1 64 1 (POTENTIAL).
CC FT TRANSMEM 41 80 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 65 80 2 (POTENTIAL).
CC FT TRANSMEM 81 100 EXTRACELLULAR (POTENTIAL).
CC FT DOMAIN 101 111 3 (POTENTIAL).
CC FT TRANSMEM 112 133 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 134 155 4 (POTENTIAL).
CC FT TRANSMEM 156 176 EXTRACELLULAR (POTENTIAL).
CC FT DOMAIN 177 201 5 (POTENTIAL).
CC FT TRANSMEM 202 221 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 222 241 6 (POTENTIAL).
CC FT TRANSMEM 242 262 EXTRACELLULAR (POTENTIAL).
CC FT DOMAIN 263 286 7 (POTENTIAL).
CC FT TRANSMEM 287 306 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 307 353 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 11 11 BY SIMILARITY.
CC FT DISULFID 110 187
CC SEQUENCE 353 AA; 39938 MW; 42FFE5BC7545505E CRC64;

Query Match 3.0%; Score 11; DB 1; Length 353;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 LFVLTLPFWAV 95
|||||
Db 87 LFVLTLPFWAV 97

RESULT 5
CCR4_FELCA STANDARD; PRT; 353 AA.
ID CCR4_FELCA
AC P56498; P79172; O02700;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)

	Matches	11;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	85	LFVLTLPFWAV	95							
DB	87	LFVLTLPFWAV	97							
RESULT	6									
ID	CKR4_HUMAN	STANDARD;	PRT;	360	AA.					
AC	P51679;									
DT	01-OCT-1996	(Rel. 34, Created)								
DT	01-OCT-1996	(Rel. 34, Last sequence update)								
DE	01-OCT-2000	(REL. 40, Last annotation update)								
DE	C-C CHEMOKINE RECEPTOR TYPE 4 (C-C CKR-4) (CCR-4) (CCR4)									
DE	(K5-5).									
GN	CKR4 OR CMKBR4.									
OS	Homo sapiens (Human).									
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;									
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.									
ON	NCBI_TaxID=9606;									
RX	[1]									
RP	SEQUENCE FROM N.A.									
RX	MEDLINE=95370289; PubMed=7642634;									
RA	Power C.A., Meyer A., Nemeth K., Bacon K.B., Hoogewerf A.J.,									
RA	Molecular cloning and functional expression of a novel CC chemokine									
RA	"Moleculefoot A.E.I., Wells T.N.C.;"									
RT	receptor CDNA from a human basophilic cell line.";									
RL	J. Biol. Chem. 270:19495-19500(1995).									
RN	[2]									
RP	FUNCTION.									
RX	MEDLINE=97313486; PubMed=9169480;									
RA	Imai T., Baba M., Nishimura M., Kakizaki M., Takagi S., Yoshie O.;									
RT	The T cell-directed CC chemokine TARC is a highly specific									
RT	biological ligand for CC chemokine receptor 4.";									
CC	J. Biol. Chem. 272:15036-15042(1997).									
CC	-!- FUNCTION: RECEPTOR FOR C-C TYPE CHEMOKINE. BINDS TO TARC, MIP-1-									
CC	ALPHA, RANTES, AND MCP-1. SUBSEQUENTLY TRANSDUCES A SIGNAL BY									
CC	INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.									
CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.									
CC	-!- TISSUE SPECIFICITY: EXPRESSED STRONGLY IN PERIPHERAL BLOOD T CELLS									
CC	BUT NOT IN B CELLS, NATURAL KILLER CELLS, MONOCYTES, OR									
CC	GRANULOCYTES.									
CC	-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.									
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration									
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -									
CC	the European Bioinformatics Institute. There are no restrictions on its									
CC	use by non-profit institutions as long as its content is in no way									
CC	modified and this statement is not removed. Usage by and for commercial									
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/									
CC	or send an email to license@isb-sib.ch).									
DR	EMBL; X85740; CAA59743.1;									
DR	MIM; 604836;									
DR	GRDB; GCR_2115;									
DR	InterPro; IPR000276;									
DR	InterPro; IPR000355;									
DR	InterPro; IPR002239;									
DR	Pfam; PF00001; 7tm_1.1.									
DR	PRINTS; PR00237; GPCRHHODOPS.									
DR	PRINTS; PR00657; CCHEMOKINER.									
DR	PRINTS; PR01109; CHEMOKINER4.									
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.									
DR	PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.									
KW	G-protein coupled receptor; Transmembrane; Glycoprotein.									
FT	DOMAIN 1 39									
FT	EXTRACELLULAR (POTENTIAL).									

FT TRANSMEM	151	175	4 (POTENTIAL).
FT DOMAIN	176	206	EXTRACELLULAR (POTENTIAL).
FT TRANSMEM	207	226	5 (POTENTIAL).
FT DOMAIN	227	242	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	243	267	6 (POTENTIAL).
FT DOMAIN	268	284	EXTRACELLULAR (POTENTIAL).
FT TRANSMEM	285	308	7 (POTENTIAL).
FT DOMAIN	309	360	CYTOPLASMIC (POTENTIAL).
FT CARBOHYD	183	183	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	194	194	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID	110	187	BY SIMILARITY.
SQ SEQUENCE	360 AA;	41402 MW;	51EBE12AD1FAFABF CRC64;

Query Match	2.7%;	Score 10;	DB 1;	Length 360;
Best Local Similarity	100.0%;	Pred. No. 0.036;	0;	
Matches 10;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	69	RSMTDYYLLN 78
Db	71	RSMTDYYLLN 80

Search completed: May 23, 2001, 15:38:14
Job time: 110 sec

GenCore version 4.5

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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:35:24 ; Search time 35.78 Seconds
(without alignments)
1195.665 Million cell updates/sec

Title: US-08-887-977-10

Perfect score: 365

Sequence: 1 MFSTPVKIIQCQSLHITQL.....NISRTSETADNDNASFTM 365

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 374700 seqs, 117207915 residues

Word size : 10

Total number of hits satisfying chosen parameters: 10

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

SPTREMBL_15:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_unclassified:*
- 13: sp_vertebrate:*
- 14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	6.0	367	11 Q9R1V0	Q9R1V0 mus musculus
2	11	3.0	353	13 Q93247	Q93247 cyprinus ca
3	11	3.0	353	13 Q9PTF7	Q9PTF7 brachydanio
4	11	3.0	357	13 Q42445	Q42445 oncorhynch
5	10	2.7	360	4 Q9ULY7	Q9ULY7 homo sapien
6	10	2.7	360	4 Q9ULY6	Q9ULY6 homo sapien
7	10	2.7	383	14 Q89609	Q89609 equine herp
8	10	2.7	394	5 Q9NJS6	Q9NJS6 aplysia kur
9	10	2.7	394	5 Q9NHF3	Q9NHF3 aplysia cal
10	10	2.7	469	4 Q9NSD7	Q9NSD7 homo sapien

ALIGNMENTS

RESULT 1
Q9R1V0 PRELIMINARY; PRT; 367 AA.
AC Q9R1V0;

DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE CC CHEMOKINE LARC SPECIFIC RECEPTOR.
GN MCCR6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Tanaka Y.;
RT "Molecular Cloning of Murine Homologue of CCR6, the Specific Receptor
for CC Chemokine LARC";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB016031; BAA82443.1; -
DR INTERPRO: IPR000190; -
DR INTERPRO: IPR000276; -
DR INTERPRO: IPR000355; -
DR PFAM: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODOPSN.
DR PRINTS: PR00635; ANGIOTENSINR.
DR PRINTS: PR00657; CCHEMOKINER.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 367 AA; 42082 MW; 207FD98B2F7A5DD3 CRC64;

Query Match 6.0%; Score 22; DB 11; Length 367;
Best Local Similarity 100.0%; Pred. No. 5.5e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 248 IAVLVFLACQIPHNNVLLVTA 269

Db 249 IAVLVFLACQIPHNNVLLVTA 270

RESULT 2

ID Q93247 PRELIMINARY; PRT; 353 AA.
AC Q93247;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE CXCR4.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RA Fujiki K., Nakao M., Shin D., Yano T.;
RT "cDNA cloning of a carp homologue of mammalian CXCR4";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AB012310; BAA32797.1; -
DR INTERPRO: IPR000276; -
DR PFAM: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODOPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
SQ SEQUENCE 353 AA; 39633 MW; 84924BE413FB3B3F CRC64;

Query Match 3.0%; Score 11; DB 13; Length 353;
Best Local Similarity 100.0%; Pred. No. 0.0094;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 85 LFVLTLPFWAV 95

Db 84 LFVLTLPFWAV 94

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Query Match      3.0%; Score 11; DB 13; Length 357;
Best Local Similarity 100.0%; Pred. No. 0.0095;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
Q9PTF7 PRELIMINARY; PRT; 353 AA.
ID AC Q9PTF7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE CHEMOKINE RECEPTOR CXCR4.
GN CXCR4.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Tseng S., Rollins B.J.;
RT "Chemokines and chemokine receptors in zebrafish.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF201451; AAF17561.1; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR000355; -
DR INTERPRO; IPR001277; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00645; LCRIORPHANR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
RW Receptor.
SQ SEQUENCE 353 AA; 39444 MW; 410F9A7F75D631BE CRC64;

Query Match      3.0%; Score 11; DB 13; Length 353;
Best Local Similarity 100.0%; Pred. No. 0.0094;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 LFVLTLPFWAV 95
DB 84 LFVLTLPFWAV 94
|||||
|||||

RESULT 4
ID 042445 PRELIMINARY; PRT; 357 AA.
AC 042445
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE CXC CHEMOKINE RECEPTOR.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Daniels G.D., Charlemagne J., Secombes C.J.;
RT "Cloning and sequencing of a rainbow trout, Oncorhynchus mykiss,
RT chemokine receptor homolog.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AJ001039; CAA04493.1; -
DR INTERPRO; IPR000276; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
RW G-protein coupled receptor; transmembrane; Glycoprotein.
SQ SEQUENCE 357 AA; 39817 MW; 14EC2F01DA1222C4 CRC64;

Query Match      2.7%; Score 10; DB 4; Length 360;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 RSMSTDVYLLN 78
DB 71 RSMSTDVYLLN 80
|||||
|||||

RESULT 6
Q9ULY6 PRELIMINARY; PRT; 360 AA.
ID Q9ULY6
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE B-CHEMOKINE RECEPTOR CCR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kato H., Tsuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki H.,
RT "New variations of human CC-chemokine receptors CCR3 and CCR4.";
RL Genes Immun. 1:97-104(1999).
DR EMBL; AB023889; BAA86966.1; -
DR INTERPRO; IPR000190; -
DR INTERPRO; IPR000248; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR000355; -
DR INTERPRO; IPR001277; -
DR INTERPRO; IPR002236; -
DR INTERPRO; IPR002239; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00241; ANGIOTENSINR.
DR PRINTS; PR00635; ANGIOTENSINR.
DR PRINTS; PR00645; LCRIORPHANR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01106; CHEMOKINER1.
DR PRINTS; PR01109; CHEMOKINER4.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
RW Receptor.
FT VARIANT 130 130 V -> L.
SQ SEQUENCE 360 AA; 41388 MW; F52DA1A8D9DA7DDB CRC64;

Query Match      2.7%; Score 10; DB 4; Length 360;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 RSMSTDVYLLN 78
DB 71 RSMSTDVYLLN 80
|||||
|||||

RESULT 6
Q9ULY6 PRELIMINARY; PRT; 360 AA.
ID Q9ULY6
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE B-CHEMOKINE RECEPTOR CCR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kato H., Tsuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki H.,

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RA Hirai K., Tokunaga K.;
RT "New variations of human CC-chemokine receptors CCR3 and CCR4.";
RL Genes Immun. 1:97-104(1999).
DR EMBL: AB023891; BAA86968.1; -
DR INTERPRO: IPR000190; -
DR INTERPRO: IPR000248; -
DR INTERPRO: IPR000276; -
DR INTERPRO: IPR000355; -
DR INTERPRO: IPR001277; -
DR INTERPRO: IPR002236; -
DR INTERPRO: IPR002239; -
DR PFAM: PF00001; 7tm.1; 1.
DR PRINTS: PRO0237; GPCRHDOPSN.
DR PRINTS: PRO0241; ANGIOTENSINR.
DR PRINTS: PRO0635; ANGIOTENSINR.
DR PRINTS: PRO0645; LCRIORPHANR.
DR PRINTS: PRO0657; CCHEMOKINER.
DR PRINTS: PRO1106; CHEMOKINER1.
DR PRINTS: PRO1109; CHEMOKINER4.
DR PRINTS: PRO0237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW RECEPTOR.
FT VARIANT 178 178 S -> C.
SQ SEQUENCE 360 AA; 41386 MW; AAF0EA3AD1EAF6D2 CRC64;

Query Match 2.7%; Score 10; DB 4; Length 360;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 RSMTDVYLLN 78
Db 71 RSMTDVYLLN 80
|||||
|||||

RESULT 7
Q89609 ID Q89609 PRELIMINARY; PRT; 383 AA.
AC Q89609;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE G PROTEIN-COUPLED RECEPTOR.
OS Equine herpesvirus 2.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Roseolovirus.
OX NCBI_TaxID=12657;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=86/67;
RX MEDLINE=95302501; PubMed=7783207;
RA Telford E.A., Watson M.S., Aird H.C., Perry J., Davison A.J.;
RT "The DNA sequence of equine herpesvirus 2.";
RL J. Mol. Biol. 249:520-528(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=86/67;
RX Telford E.A.R.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: U20824; AAC13866.1; -
DR EMBL: U20824; AAC13788.1; -
DR INTERPRO: IPR000276; -
DR PFAM: PF00001; 7tm.1; 1.
DR PRINTS: PRO0237; GPCRHDOPSN.
SQ SEQUENCE 383 AA; 43667 MW; 0C65C53EAF539F72 CRC64;

Query Match 2.7%; Score 10; DB 14; Length 383;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GLLGNILWVI 60
Db 86 GLLGNILWVI 95
|||||
|||||

RESULT 8
Q9NJS6 ID Q9NJS6 PRELIMINARY; PRT; 394 AA.
AC Q9NJS6;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE OCTOPAMINE RECEPTOR.
OS Aplysia kurodai (Kuroda's sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;
OC Aplysiidae; Aplysia.
OX NCBI_TaxID=6501;
RN [1]
RP SEQUENCE FROM N.A.
RA Chang D.J., Li X.C., Kim H.K., Kim U.S., Cho N.J., Lo X., Weiss K.R.,
RA Kandel E.R., Kaang B.K.;
RT "Activation of a heterologously expressed octopamine receptor coupled
RT only to adenylyl cyclase produces all the features of presynaptic
RT facilitation in Aplysia sensory neurons.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:1829-1834(2000).
DR EMBL: AF117654; AAF28802.1; -
KW Receptor.
SQ SEQUENCE 394 AA; 44423 MW; 8C7FE47EC686B0F4 CRC64;

Query Match 2.7%; Score 10; DB 5; Length 394;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 CISMDRYIAI 138
Db 131 CISMDRYIAI 140
|||||
|||||

RESULT 9
Q9NHF3 ID Q9NHF3 PRELIMINARY; PRT; 394 AA.
AC Q9NHF3;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE OCTOPAMINE RECEPTOR.
GN APOA.
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;
OC Aplysiidae; Aplysia.
OX NCBI_TaxID=6500;
RN [1]
RP SEQUENCE FROM N.A.
RA Chang D.J., Li X.C., Kim H.K., Kim U.S., Cho N.J., Lo X., Weiss K.R.,
RA Kandel E.R., Kaang B.K.;
RT "Activation of a heterologously expressed octopamine receptor coupled
RT only to adenylyl cyclase produces all the features of presynaptic
RT facilitation in Aplysia sensory neurons.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:1829-1834(2000).
DR EMBL: AF222978; AAF37686.1; -
KW Receptor.
SQ SEQUENCE 394 AA; 44334 MW; 1204086FEB6CD599 CRC64;

Query Match 2.7%; Score 10; DB 5; Length 394;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 CISMDRYIAI 138
Db 131 CISMDRYIAI 140
|||||
|||||

RESULT 10
Q9NSD7

```

ID Q9NSD7 PRELIMINARY; PRT; 469 AA.
AC Q9NSD7;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE G-PROTEIN COUPLED RECEPTOR SALPR.
GN SALPR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Matsumoto M., Kamohara M., Sugimoto T., Hidaka K., Takasaki J.,
RA Saito T., Okada M., Yamaguchi T., Furuichi K.;
RT "The novel G-protein coupled receptor SALPR shares sequence similarity
RT with somatostatin and angiotensin receptors."
RL Gene 248:183-189(2000).
DR EMBL; D88437; BAA93001.1; -.
KW Receptor; G-protein coupled receptor.
SQ SEQUENCE 469 AA; 51123 MW; 932E7B3001689F7B CRC64;

Query Match      2.7%; Score 10; DB 4; Length 469;
Best Local Similarity 100.0%; Pred.No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 FVLTLFWAV 95
Db 131 FVLTLFWAV 140
|||||

```

Search completed: May 23, 2001, 15:37:59
Job time: 155 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:21:43 ; Search time 184.73 Seconds
(without alignments)
112.946 Million cell updates/sec

Title: US-08-887-977-10
Perfect score: 1894
Sequence: 1 MFSTPVKILLCQSLHITQL.....NISROTSETADNDNASSFTM 365

Scoring table:
BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
A.Geneseq_0401.*
1: /SID56/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID56/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID56/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SID56/gcgdata/geneseq/geneseq/AA1983.DAT.*
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8: /SID56/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SID56/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SID56/gcgdata/geneseq/geneseq/AA1989.DAT.*
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12: /SID56/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SID56/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SID56/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SID56/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SID56/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SID56/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SID56/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SID56/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SID56/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID56/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID56/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1894	100.0	365	19	W48086 Human dendritic ce
2	1888	99.7	365	21	Y97077 Primate (human) ch
3	683	36.1	378	21	Y90629 Human G protein-co
4	682	36.0	378	19	W48724 Human V31 seven tr
5	682	36.0	378	21	B21688 Human 7TM receptor
6	682	36.0	378	21	B21699 7TM receptor prote
7	682	36.0	378	22	B50859 Human CCR7. Homo
8	680	35.9	378	15	R53744 Putative seven tra
9	678.5	35.8	410	15	R53743 Polypeptide sequen
10	678.5	35.8	410	19	W48723 Genomic clone of 7
11	678.5	35.8	410	21	B21687

12	677	35.7	358	15	R53745
13	677	35.7	358	21	B21689
14	675	35.6	378	21	Y90663 Human mutant G pro
15	668.5	35.3	359	15	R53747 Seven transmembran
16	668.5	35.3	359	19	W48728 Murine V31 seven t
17	668.5	35.3	359	21	B21691 Epstein Barr virus
18	663	35.0	378	19	R54079 G-protein coupled
19	663	35.0	378	15	W56164 Epstein Barr virus
20	663	35.0	378	19	W53622 Epstein Barr virus
21	662	35.0	350	13	R27791 Interleukin-8 rece
22	662	35.0	350	16	R68811 Interleukin-8 rece
23	662	35.0	350	16	R80756 Interleukin 8 rece
24	662	35.0	350	16	R80951 Recombinant high a
25	662	35.0	350	17	B09989 Human IL-8 recepto
26	662	35.0	1060	16	R70123 IL8-R type 1-GBP 1
27	654	34.5	355	13	R28272 Sequence in a high
28	654	34.5	355	16	R80950 Recombinant high a
29	643.5	34.0	361	20	W97348 An Epstein-Barr vi
30	636.5	33.6	358	16	R80952 Recombinant high a
31	629.5	33.2	355	14	R33420 Human IL-8 recepto
32	629.5	33.2	355	17	B09980 Human IL-8 recepto
33	629.5	33.2	360	13	R28273 Sequence in a low
34	629.5	33.2	360	16	R80758 Interleukin 8 rece
35	629.5	33.2	1064	16	R70124 IL8-R type 2-GBP 1
36	623.5	32.9	351	20	Y23825 A7 times membrane
37	615.5	32.5	360	15	R80953 Recombinant high a
38	610.5	32.2	360	21	B07498 A human CCR4 chemo
39	607.5	32.1	360	17	R99274 Chemokine receptor
40	605.5	32.0	358	13	R28274 Sequence in a low
41	600.5	31.7	312	15	R48717 G-protein coupled
42	600.5	31.6	312	17	W02689 African green monk
43	598.5	31.4	342	20	W97784 pig-tailed macaque
44	594.5	31.4	342	20	W97785 Human CC chemokine
45	593.5	31.3	357	21	B19605

ALIGNMENTS

RESULT 1	
W48086	W48086 standard; Protein: 365 AA.
XX	
AC	W48086;
XX	
DT	11-JUN-1998 (first entry)
XX	
DE	Human dendritic cell chemokine receptor.
XX	
KW	Human: thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta;
KW	receptor; dendritic cell; macrophage; inflammation; asthma.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Misc-difference 193
FT	/note= "encoded by CAN"
XX	
PN	W09801557-A2.
XX	
PD	15-JAN-1998.
XX	
PF	02-JUL-1997; 97WO-US10819.
XX	
PR	04-JUN-1997; 97US-0048593.
PR	05-JUL-1996; 96US-0675814.
PR	11-OCT-1996; 96US-0028329.
XX	
PA	(SCHE) SCHERING CORP.
XX	
PI	Gish KC, Schall TJ, Vicari A, Wang W, Zlotnik A;
XX	
DR	WPI; 1998-101054/09.

Partial sequence o
Human 7TM receptor
Human mutant G pro
Seven transmembran
Murine V31 seven t
Epstein Barr virus
G-protein coupled
Epstein Barr virus
Interleukin-8 rece
Interleukin-8 rece
Interleukin 8 rece
Recombinant high a
Human IL-8 recepto
IL8-R type 1-GBP 1
Sequence in a high
Recombinant high a
An Epstein-Barr vi
Recombinant high a
Human IL-8 recepto
Human IL-8 recepto
Sequence in a low
Interleukin 8 rece
IL8-R type 2-GBP 1
A7 times membrane
Recombinant high a
A human CCR4 chemo
Chemokine receptor
Sequence in a low
G-protein coupled
African green monk
pig-tailed macaque
Human CC chemokine

DR N-PSDB; V15418.
 XX
 PT Novel chemokines, e.g. thymus expressed chemokine - used for
 PT treating inflammatory conditions including asthma.
 XX
 PS Claim 3; Page 94-95; 202pp; English.
 XX
 CC The present sequence represents human dendritic cell chemokine receptor.
 CC Antibodies which bind to the protein can be used in detecting or
 CC diagnosing various immunological conditions related to expression
 CC of the protein. The nucleic acid can be used for screening and
 CC isolating DNA clones for the chemokines, especially from other
 CC species. The chemokine can be used in the treatment of conditions
 CC associated with abnormal physiology or development, including
 CC inflammatory conditions such as asthma.
 CC
 XX Sequence 365 AA;
 SQ

Query Match 100.0%; Score 1894; DB 19; Length 365;
 Best Local Similarity 100.0%; Pred. No. 1.2e-209;
 Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MFSPVKIILCOSILHTQLRLRCYCAPCRSSGSPGYIRIAYSLICVGLGNILVI 60
 DB 1 mstfpvkilicqslhtqlrlrcycapcrssgspgylyriayslilcvlgllnllvli 60
 OY 61 TFAFYKARSMTDYLNNMAIADILFVLTLPFAVSHATGAWFNSATCKLKGIYAINF 120
 DB 61 tfafykkarsmtdyllnmaiadilfvltlpfawshatgawfnsatckllkgyiainf 120
 OY 121 NCGMLLTCTISMDRYAIYQATKSFRLSRTPRSKIIICLVWGLSVIISSTFVNOKY 180
 DB 121 ncgmlltctismdryaiyqatkstfrrslprskiliclvwglsviisstfvdnqy 180
 OY 181 NTQGSVCEPKYQYSEPIRKMLMLGLLELFGFPIPLMFCTFTFYKTLVQANSKR 240
 DB 181 ntgsdvcepkyytsepirkmlmlgllelfgfpiplmfctftfyktlvqanskr 240
 OY 241 HKAIRVIIVAVLVFLACQIPHNMLVLTAAANLGMNRSQSEKILGYTKVTEVLAFLHC 300
 DB 241 hkaivriiavvlvflacqiphnmvlttaanlgmnrsqsekiigytkvtevlaflhc 300
 OY 301 CLNPVLYAFIGKERNYFLKILKDLWCYRRKYSKSGFCAGRYSENISROTSETADNDNA 360
 DB 301 clnpvlyafigkfrnyflkilkdlwcrrkykssgfcagrysenisrotsetadndna 360
 OY 361 SSFTM 365
 DB 361 ssftm 365

RESULT 2
 Y97077
 ID Y97077 standard; Protein; 365 AA.
 XX
 AC Y97077;
 XX
 DT 04-DEC-2000 (first entry)
 XX
 DE Primate (human) chemokine receptor CCR6.
 XX
 KW MIP-3-alpha; chemokine; CCR6 receptor; ligand; cytosolic; agonist;
 KW antagonist; anti-psoriatic; dermatological; immunosuppressive;
 KW anti-inflammatory.
 XX
 OS Homo sapiens.
 XX
 FH Key location/Qualifiers
 FT Misc-difference 193 /note= "Encoded by CAN#"
 XX
 PN WO200046248-A1.

XX
 PD 10-AUG-2000.
 XX
 PF 02-FEB-2000; 2000WO-US00511.
 XX
 PR 03-FEB-1999; 99US-0244281.
 XX
 PA (SCHE) SCHERING CORP.
 XX
 DR Oldham ER, Honey B, Dieu-Nosjean M, Caux C, Zlotnik A;
 XX
 DR WPI. 2000-543477/49.
 XX
 PS N-PSDB; A51971.
 XX
 PT Novel methods for modulating the migration of cells within or to the
 PT skin using MIP-3-alpha or CCR6 agonists or antagonists, useful for
 PT treating skin disorders, e.g. cancer
 XX
 PS Disclosure; Page 53-54; 61pp; English.
 XX
 CC The MIP-3-alpha chemokine is expressed in inflamed skin cells. This
 CC chemokine is the ligand for the CCR6 receptor. MIP-3-alpha or CCR6
 CC agonists or antagonists can be used to modulate the migration of a cell
 CC within or to the skin of a mammal. MIP-3-alpha can be used to purify a
 CC population of cells expressing a MIP-3-alpha receptor. The methods are
 CC useful for treating a mammalian subject with a skin disease or condition,
 CC e.g. cancer, metastasis, psoriasis, atopic or contact dermatitis,
 CC systemic lupus erythematosus and lichen ruber planus, or for treating
 CC skin transplants or grafts.
 CC
 XX Sequence 365 AA;
 SQ

Query Match 99.7%; Score 1888; DB 21; Length 365;
 Best Local Similarity 99.7%; Pred. No. 5.8e-209;
 Matches 364; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MFSPVKIILCOSILHTQLRLRCYCAPCRSSGSPGYIRIAYSLICVGLGNILVI 60
 DB 1 mstfpvkilicqslhtqlrlrcycapcrssgspgylyriayslilcvlgllnllvli 60
 OY 61 TFAFYKARSMTDYLNNMAIADILFVLTLPFAVSHATGAWFNSATCKLKGIYAINF 120
 DB 61 tfafykkarsmtdyllnmaiadilfvltlpfawshatgawfnsatckllkgyiainf 120
 OY 121 NCGMLLTCTISMDRYAIYQATKSFRLSRTPRSKIIICLVWGLSVIISSTFVNOKY 180
 DB 121 ncgmlltctismdryaiyqatkstfrrslprskiliclvwglsviisstfvdnqy 180
 OY 181 NTQGSVCEPKYQYSEPIRKMLMLGLLELFGFPIPLMFCTFTFYKTLVQANSKR 240
 DB 181 ntgsdvcepkyytsepirkmlmlgllelfgfpiplmfctftfyktlvqanskr 240
 OY 241 HKAIRVIIVAVLVFLACQIPHNMLVLTAAANLGMNRSQSEKILGYTKVTEVLAFLHC 300
 DB 241 hkaivriiavvlvflacqiphnmvlttaanlgmnrsqsekiigytkvtevlaflhc 300
 OY 301 CLNPVLYAFIGKERNYFLKILKDLWCYRRKYSKSGFCAGRYSENISROTSETADNDNA 360
 DB 301 clnpvlyafigkfrnyflkilkdlwcrrkykssgfcagrysenisrotsetadndna 360
 OY 361 SSFTM 365
 DB 361 ssftm 365

RESULT 3
 Y90629
 ID Y90629 standard; Protein; 378 AA.
 XX
 AC Y90629;
 XX
 DT 21-AUG-2000 (first entry)

[illegible]

Db	358	chrhrrssmsveaetttt	375	
	RESULT	8		
	R53744			
ID	R53744	standard; Protein; 378 AA.		
XX	AC	R53744;		
XX	XX	02-FEB-1995 (first entry)		
XX	XX	Putative seven transmembrane receptor (V31).		
XX	XX	Primer; seven transmembrane receptor; receptor; amplification; PCR;		
XX	XX	polymerase chain reaction.		
XX	OS	Homo sapiens.		
XX	XX	WO9412635-A.		
XX	XX	09-JUN-1994.		
XX	XX	17-NOV-1993; 93WO-US11153.		
XX	XX	17-NOV-1992; 92US-0977452.		
XX	XX	(ICOS-) ICOS CORP.		
XX	XX	Godiska R, Gray PW, Schweickart VL;		
XX	XX	WPI; 1994-200264/24.		
XX	XX	N-PSDB; Q66160.		
XX	XX	DNA encoding seven transmembrane receptors - used to develop		
XX	XX	prods. for use as therapeutic or diagnostic agents for conditions		
XX	XX	involving the receptors.		
XX	XX	Claim 1; Page 52-53; 100pp; English.		
XX	XX	A human cDNA encoding the seven transmembrane receptor V31 was		
XX	XX	isolated by first amplifying a partial cDNA clone from a human		
XX	XX	tonsil cDNA library using two primers (Q66154, Q66155). The resulting		
XX	XX	amplified products were probed using two radioactively labelled		
XX	XX	sequences (Q66156, Q66157). A hybridising band was isolated from the		
XX	XX	cell and cloned. The resulting clone was named pv31-5'end (Q66158). A		
XX	XX	full length cDNA clone was isolated from a peripheral blood		
XX	XX	mononuclear cell library using V31 specific primers (Q66159, Q66152).		
XX	XX	Clone PBMC75 was isolated and the V31 cDNA insert in the clone was		
XX	XX	designated cDNA V31-B (Q66160).		
XX	XX	Sequence. 378 AA;		
	Query Match	35.9%; Score 680; DB 15; Length 378;		
	Best Local Similarity	39.4%; Pred. No. 9.5e-70;		
	Matches 149; Conservative	79; Mismatches 114; Indels 36; Gaps 8;		
QY	5	PVKILQCQSIHITQLIRVCY-----		
Db	6	pmksavlvalvifvgv---clcqdevtdyignttdvtylfeslcskdkvnrkafwflp 62		
QY	42	IAYSLLICVLGNTLVITAFYKAKRSMTDYLNNMAIADILFVLTLPFWAVSHATGA 101		
Db	63	imysliicfvllnglvitvityfkrklmctctyllnlavadiilfltpfways-aaks 121		
QY	102	WVFSNATCKLKGHYAINFNCGMLLLTICISMDRYIAIVQATKSFRLRSRTLPKSKICLV 161		
Db	122	wfvgvhckllfaykmsffgmllllcisidryaivqavsahrhrarvlliskiscvg 181		
QY	162	WGLSVLISSSTFVEN--QKNTQSDVCEPKYQVSEPIRWKLLMGLLELFGFFIPLM 219		
Db	182	ilwlatvlsipellysdlqrsseqamrc---slitheveafitiquaqmvgifvpll 237		

Db 107 gnglvltiyfkrklmttdtllnlavadihlitlpfways-aakswvfgvhfcklif 165
 QY 114 GIYAINENCGMLLTCTISMDRYIAIVQATKSPRLRSRTLPRSKIIICLVVWGLSVIISST 173
 Db 166 aiykmsffsgmllilcisdryvaivqavsaahrarvllisklscvgiwiatiwise 225
 QY 174 FVFN--QKYNTOGSDVCEPKYQTVSEPIRWKLLMLGLELFGFFIPLMFIMFYTFIVKT 231
 Db 226 llysdldgrsseqamrc-----slitehveafitigvaqmvigflvpllamscfylviirt 281
 QY 232 LVQAQNSKRHKAIIRVITAVLVFLACQIPHN--WVLLVTAANLGKMNRSQSEKLIGYTKT 290
 Db 282 llqarnfernkaiikaivavvvfivfipyngvvaqtvanfnitsstcelskqlniayd 341
 QY 291 VTEVLAFLHCLNPVLVAFIGOKPRNYELKILKDLWCVRKRYKSSGFSC--AGRYSENIS 348
 Db 342 vtsylacvrccvnpflyafigvkkfrndlkfkdglgclseqdlrqwsscrhrrssmsve 401
 QY 349 RQTSSET 354
 Db 402 aetttt 407

RESULT 10

W48723
 ID W48723 standard; Protein; 410 AA.

AC W48723;

XX

DT 25-SEP-1998 (first entry)

XX

DE Polypeptide sequence encoded by the human V31 genomic DNA.

XX V28; placenta; seven transmembrane receptor; 7TM; signal transduction;

XX Immunology; inflammation; V31.

XX Homo sapiens.

XX US5759804-A.

XX 02-JUN-1998.

XX 17-NOV-1993; 93US-0153848.

XX 17-NOV-1992; 92US-0977452.

XX (ICOS-) ICOS CORP.

XX Godiska R, Gray PW, Schweickart VL;

XX WPI; 1998-332132/29.

XX N-PSDB; V18345.

XX DNA encoding V28 seven transmembrane receptor polypeptide - useful

XX for producing recombinant polypeptide and anti-V28 antibodies, and

XX in screening assays for V28 agonists and antagonists

XX Example 2; Columns 31-34; 56pp; English.

XX The present sequence represents the deduced polypeptide sequence encoded

XX by the V31 genomic DNA (V18345) which was isolated from a human placenta

XX genomic library. The invention claims for a full length V28 genomic DNA

XX (V18343) and the V28 (W48722) protein it encodes. V28 and V31 (W48723)

XX proteins are seven transmembrane (7TM) receptors which are probably

XX involved in signal transduction. The invention also claims that cells

XX transformed with V28 DNA can be used to produce the recombinant

XX polypeptide, to produce anti-V28 antibodies or in screening assays for

XX V28 agonists or antagonists. The antibodies, agonists and antagonists

XX could then be used to modulate V28 receptor-ligand binding, for e.g. in

XX immunological and/or inflammatory events in vivo.

XX Sequence 410 AA;

SQ

Query Match 35.8%; Score 678.5; DB 19; Length 410;
 Best Local Similarity 40.7%; Pred. No. 1-6e-69;
 Matches 149; Conservative 78; Mismatches 120; Indels 19; Gaps 8;
 QY 2 FSTPVKIILOS-----ILHTQILIRCYCAPCRRSG--SSPGYLYRIAYSILICVLGLL 53
 Db 48 fsp-kvclqcdevtdddyigdnnttdytlfesleskdvrfnkawflplmysilicfvgl 106
 QY 54 GNILVVITFARYKKARSMTDVYLLNMAADILFVLTLPFWAYSHATGAWFSNATCKLLK 113
 Db 107 gnglvltiyfkrklmttdtllnlavadihlitlpfways-aakswvfgvhfcklif 165
 QY 114 GIYAINENCGMLLTCTISMDRYIAIVQATKSPRLRSRTLPRSKIIICLVVWGLSVIISST 173
 Db 166 aiykmsffsgmllilcisdryvaivqavsaahrarvllisklscvgiwiatiwise 225
 QY 174 FVFN--QKYNTOGSDVCEPKYQTVSEPIRWKLLMLGLELFGFFIPLMFIMFYTFIVKT 231
 Db 226 llysdldgrsseqamrc-----slitehveafitigvaqmvigflvpllamscfylviirt 281
 QY 232 LVQAQNSKRHKAIIRVITAVLVFLACQIPHN--WVLLVTAANLGKMNRSQSEKLIGYTKT 290
 Db 282 llqarnfernkaiikaivavvvfivfipyngvvaqtvanfnitsstcelskqlniayd 341
 QY 291 VTEVLAFLHCLNPVLVAFIGOKPRNYELKILKDLWCVRKRYKSSGFSC--AGRYSENIS 348
 Db 342 vtsylacvrccvnpflyafigvkkfrndlkfkdglgclseqdlrqwsscrhrrssmsve 401
 QY 349 RQTSSET 354
 Db 402 aetttt 407

RESULT 11

B21687

ID B21687 standard; Protein; 410 AA.

XX B21687;

XX 26-JAN-2001 (first entry)

XX Genomic clone of 7TM receptor V31 protein.

XX Seven transmembrane receptor; 7TM; heptahelical; serpentine;

XX G-protein-coupled; V28; V31; V112; R20; R2; R12; RM3; gene therapy;

XX cancer.

XX Homo sapiens.

XX US6107475-A.

XX 22-AUG-2000.

XX 26-APR-1999; 99US-0299843.

XX 17-MAY-1994; 94US-0245242.

XX 01-JUN-1998; 98US-0088337.

XX 17-NOV-1992; 92US-0977452.

XX 17-NOV-1993; 93US-0153848.

XX (ICOS-) ICOS CORP.

XX Schweickart VL, Gray PW, Godiska R;

XX WPI; 2000-571335/53.

XX N-PSDB; A90600.

XX Polynucleotide encoding seven transmembrane receptors, antibody

XX specific to the receptor, agonist and antagonist of the receptor useful

XX for treating inflammation in a mammal

XX Example 3; Columns 33-36; 61pp; English.

PS

XX The present sequence is a novel seven transmembrane (7TM) receptors
 CC (also known as heptahelical, serpentine or G-protein-coupled receptors).
 CC The coding sequence for the present sequence may be used for gene
 CC therapy for diseases such as cancer.
 XX Sequence 410 AA;

Query Match 35.8%; Score 678.5; DB 21; Length 410;
 Best Local Similarity 40.7%; Pred. No. 1.6e-69;
 Matches 149; Conservative 78; Mismatches 120; Indels 19; Gaps 8;

QY 2 FSTPKVILQCS-----ILHITQLILRCYCPCRRSG--SSPGYLRYIAYSLICVLGLL 53
 Db 48 fsp-kvelcqvdevtdygdnttdvtylifeslckkdvnfkawflpimysliicfvgl 106

QY 54 GNILVITFAFYKKARSMTDVLLNMAIADILFVLFPFVAVSHATGAWFVSNATCKLLK 113
 Db 107 gnglvltviyfrkrlkmttdtynlnlavadilfltlpways-aakswvfgvhfcklif 165

QY 114 GIYAINFCGMILLTICISMDRYTAIVQATKSPRLSRTLPRSKIICLVNGLSVIISST 173
 Db 166 alykmsffgmlilicisdryvalqavsahrarvllisclscvgiilatvlsipe 225

QY 174 FVEN--QKNTQGSVDCEPKYQTVSEPIRWKLLMLGLLELFGFFIPLMFVCFVTVTKT 231
 Db 226 llysdqlrsseqamrc-----slitehveafitqvaqmgivflvplamsfcylviirt 281

QY 232 LVQAKSRHKRAIRVIAVVLVFLACQIPHNVLLVTAANLGMNRSQSEKLGITYTKT 290
 Db 282 llqarnfernkakvliavvvvfiqvglyngvvlqvtvanfnitscelsqnlaiyd 341

QY 291 VTEVLAFLHCLLPVLYAFIGQKERNYFLKLDLCVCRKYSKSGFSC--AGRYSENIS 348
 Db 342 vtyslacvrccvnpflyafigvkrndlfklfdlglcslqeqrlqwsrchrirssmsve 401

QY 349 ROTSET 354
 Db 402 aetttt 407

RESULT 12
 ID R53745 standard; Protein; 358 AA.
 XX R53745;
 AC R53745;
 XX

02-FEB-1995 (first entry)
 Partial sequence of seven transmembrane receptor (V31).
 XX

Primer; seven transmembrane receptor; receptor; amplification; PCR;
 polymerase chain reaction.
 XX

Homo sapiens.
 OS
 WO9412635-A.
 XX

09-JUN-1994.
 XX

17-NOV-1993; 93WO-US11153.
 XX

17-NOV-1992; 92US-0977452.
 XX

(ICOS-) ICOS CORP.
 XX

Godiska R, Gray PW, Schweickart VL;
 XX

WPI; 1994-200264/24.
 DR

N-PSDB; Q66162.
 DR

DNA encoding seven transmembrane receptors - used to develop
 PT

prods. for use as therapeutic or diagnostic agents for conditions
 involving the receptors.
 XX

Example 3; Page 56-57; 100pp; English.
 XX

Two primers (Q66148, Q66149) were used to amplify human genomic DNA
 purified from leukocytes. Approximately 1000 clones were isolated
 after the initial amplification reaction and probed with sequences
 CC specific for seven transmembrane receptors IL8R1, AT2R and R20.
 CC Clones which did not hybridise were then chosen for sequence
 CC analysis. Three new clones were identified that appeared to encode
 CC seven transmembrane receptor segments. Two more primers (Q66151,
 CC Q66152) were used to isolate a full length version of one of these
 CC clones designated V31 (see Q66153). This is the sequence encoded
 CC by exon 3 of the V31 genomic clone
 XX Sequence 358 AA;

Query Match 35.7%; Score 677; DB 15; Length 358;
 Best Local Similarity 44.0%; Pred. No. 1.9e-69;
 Matches 140; Conservative 70; Mismatches 98; Indels 10; Gaps 5;

QY 42 TAYSILICVGLGNILVITFAFYKKARSMTDVLLNMAIADILFVLFPFVAVSHATGA 101
 Db 43 lmyslicfvglnglvltviyfrkrlkmttdtynlnlavadilfltlpways-aaks 101

QY 102 WVFENATCKLLGIYAINFCGMILLTICISMDRYTAIVQATKSPRLSRTLPRSKIICLV 161
 Db 102 wvfgvhfcklifaykmsffgmlilicisdryvalqavsahrarvllisclscvg 161

QY 162 VWGLSVIISSTSSVFVN--QKNTQGSVDCEPKYQTVSEPIRWKLLMLGLLELFGFFIPLM 219
 Db 162 lwtatvisipellysdqlrsseqamrc-----slitehveafitqvaqmgivflvpl 217

QY 220 FMICYTTFIVTLVQAKSRHKRAIRVIAVVLVFLACQIPHNVLLVTAANLGMNRS 278
 Db 218 amsfcylviirtllqarnfernkakvliavvvvfiqvglyngvvlqvtvanfnitsst 277

QY 279 COSEKLGITYTKTVEVLAFLHCLLPVLYAFIGQKERNYFLKLDLCVCRKYSKSGFS 338
 Db 278 celsqnlaiydvtyslacvrccvnpflyafigvkrndlfklfdlglcslqeqrlqws 337

QY 339 C--AGRYSENISROTSET 354
 Db 338 crhrirssmsveaetttt 355

RESULT 13
 ID B21689 standard; Protein; 358 AA.
 XX B21689;
 AC B21689;
 XX

26-JAN-2001 (first entry)
 Human 7TM receptor V31-B cDNA clone exon 1 protein.
 XX

Seven transmembrane receptor; 7TM; heptahelical; serpentine;
 G-protein-coupled; V28; V31; V112; R20; R2; R12; RM3; gene therapy;
 cancer.
 XX

Homo sapiens.
 OS
 US6107475-A.
 XX

22-AUG-2000.
 XX

26-APR-1999; 99US-0299843.
 XX

17-MAY-1994; 94US-0245242.
 XX

01-JUN-1998; 98US-0088337.
 XX

17-NOV-1992; 92US-0977452.
 XX

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PR 17-NOV-1993; 93US-0153848.
XX (ICOS-) ICOS CORP.
PA Schweickart VL, Gray PW, Godiska R;
PI WPI; 2000-571335/53.
XX DR N-PSDB; A91709.
XX Polynucleotide encoding seven transmembrane receptors, antibody
PT specific to the receptor, agonist and antagonist of the receptor useful
PT for treating inflammation in a mammal
XX Example 3; Columns 49-52; 61pp; English.
XX The present sequence is a novel seven transmembrane (7TM) receptors
CC (also known as heptahelical, serpentine or G-protein-coupled receptors).
CC The coding sequence for the present sequence may be used for gene
CC therapy for diseases such as cancer.
XX Sequence 358 AA;

Query Match 35.7%; Score 677; DB 21; Length 358;
Best Local Similarity 44.08; Pred. No. 1.9e-69;
Matches 140; Conservative 70; Mismatches 98; Indels 10; Gaps 5;

QY 42 IAYSLICVLGILNVLVITFAFYKARSMVDVLLNMAIADILFVLTPFWAVSHATGA 101
DB 43 Imsyilcfvllnglvgvltvtyifkrktmttdtynlnlavadiiflllpfways-aaks 101

QY 102 WVFNSATCKLLGIYAINFCNGMLLLTICISMDRYAIVQATKSFRLSRTPRSKIICLV 161
DB 102 wvfghvcklifaikmsffsgmlllscisidryvaivqavsahrarvllisklscvg 161

QY 162 VWGLSVIISSTFFVN--QKYNTOGSDVCEPKYQTVSEPIRKLMLGLLELFGFPIPLM 219
DB 162 iwlatvisipellysdqrsseqamrc-----slitehveafitqvaqmvglfvlpl 217

QY 220 FMIFCYFIVKTLVQAQNSKRHRKAIRVIAVVLVFLACQIPHN--WVLLVTAANLGMNRS 278
DB 218 amsfylviirtllqarnfernkakvllavvvvfvfqlpyngvvlqgtvanfnitst 277

QY 279 COSEKLIQYTKTVEVLAFLHCLLPVLYAFIGQKFRNYFLKILKDLWCVRKRYKSSGFS 338
DB 278 celskqlniaydvtyslacvrcvnpflyafigvkfrndlkfklgclsgqlrgwss 337

QY 339 C--AGRYSENISROTSET 354
DB 338 crhirssmsveaetttt 355

RESULT 14
Y90663
ID Y90663 standard; Protein; 378 AA.
XX Y90663;
AC Y90663;
XX 21-AUG-2000 (first entry)
XX Human mutant G protein-coupled receptor EB11 (I262K).
XX G protein-coupled receptor; GPCR; constitutively active;
KW intracellular loop 3; transmembrane domain 6; drug screening;
KW agonist; antagonist; mutant; mutein.
XX Homo sapiens.
OS Synthetic.
XX WO200022129-A1.
XX PN
XX PD
XX 20-APR-2000.
XX

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PF 12-OCT-1999; 99WO-US23938.
XX 13-OCT-1998; 98US-0170496.
XX (AREN-) ARENA PHARM INC.
XX Behan DP, Chalmers DT, Liaw CW;
PI WPI; 2000-329165/28.
XX DR N-PSDB; A30729.
XX Non-endogenous constitutively activated human G protein-coupled
PT receptors, useful for identifying agonists for use as pharmaceutical
PT agents
XX Example 2; Page 259-260; 341pp; English.
XX The invention relates to constitutively active, non-endogenous versions
CC of endogenous human orphan G protein-coupled receptors (GPCRs, Y90643-
CC Y90677 and Y90683-Y90687), and to DNA encoding them (A30709-A30743 and
CC A30775-A30779). The mutant proteins of the invention contain a
CC mutation in a portion of the protein comprising intracellular loop 3
CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
CC is substituted for an endogenous residue in IC3 at a position 16 amino
CC acids N-terminal of an endogenous proline in TM6 to form a sequence
CC X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or
CC Ala, and is preferably Lys. When the endogenous residue at this position
CC is Lys, this residue is replaced by His, Arg or preferably Ala. The 15
CC amino acid stretch between the substituted amino acid and the Pro may be
CC endogenous, non-endogenous, or a mixture of endogenous and non-endogenous
CC residues. The constitutively active GPCRs are useful for identifying
CC antagonists, agonists and partial agonists for use as pharmaceutical
CC agents. The mutant proteins are also useful in research settings for
CC elucidating the roles of the receptors in normal and diseased conditions.
CC Antagonists for a particular GPCR are useful for treating diseases and
CC disorders associated with that receptor. Because the novel mutant GPCRs
CC are constitutively active, they can be used directly for screening of
CC compounds without the need for endogenous ligands. Sequences Y90643-
CC Y90677 and Y90683-Y90687 the mutant human GPCRs of the invention.
XX Sequence 378 AA;

Query Match 35.6%; Score 675; DB 21; Length 378;
Best Local Similarity 39.2%; Pred. No. 3.6e-69;
Matches 148; Conservative 79; Mismatches 115; Indels 36; Gaps 8;

QY 5 PVKIIQCQSILHITQILRCYC-----clcqdevtdyigdnrtvdlfscskkdvrfkawflp 62
DB 6 pmksvlvvalvifqv---clcqdevtdyigdnrtvdlfscskkdvrfkawflp 62

QY 42 IAYSLICVLGILNVLVITFAFYKARSMVDVLLNMAIADILFVLTPFWAVSHATGA 101
DB 63 Imsyilcfvllnglvgvltvtyifkrktmttdtynlnlavadiiflllpfways-aaks 121

QY 102 WVFNSATCKLLGIYAINFCNGMLLLTICISMDRYAIVQATKSFRLSRTPRSKIICLV 161
DB 122 wvfghvcklifaikmsffsgmlllscisidryvaivqavsahrarvllisklscvg 181

QY 162 VWGLSVIISSTFFVN--QKYNTOGSDVCEPKYQTVSEPIRKLMLGLLELFGFPIPLM 219
DB 182 iwlatvisipellysdqrsseqamrc-----slitehveafitqvaqmvglfvlpl 237

QY 220 FMIFCYFIVKTLVQAQNSKRHRKAIRVIAVVLVFLACQIPHN--WVLLVTAANLGMNRS 278
DB 238 amsfylviirtllqarnfernkakvllavvvvfvfqlpyngvvlqgtvanfnitst 297

QY 279 COSEKLIQYTKTVEVLAFLHCLLPVLYAFIGQKFRNYFLKILKDLWCVRKRYKSSGFS 338
DB 298 celskqlniaydvtyslacvrcvnpflyafigvkfrndlkfklgclsgqlrgwss 357

QY 339 C--AGRYSENISROTSET 354
DB 339 C--AGRYSENISROTSET 354

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:23:13 ; Search time 95.91 seconds
(without alignments)
73.110 Million cell updates/sec

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Perfect score: 1894
Sequence: 1 MFSTPVKILQCSILHITQL.....NISRTSETADNDNASFTM 365

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA.*

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- 2: /cgn2.6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2.6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2.6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2.6/ptodata/2/iaa/PCTUS_COMB.pep.*
- 6: /cgn2.6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	682	36.0	378	1 US-08-153-848-15	Sequence 15, Appl
2	682	36.0	378	3 US-09-299-843A-15	Sequence 15, Appl
3	682	36.0	378	3 US-09-299-843A-66	Sequence 66, Appl
4	682	36.0	378	4 US-09-251-545-1	Sequence 1, Appl
5	682	36.0	378	5 PCT-US93-11153-15	Sequence 15, Appl
6	678.5	35.8	410	1 US-08-153-848-7	Sequence 7, Appl
7	678.5	35.8	410	3 US-09-299-843A-7	Sequence 7, Appl
8	678.5	35.8	410	5 PCT-US93-11153-7	Sequence 7, Appl
9	677	35.7	358	1 US-08-153-848-19	Sequence 19, Appl
10	677	35.7	358	3 US-09-299-843A-19	Sequence 19, Appl
11	677	35.7	358	5 PCT-US93-11153-19	Sequence 19, Appl
12	668.5	35.3	359	1 US-08-153-848-24	Sequence 24, Appl
13	668.5	35.3	359	3 US-09-299-843A-24	Sequence 24, Appl
14	668.5	35.3	359	5 PCT-US93-11153-24	Sequence 24, Appl
15	663	35.0	378	1 US-08-383-750-2	Sequence 2, Appl
16	663	35.0	378	1 US-08-383-751A-2	Sequence 2, Appl
17	663	35.0	378	3 US-08-352-678-2	Sequence 2, Appl
18	663	35.0	378	5 PCT-US93-09636-2	Sequence 2, Appl
19	662	35.0	350	1 US-08-202-056-1	Sequence 1, Appl
20	662	35.0	350	1 US-08-076-093A-2	Sequence 2, Appl
21	662	35.0	350	1 US-08-450-393A-7	Sequence 7, Appl
22	662	35.0	350	1 US-08-410-453A-1	Sequence 1, Appl
23	662	35.0	350	1 US-08-701-265-2	Sequence 2, Appl
24	662	35.0	350	1 US-08-410-454A-1	Sequence 1, Appl
25	662	35.0	350	2 US-08-284-586-2	Sequence 2, Appl
26	662	35.0	350	2 US-08-410-456A-1	Sequence 1, Appl
27	662	35.0	350	2 US-08-805-478-2	Sequence 2, Appl

Sequence 2, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 1, Appl
Sequence 8, Appl
Sequence 5, Appl
Sequence 8, Appl
Sequence 8, Appl
Sequence 7, Appl
Sequence 20, Appl
Sequence 38, Appl
Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-153-848-15
: Sequence 15, Application US/08153848
: Patent No. 5759804
: GENERAL INFORMATION:
: APPLICANT: Godiska, Ronald
: APPLICANT: Gray, Patrick W.
: APPLICANT: Schweikart, Vicki L.
: TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
: NUMBER OF SEQUENCES: 64
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
: ADDRESS: Bicknell
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION NUMBER: US/08/153,848
: APPLICATION NUMBER: 514
: FILING DATE: 17-NOV-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/977,452
: FILING DATE: 17-NOV-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: No. 5759804and, Greta E.
: REGISTRATION NUMBER: 35,302
: REFERENCE/DOCKET NUMBER: 31794
: TELEPHONE: (312) 474-6300
: TELEFAX: (312) 474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 15:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 378 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-153-848-15

Query Match 36.0%; Score 682; DB 1; Length 378;
Best Local Similarity 39.4%; Pred. No. 4, 9e-56;
Matches 149; Conservative 79; Mismatches 114; Indels 36; Gaps 8;

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; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-299-843A-15
;
; Query Match 36.08; Score 682; DB 3; Length 378;
; Best Local Similarity 39.48; Pred. No. 4.9e-56;
; Matches 149; Conservative 79; Mismatches 114; Indels 36; Gaps 8;
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QY 5 PVKILCOQILHITQILRCYC-----APCRRSG--SSPGYLRY 41
Db 6 PKMSVLVALLVIFQV---CLCQDEVTDYIGDNTTVDYTLFESLCSKKDVRNFKAWFLP 62
QY 42 IAYSILICVLGLGNILVITFAFYKARSMTDVYLLNMAIADILFVLTPFWAYSHATGA 101
Db 63 IMYSIIICFVGLLGNLVLTIVYFKRLKMTDTYLLNLAVADILFLLTPFWAYS-AAKS 121
QY 102 WYFSNATCKLLGIYAINFCNCGMLLITCISMDRYIAIVQATKSFRLSRTPLRSKIICLV 161
Db 122 WYFGVHFECKLIYAIKMSFSGMLLILCISIDRYIAIVQASHRHARVLLISKLSVCG 181
QY 162 WYGLSVIISSTFVN--QKYNTOGSDVCEPKYQTVSEPIRWKLLMLGLELFGFFIPLM 219
Db 182 IWILATVLSIPELLYDLQSSSEQAMRC---SLITEHVEAFITIQVAQWVIGFLVPLL 237
QY 220 FMIFCYTFIVKTLVQAQNSKRKAIRVITAVLVFLACQIPH-N-MVLVTAANLGMKNRS 278
Db 238 AMSFCYLVIRTLQARNFERNKAIVIAVVVFIVFQLPYNGVLAQTVAENFNTSST 297
QY 279 COSEKLGITKVTVEVLAFLHCLNPLVYAFIGOKERNYFLKILKDLWCVRKYKSSGFS 338
Db 298 CELSKQLNIAYDVTYSLACVRCVNPFLYAFIGVFRNDLFKDLGCLSQEQLROWSS 357
QY 339 C--AGRYSENISROTSET 354
Db 358 CRHRRSSMSVEAETTTT 375

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RESULT 2
US-09-299-843A-15
; Sequence 15, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESS: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,843A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/088,337
; FILING DATE: 01-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jill E. Uhl
; REGISTRATION NUMBER: 43,213
; REFERENCE/DOCKET NUMBER: 27866/32059B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448

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; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-299-843A-15
;
; Query Match 36.08; Score 682; DB 3; Length 378;
; Best Local Similarity 39.48; Pred. No. 4.9e-56;
; Matches 149; Conservative 79; Mismatches 114; Indels 36; Gaps 8;
;
QY 5 PVKILCOQILHITQILRCYC-----APCRRSG--SSPGYLRY 41
Db 6 PKMSVLVALLVIFQV---CLCQDEVTDYIGDNTTVDYTLFESLCSKKDVRNFKAWFLP 62
QY 42 IAYSILICVLGLGNILVITFAFYKARSMTDVYLLNMAIADILFVLTPFWAYSHATGA 101
Db 63 IMYSIIICFVGLLGNLVLTIVYFKRLKMTDTYLLNLAVADILFLLTPFWAYS-AAKS 121
QY 102 WYFSNATCKLLGIYAINFCNCGMLLITCISMDRYIAIVQATKSFRLSRTPLRSKIICLV 161
Db 122 WYFGVHFECKLIYAIKMSFSGMLLILCISIDRYIAIVQASHRHARVLLISKLSVCG 181
QY 162 WYGLSVIISSTFVN--QKYNTOGSDVCEPKYQTVSEPIRWKLLMLGLELFGFFIPLM 219
Db 182 IWILATVLSIPELLYDLQSSSEQAMRC---SLITEHVEAFITIQVAQWVIGFLVPLL 237
QY 220 FMIFCYTFIVKTLVQAQNSKRKAIRVITAVLVFLACQIPH-N-MVLVTAANLGMKNRS 278
Db 238 AMSFCYLVIRTLQARNFERNKAIVIAVVVFIVFQLPYNGVLAQTVAENFNTSST 297
QY 279 COSEKLGITKVTVEVLAFLHCLNPLVYAFIGOKERNYFLKILKDLWCVRKYKSSGFS 338
Db 298 CELSKQLNIAYDVTYSLACVRCVNPFLYAFIGVFRNDLFKDLGCLSQEQLROWSS 357
QY 339 C--AGRYSENISROTSET 354
Db 358 CRHRRSSMSVEAETTTT 375

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RESULT 3
US-09-299-843A-66
; Sequence 66, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESS: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,843A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/088,337
; FILING DATE: 01-JUN-1998

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; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/153,848
 ; FILING DATE: 17-NOV-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/977,452
 ; FILING DATE: 17-NOV-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: JILL E. UHL
 ; REGISTRATION NUMBER: 43,213
 ; REFERENCE/DOCKET NUMBER: 27866/32059B
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 474-6300
 ; TELEFAX: (312) 474-0448
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 66:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 378 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-299-843A-66

Query Match 36.0%; Score 682; DB 3; Length 378;
 Best Local Similarity 38.8%; Pred. No. 4.9e-56;
 Matches 145; Conservative 76; Mismatches 123; Indels 30; Gaps 6;

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 QY 42 IAYSLICVLGLGNILVVITFAFYKARSDTDVYLLNMAIADILEVLTPFWAVSHATGA 101
 Db 63 LMYSVICFVGLGNLGLVLTYYFKRLKTMDDTYLLNLAVALDILFLILPFWAYSEAK-S 121
 QY 102 WYFSNATCKLLKGIYAINFCNGMMLLTICISMDRYTAIVQATKSPRLSRTLPKSKILCV 161
 Db 122 WIFGVLCGIFGYIKLSFFSGMULLLCISIDRYVAIVQAVSHRHRARVLLISKLSVCG 181
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RESULT 4
 US-09-251-545-1
 ; Sequence 1, Application US/09251545
 ; Patent No. 6153441
 ; GENERAL INFORMATION:
 ; APPLICANT: Edward R. Appelbaum
 ; APPLICANT: Henry M. Sarau
 ; APPLICANT: John R. White
 ; TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND
 ; TITLE OF INVENTION: ANTAGONISTS OF THE INTERACTION BETWEEN HUMAN CCR7 RECEPTOR
 ; TITLE OF INVENTION: AND CK(-9) LIGAND AND INTERACTION THEREOF
 ; FILE REFERENCE: P50753
 ; CURRENT APPLICATION NUMBER: US/09/251,545
 ; EARLIER FILING DATE: 1999-02-17
 ; EARLIER APPLICATION NUMBER: 60/074,883
 ; EARLIER FILING DATE: 1998-02-17
 ; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 378
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-09-251-545-1

Query Match 36.0%; Score 682; DB 4; Length 378;
 Best Local Similarity 39.4%; Pred. No. 4.9e-56;
 Matches 149; Conservative 79; Mismatches 114; Indels 36; Gaps 8;

QY 5 PVKILQCSILHITLILRCYC-----APCRSG--SSPGYLVR 41
 Db 6 PMKSVLVALLVIFQV---CLCQDEVTDDYIGDNTVDTYTLFESCSKKDVRNFKAWFLP 62
 QY 42 IAYSLICVLGLGNILVVITFAFYKARSDTDVYLLNMAIADILEVLTPFWAVSHATGA 101
 Db 63 IMYSIICFVGLGNLGLVLTYYFKRLKTMDDTYLLNLAVALDILFLILPFWAYS-AKS 121
 QY 102 WYFSNATCKLLKGIYAINFCNGMMLLTICISMDRYTAIVQATKSPRLSRTLPKSKILCV 161
 Db 122 WYFSNATCKLLKGIYAINFCNGMMLLTICISMDRYTAIVQATKSPRLSRTLPKSKILCV 161
 QY 162 VWGLSVIISSTVFVN--QKNTQGSVDCEPKYQTVSEPIRWKLLMLGLELFGFFIPLM 219
 Db 182 IWMLAFSLPELISYGLKNSGDTL--RCSLVSAQVEALITIOVAQWVFGFLVPMFLAM 239
 QY 222 IFCTYFTVKTVAQONSKRHKRAIRVIAVVLVFLACQIPHIN--WVLLVTAANLGNMRS 278
 Db 238 AMSFCVLIIRTLQARNFERNKAIRVIAVAVVVFVIFQLPYNGVLAQTVANFNITNS 297
 QY 279 COSEKLGITKTVTEVLAFHCCNPNVLYAFIGOKFRNYFLKILKDLWCVRKYKSSGFS 338
 Db 298 CELSKQLNAYDVITYSLASVRCVNPFLYAFIGVFRSDLFKFLKDLGCLSGQLRHWSCK 357
 QY 339 C--AGRYSENISROTSET 354
 Db 358 CRHRRSSMSVEAETTTT 375

RESULT 5
 PCT-US93-11153-15
 ; Sequence 15, Application PC/TUS9311153
 ; GENERAL INFORMATION:
 ; APPLICANT: Godiska, Ronald
 ; APPLICANT: Gray, Patrick W.
 ; APPLICANT: Schweikart, Vicki L.
 ; TITLE OF INVENTION: Novel Seven Transmembrane Receptors
 ; NUMBER OF SEQUENCES: 64
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ; ADDRESSEE: Bicknell
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US93/11153
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/977,452
 ; FILING DATE: 17-NOV-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Noland, Greta E.
 ; REGISTRATION NUMBER: 35,302

```

; REFERENCE/DOCKET NUMBER: 31794
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-11153-15

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Query Match      36.0%; Score 682; DB 5; Length 378;
Best Local Similarity 39.4%; Pred. No. 4.9e-56;
Matches 149; Conservative. 79; Mismatches 114; Indels 36; Gaps 8;

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QY 5 PVKIIICOSILHITQILRCYC-----CLCQDEVTDDYIGDNTTVDYTLFESLCSKDKVRNFKAWFLP 41
DB 6 PMKSVLVVALLVIFQV-----APCRRSG--SSPGYLXR 62
QY 42 TAYSLICVLGLNLIVITFAFYKARSMTDVLNMAIADILFVLTLPFWAVSHATGA 101
DB 63 IMYSICFVGLNGLVLTYYIFKRLKMTDTYLLNLAVADILFVLTLPFWAYS-AAKS 121
QY 102 WYFSNATKLLGIYAINFCMGLLTCTISMDRYIAIVQATKSFRLRSRLPRSKIIICLV 161
DB 122 WYGVHFCFLFAIYKMSFSGMLLCTISIDRYIAIVQAVSAHRARVLLISKUSCVG 181
QY 162 WGLSVIISSTFVFN--QKYNTOGSDVCEPKYQTVSEPIRWKLLMLGLLELFGFFIPLM 219
DB 182 IWILATVLSIPPELLYDLQRSSEQAMRC----SLITEHVEAFITIQVQAVMIGFLVPLL 237
QY 220 PMFYCYTIVTLVQAKNSKRIKARVITAVLVFLACQIPHN--MVLVTAANLGMKNRS 278
DB 238 AMSFCVLIIRTLQARNFERNKAIKVIIVVVFVIFQLPYNGVVLQAQVANFNITST 297
QY 279 COSEKLGIVTKVTEVLAFLHCLNPLVYAFIGOKFRNYFLKILKDLWCVRKYSKSGFS 338
DB 298 CELSKQLNIAYDVTYSLACVRCVNPFLYAFIGVKFRNDFLKFQDLGCLSQEOLROWSS 357
QY 339 C--AGRYSENISRTSET 354
DB 358 CRHRRSSMSVEATTTT 375

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RESULT 6
US-08-153-848-7
; Sequence 7, Application US/08153848
; Patent No. 5759804
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153.848
; FILING DATE:

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; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5759804and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 410 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-153-848-7
; Query Match      35.8%; Score 678.5; DB 1; Length 410;
; Best Local Similarity 40.7%; Pred. No. 1.1e-55;
; Matches 149; Conservative 78; Mismatches 120; Indels 19; Gaps 8;
QY 2 FSTPVKIIICOS-----ILHITQILRCYCPCRRSG--SSPGYLRYIAYSLICVLGLL 53
DB 48 FPSP-KVCLCQDEVTDDYIGDNTTVDYTLFESLCSKDKVRNFKAWFLPIMYSIICFVGLL 106
QY 54 GNILVITFAFYKARSMTDVLNMAIADILFVLTLPFWAVSHATGAWFSNATCKLLK 113
DB 107 GNLGVLTYYIFKRLKMTDTYLLNLAVADILFVLTLPFWAYS-AAKSNVFGVHCEKLI 165
QY 114 GIYAINFCMGLLTCTISMDRYIAIVQATKSFRLRSRLPRSKIIICLVVGLSVIISST 173
DB 166 AIYKMSFSGMLLCTISIDRYIAIVQAVSAHRARVLLISKUSCVGIWILATVLSIPE 225
QY 174 FVFN--QKYNTOGSDVCEPKYQTVSEPIRWKLLMLGLLELFGFFIPLMFIFCYTIVK 231
DB 226 LLYSDQRSSEQAMRC----SLITEHVEAFITIQVQAVMIGFLVPLLAMSFVLIIRT 281
QY 232 LVQAKNSKRIKARVITAVLVFLACQIPHN--MVLVTAANLGMKNRSQSKELGYTKT 290
DB 282 LLQARNFERNKAIKVIIVVVFVIFQLPYNGVVLQAQVANFNITSTCELSKQLNIAYD 341
QY 291 VTEVLAFLHCLNPLVYAFIGOKFRNYFLKILKDLWCVRKYSKSGFS--AGRYSENIS 348
DB 342 VTYSLACVRCVNPFLYAFIGVKFRNDFLKFQDLGCLSQEOLROWSSCRHRRSSMSVE 401
QY 349 RQTSSET 354
DB 402 AETTTT 407

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RESULT 7
US-08-299-843A-7
; Sequence 7, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:

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RESULT 9
US-08-153-848-19
; Sequence 19, Application US/08153848
; Patent No. 5759804
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153,848
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5759804and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-153-848-19

Query Match 35.7%; Score 677; DB 1; Length 358;
Best Local Similarity 44.0%; Pred. No. 1.3e-55;
Matches 140; Conservative 70; Mismatches 98; Indels 10; Gaps 5;
Qy 42 IAYSLICVLGLGILVITFAFYKARSMTDYLNNMAIADILFVLTLPFWAVSHATGA 101
Db 43 IMYSICFVGLGVLGVLVITFYFKRLKMTDYLNNLAVADILFLLTLPFWAYS-AAKS 101
Qy 102 WYFSNATCKLKGIVAINFCNGMLLTCTISMDRYTAIVQATKSFRLSRTLPRSKIICLV 161
Db 102 WYFVGHFCKLFAIKYKMSFFSGMLLLCISIDRYVAIVQAVSAHRARVLLISKLCV 161
Qy 162 WYGLSVIISSTFVFN--QKYNQSGDVCPEKYQTVSEPIRWKLLMLGLLELFGFFIPLM 219
Db 162 IWILATVLSIPELLYSDLQSSSEQAMRC----SLITERVEAFITIQVQAWMIGFLVPL 217
Qy 220 FMIFCYTFVTKLVQAOQNSKRHKAIRVIAVVLVFLACQIPH-NVLLVTAANLGMNRS 278
Db 218 AMSFCVLIIRTLQARNERNKAIRVIAVVFVQLPVGNGVLAQVAFNFIISST 277
Qy 279 COSEKLGITKVTVEVLAFLHCLNPLVAFIGOKFRNYFLKILKDLWCVRKRYKSGFS 338
Db 278 CELSKQLNAYDVTVSLACVRCVNFVIAFGVGRNDLFKFLKDLGCLSQEQLQWSS 337
Qy 339 C--AGRYSENISRTSET 354

Db 338 CRHRRSSMSVEAETTTT 355
RESULT 10
US-09-299-843A-19
; Sequence 19, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,843A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/088,337
; FILING DATE: 01-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jill E. Uhl
; REGISTRATION NUMBER: 43,213
; REFERENCE/DOCKET NUMBER: 27866/32059B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-299-843A-19

Query Match 35.7%; Score 677; DB 3; Length 358;
Best Local Similarity 44.0%; Pred. No. 1.3e-55;
Matches 140; Conservative 70; Mismatches 98; Indels 10; Gaps 5;
Qy 42 IAYSLICVLGLGILVITFAFYKARSMTDYLNNMAIADILFVLTLPFWAVSHATGA 101
Db 43 IMYSICFVGLGVLGVLVITFYFKRLKMTDYLNNLAVADILFLLTLPFWAYS-AAKS 101
Qy 102 WYFSNATCKLKGIVAINFCNGMLLTCTISMDRYTAIVQATKSFRLSRTLPRSKIICLV 161
Db 102 WYFVGHFCKLFAIKYKMSFFSGMLLLCISIDRYVAIVQAVSAHRARVLLISKLCV 161
Qy 162 WYGLSVIISSTFVFN--QKYNQSGDVCPEKYQTVSEPIRWKLLMLGLLELFGFFIPLM 219
Db 162 IWILATVLSIPELLYSDLQSSSEQAMRC----SLITERVEAFITIQVQAWMIGFLVPL 217
Qy 220 FMIFCYTFVTKLVQAOQNSKRHKAIRVIAVVLVFLACQIPH-NVLLVTAANLGMNRS 278

Db	218	AMSECVLVIIRTLQARNERNKAIVTAVVVFVQLPYGVVLAQTVANFNITST	277
QY	279	COSEKLIGYKTYTEVLAFLHCCNLPVLYAFIGQKFNRYFLKILKDLWCVRKRYKSSGFS	338
Db	278	CELSKQLNITAYDYTYSILACVRCVNFPLAFYAFIGKFRNDLFKFLKDLGCLSQEQLQWSS	337
QY	339	C--AGRYSENISROTSET	354
Db	338	CRHRIIRSSMSVEAEITTT	355

RESULT 11

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PCT-US93-11153-19
: Sequence 19, Application PC/TUS9311153
: GENERAL INFORMATION:
: APPLICANT: Godiska, Ronald
: APPLICANT: Gray, Patrick W.
: APPLICANT: Schweikart, Vicki L.
: TITLE OF INVENTION: Novel Seven Transmembrane Receptors
: NUMBER OF SEQUENCES: 64
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
: ADDRESSEE: Bicknell
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/11153
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/977,452
: FILING DATE: 17-NOV-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Noland, Greta E.
: REGISTRATION NUMBER: 35,302
: REFERENCE/DOCKET NUMBER: 31794
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312) 474-6300
: TELEFAX: (312) 474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 358 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: PCT-US93-11153-19

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Query Match	35.7%	Score 677;	DB 5;
Best Local Similarity	44.0%;	Pred. No. 1.3e-55;	
Matches 140;	Conservative	70;	Mismatches 98;
			Indels 10;
			Gaps 5;

[illegible][illegible]

RESULT 12

US-08-153-848-24
Sequence 24, Application US/08153848
Patent No. 5759804
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-153-848-24

	Query Match	35.3%	Score 668.5	DB 1	Length 359
Best Local Similarity	43.2%				
Matches 136: Conservative				Pred. NO. 8.3e-55;	
				67: Mismatches 107:	Indels 5: Gaps 4:

	Qy	42	IATSLICVLGELLGNILVITFAFYKKARSMTDVTYLLNMAIADILFVLTLPFWAVSHATGA	101
			: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
	Db	43	LMYSVFICVGLLNGUWILTYIFYFKRUKTDTDTYLLNLAVADILFLILFPWAYSEAK-S	101
			: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
	Qy	102	WFVSFNATCKLLKGIYAFNFCNGMLLFTCSIMDRYIAIVQATKSPRLRSRTIPRSKIICLV	161
			: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
	Db	102	WIFGVYLCKGFIGYIKLSFFSGMILLUCISIDRVXVAIVQAVSRHRHRAVELLIISKSCVG	161
			: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	

88

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1670	88.2	369	2	JC5068	G protein-coupled
2	682	36.0	378	2	B55735	lymphocyte-specific
3	682	36.0	378	2	A55735	G protein-coupled
4	665	35.1	350	2	A39445	interleukin-8 rece
5	663	35.0	378	2	A45680	G protein-coupled
6	654	34.5	355	2	JQ1231	interleukin-8 rece
7	636.5	33.6	358	2	A53752	interleukin-8 rece
8	629.5	33.2	360	2	A53611	interleukin-8 rece
9	610.5	32.2	360	2	A57160	chemokine (C-C) re
10	593	31.3	356	2	S42096	interleukin-8 rece
11	580.5	30.6	359	2	A48921	interleukin-8 rece
12	574.5	30.3	360	2	JC4587	chemokine (C-C) re
13	571.5	30.2	359	2	I49341	MIP-1 alpha recept
14	564.5	29.8	354	2	A23669	interleukin-8 rece
15	547.5	28.9	355	2	A45177	chemokine (C-C) re
16	545	28.8	360	2	JC2443	chemokine (C-C) re
17	538	28.4	354	2	I58186	probable G protein
18	536.5	28.3	374	2	I38450	chemokine (C-C) re
19	532.5	28.1	367	2	JE0349	interferon-inducib
20	531	28.0	355	2	G02436	chemokine (C-C) re
21	527.5	27.9	352	2	A43113	chemokine (C-C) re
22	518	27.3	355	2	JC5067	G protein-coupled
23	512	27.0	355	2	JC4304	orphan G protein-c
24	504.5	26.6	355	2	I49339	macrophage inflamm
25	503	26.6	383	2	S55594	G protein-coupled
26	502.5	26.5	350	2	JN0621	G protein-coupled
27	496.5	26.2	352	2	A45747	neuropeptide Y/pep
28	492.5	26.0	352	2	G00048	fusin (LESTRA) - c
29	489	25.8	359	2	S15403	angiotensin II rec

240 RHKAIRVIIAVLVFLACOIPHNMVLLVTAANLGKMNRSCESE

Pred No is the number of results predicted by chance to have a

Ov 339 C--AGRYSENISBOTSET 354

J. BIOT. CHEM. 269, 26381-26389, 1994

Ov 339 C--AGRYSENISBOTSET 354

QY 98 ATGAWFNSATCKLLKGIYAINFNCGLMLLTCTISMDRYIAIQAQTSFRLRSRTLPKSKI 157
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 105 EKG-WIFGTPCKVSLVKEVNFYSGILLACISVDYLAIVAHRTLTOKRHLV---KF 160
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 158 ICLVWGLSVLISSSTFFVFNQYN-TQSDVCEPKYQTVS-EPKRWKLLMGLLELFGFF 215
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 161 ICLGTAWSLILSLPFFLEFRQVSPNNSPVC---YEDLGHNTAKRWMLRILPHFGFI 217
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 216 IPLMFIMFYCTEIVKTLVQAQSKRKAIRVIAVVLVFLACQIPHNVLV-
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 218 LPLVWMLFCYGTLTFLQAHGQKRAIRVIAVVLVFLACQIPHNVLV-
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 275 MNRSCQSEKLIQYTKTVTEVLAFLHCLLPVLYAFTGQFRNYFLKILKDLKMCVRRKYS 334
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 278 IQETCORNDIDRALDATEILGLHCLNPIIYAFIQGNFGLKMLAARGLSKEFLT 337
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 335 SGFSCAGRYSENISQTSSTANDNASS 362
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 338 R-----HRVTSYTSSTNVPS 353
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
RESULT 7
A53752
interleukin-8 receptor (clone 5B1a) - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: A53752
R:Prado, G.N.; Thomas, K.M.; Suzuki, H.; LaRosa, G.J.; Wilkinson, N.; Folco, E.; Navarro
J. Biol. Chem. 269, 12391-12394, 1994
A:Title: Molecular characterization of a novel rabbit interleukin-8 receptor isotype.
A:Reference number: A53752; MUID:94230294
A:Accession: A53752
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-358 <PRA>
A:Cross-references: GB:L24445; NID:9437661; PIDN:AAA31378.1; PID:9437662
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein
Query Match 33.6%; Score 636.5; DB 2; Length 358;
Best Local Similarity 42.7%; Pred. No. 4.2e-46;
Matches 140; Conservative 59; Mismatches 116; Indels 13; Gaps 9;
QY 27 APCR-RSGSPGYLYRIAYSLICVLGLNGLWITFAFYKKARSMTDVYLLNMAIADIL 85
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 35 APCRSELETNSYVLIYILVFLSLGNSLVMLVILYRSCTCSVDYLLNLAIDL 94
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 86 FVLTLPTWAVSHATGAWFNSATCKLLKGIYAINFNCGLMLLTCTISMDRYIAIQAQTSF 145
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 95 FATLPIWAASKVHG-WTFTGTPCKVSLVKEVNFYSGILLACISVDYLAIVAHATRM 153
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 146 RLRSRTLPKSKIYVWGLSVLISSSTFFVFNQYN-TQSDVCEPKYQTV-SEPIRWKL 203
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 154 -IQRHL--VRFICLSMGMVSLILPLILFRNAPPPNNSPVC---YEDMGNSTAKRM 207
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 204 LMLGLELLEFFIPLMFIMFYCTEIVKTLVQAQSKRKAIRVIAVVLVFLACQIPHN 263
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 208 VLRIPLPOTFGFPLVLMVFCYVTLRLVFAHMGQKRAIRVIAVVLVFLACQIPHN 267
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 264 VLLV-TAANLGMKMRSCQSEKLIQYTKTVTEVLAFLHCLNPLVYAFIQGFRNYFLKIL 322
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 268 VLLTDTLMRTHVIOETCERRNDIDRALDATEILGLHCLNPIIYAFIQGFRNYFLKIL 327
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 323 KDLWCVRKY--KSGFSCAGRYSENIS 348
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 328 AAHLISKEFLAKESRPSFVASSSGNTS 355
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
RESULT 8
A53611
interleukin-8 receptor type B - human
C:Species: Homo sapiens (man)

C:Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 05-Nov-1999
C:Accession: I37898; I38712; A53611; A39446
R:Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
J. Biol. Chem. 269, 26381-26389, 1994
A:Title: Comparison of the genomic organization and promoter function for human inter
A:Reference number: I37898; MUID:95014476
A:Accession: I37898
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-360 <RES>
A:Cross-references: EMBL:U11801; NID:9511801; PIDN:AAB60656.1; PID:9511803
A:Accession: I38712
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-15 <RE2>
A:Cross-references: EMBL:U11872; NID:9511808; PIDN:AAA64380.1; PID:9511809; EMBL:U118
11876; NID:9511816; PID:9511817; EMBL:U11877; NID:9511818; PID:9511819; EMBL:U11878;
R:Sprenger, H.; Lloyd, A.R.; Lautens, L.L.; Bonner, T.I.; Kelvin, D.J.
J. Biol. Chem. 269, 11065-11072, 1994
A:Title: Structure, genomic organization, and expression of the human interleukin-8 r
A:Reference number: A53611; MUID:94209273
A:Accession: A53611
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 6-360 <SPR>
A:Cross-references: GB:M99412; GB:L19593
R:Murphy, P.M.; Tiffany, H.L.
Science 253, 1280-1283, 1991
A:Title: Cloning of complementary DNA encoding a functional human interleukin-8 recep
A:Reference number: A39446; MUID:91368200
A:Accession: A39446
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 6-360 <MUR>
A:Cross-references: GB:M73969
C:Comment: This receptor, unlike IL8RA, binds several peptides besides interleukin-8,
C:Genetics:
A:Gene: GDB:IL8RB; IL8RA
A:Cross-references: GDB:127868; OMIM:146928
A:Map position: 2q35-2q35
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein
Query Match 33.2%; Score 629.5; DB 2; Length 360;
Best Local Similarity 43.4%; Pred. No. 1.6e-45;
Matches 132; Conservative 56; Mismatches 97; Indels 19; Gaps 8;
QY 27 APCR-RSGSPGYLYRIAYSLICVLGLNGLWITFAFYKKARSMTDVYLLNMAIADIL 85
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 37 APCPESLEINKYFVVIYALVFLSLGNSLVMLVILYRSVGRSVDYLLNLAIDL 96
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 86 FVLTLPTWAVSHATGAWFNSATCKLLKGIYAINFNCGLMLLTCTISMDRYIAIQAQTSF 145
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 97 FATLPTWAASKVNG-WIFGTFLCKVSVLSLKEVNFYSGILLACISVDYLAIVAHAT--- 152
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 146 RLRSRTLPKSKIYVWGLSVLISSSTFFVFNQYN-TQSDVCEPKYQTV-SEPI 199
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 153 ----RTLTQRYLVKFCISLWGLSLLALPVLFRRVYSSNVSPAC---YEDMGNTA 205
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 200 RWKLLMGLLELLEFFIPLMFIMFYCTEIVKTLVQAQSKRKAIRVIAVVLVFLACQI 259
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 206 NWRMLRLPQSGFIVPPLLIMLFCYGTTLRTLFKAHMGQKRAIRVIAVVLVFLCWL 265
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 260 PHNVLV-TAANLGMKMRSCQSEKLIQYTKTVTEVLAFLHCLNPLVYAFIQGFRNYF 318
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 266 PYNLVLADTLMRVIOETCERRNHIDRALDATEILGLHCLNPIIYAFIQGFRHGL 325
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 319 LKIL 322
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 326 LKIL 329
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

A:Residues: 1-359 <RES>
A:Cross-references: EMBL:U31207; NID:g950174; PIDN:AA052239.1; PID:g950175
R:Bozic, C.R.; Gerard, N.P.; von Uexkull-Guldenband, C.; Kolakowski, L.F.
J. Biol. Chem. 269, 29355-29358, 1994
A:Title: The murine interleukin 8 type B receptor homologue and its ligands. Expression
A:Reference number: 155421; MUID:95050766
A:Accession: 153421
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-359 <RE2>
A:Cross-references: GB:L13239; NID:g293665; PIDN:AAA62109.1; PID:g293666
R:Wilkie, T.M.; Chen, Y.; Gilbert, D.J.; Moore, K.J.; Yu, L.; Simon, M.I.; Copeland, N.C.
Genomics 18, 175-184, 1993
A:Title: Identification, chromosomal location, and genome organization of mammalian G-protein coupled receptor 8
A:Reference number: A48909; MUID:94116980
A:Accession: H48909
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 145-258 <WIL>
A:Cross-references: GB:L20337; NID:g438800; PIDN:AAA16853.1; PID:g438801
R:Harada, A.; Kuno, K.; Nomura, H.; Mukaida, N.; Murakami, S.; Matsushima, K.
Gene 142, 297-300, 1994
A:Title: Cloning of a cDNA encoding a mouse homolog of the interleukin-8 receptor.
A:Reference number: 153774; MUID:94252584
A:Accession: 153774
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-359 <RE3>
A:Cross-references: GB:D17630; NID:g493671; PIDN:BAA04536.1; PID:g493672
C:Genetics:
A:Gene: 118rb
A:Introns: #status absent
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
F:49-74/Domain: transmembrane #status predicted <TM1>
F:84-106/Domain: transmembrane #status predicted <TM2>
F:120-141/Domain: transmembrane #status predicted <TM3>
F:163-182/Domain: transmembrane #status predicted <TM4>
F:213-234/Domain: transmembrane #status predicted <TM5>
F:251-271/Domain: transmembrane #status predicted <TM6>
F:308-328/Domain: transmembrane #status predicted <TM7>
Query Match 30.6%; Score 580.5; DB 2; Length 359;
Best Local Similarity 39.0%; Pred. No. 2.1e-41;
Matches 130; Conservative 59; Mismatches 127; Indels 17; Gaps 10;
QY 28 PCRRSG-SSPGVLYRYATSLICVLGILGNLTVITFAFYKKARSMYDVLNMAIADILF 86
DB 37 PCHSENLEINSYAVVYVYVLLVLLSVGNSLVMLVILYNRSTGCVTDVLLNLAIDLFF 96
QY 87 VLTLPWAVSHATGAWVFNATCKLLGIYAINFNCGMILLTCSMDRYTAIVQATKSF 146
DB 97 AULPWAAKNGV-WTFGSTLKIFSYKVEVTFYSSVLLACISMDRYTAIVHATSTL- 154
QY 147 LRSRLPRSKIIICLVWGLSVIISSTFVFNQYNTQGSQ-VCEPKYQTV-SEPIRWKLL 204
DB 155 IQKRHL--VKFVCIAMWLLSVLALPILIRNPVKYNLTLVC---YEDVGNNTSRLRV 209
QY 205 MGLLELFGFFIPLMPMIFCYTFIVKTLVQAQNSKRHKAIKRVIIAVLVFLACQIPHNW 264
DB 210 LRILPOTFGFLVPLLLMFCYGTFTLTLFKAHMGQKRAHMRVIFAVVLVFLCWLPLNLY 269
QY 265 LLV-TAANLGNKMRSCQSEKLIQYTVTEVLAFLHCLLPVLYAFYQKFRNFKILK 323
DB 270 LFTDLMRTKLKETCERDDDKALNATYETILGLHSLNPLIYAFYQKFRHGLLKIMA 329
QY 324 DLWCVRKYSKSGFSCAGR--YSENISROTSET 354
DB 330 TYGLVSKFEFLAK----EGRPSFVSSSANTSTT 358

RESULT 12

JC4587
chemokine (C-C) receptor 4 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
C:Accession: JC4587
R:Hoogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
Biochem. Biophys. Res. Commun. 218, 337-343, 1996
A:Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines
A:Reference number: JC4587; MUID:96136324
A:Accession: JC4587
A:Molecule type: mRNA
A:Residues: 1-360 <HOO>
A:Cross-references: EMBL:X90862; NID:g1167851; PIDN:CAA62372.1; PID:g1167852
A:Experimental source: thymus
C:Genetics:
A:Gene: cc ckr-4
C:Superfamily: vertebrate rhodopsin
C:Keywords: glycoprotein; phosphoprotein; receptor; thymus
F:2,183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status p
F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicte
F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicte
Query Match 30.3%; Score 574.5; DB 2; Length 360;
Best Local Similarity 36.2%; Pred. No. 6.8e-41;
Matches 126; Conservative 67; Mismatches 118; Indels 37; Gaps 10;
QY 28 PCRRSG-SSPGVLY-RIATSLICVLGILGNLTVITFAFYKKARSMYDVLNMAIADIL 85
DB 28 PCTKEGIRKAFGEVFLPPLYSLVFLGLFGNSVVVLFVFKYKRLKSMYDVLNLAISDLL 87
QY 86 FVLTLPWAVSHATGAWVFNATCKLLGIYAINFNCGMILLTCSMDRYTAIVQATKSF 145
DB 88 FVLSLPFWCY-YAQQWVFLGCLKIVSWMYLVGVSGIFFIMLSIDRYLAIVHAV--F 144
QY 146 LRSRLPRSKIIICLVWGLSVIISSTFVFNQYNTQGSQVCEPKYQTVSEPIRWKLLM 205
DB 145 SLKARTLTIVGVTISLTISVAVFASLPGLLFSTCYTEHNHTYCKTQYSVNS--TTWKVLS 202
QY 206 LGLEL-LFGFFIPLMPMIFCYTFIVKTLVQAQNSKRHKAIKRVIIAVLVFLACQIPHNW 264
DB 203 -SLEINVLGLLPIGLIMLFWSMIITLQHCNKKRKNRAVRMIFGVVLFGLFWTPYV 261
QY 265 LLVTAANLGNKMRSCQSEKLIQYTVTEVLAFLHCLLPVLYAFYQKFRNFKILK 324
DB 262 LFLETIVLEVLQDCTLEKLYDAIQATETLGLHCLLPVLYIFFLGERKRYITQLFR- 320
QY 325 LWCVRKYSKSGFSCAGR-----YSENISRQ--TSETADND 358
DB 321 -----TCRGLVLCCKHCDFLQVYSADMSSSSYTQSTVDHD 355
RESULT 13
149341
MP-1 alpha receptor like-2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 02-Jul-1998
C:Accession: 149341
R:Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A:Title: Cloning and differential tissue-specific expression of three mouse beta chem
A:Reference number: 149339; MUID:95340546
A:Accession: 149341
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-359 <RES>
A:Cross-references: EMBL:U28406; NID:g881551; PID:g881552
C:Superfamily: vertebrate rhodopsin
Query Match 30.2%; Score 571.5; DB 2; Length 359;
Best Local Similarity 37.3%; Pred. No. 1.2e-40;

Matches 110; Conservative 67; Mismatches 113; Indels 5; Gaps 3;

QY 25 YCAPCR--RSGSPGYRIAYSLICVLGNILVITFAFYKKARSMTDVYLLNMAIA 82
 Db 24 WAPCEKRIEELGSLWLPPLSLVIFGLGNMAMVLLIKYKQIMNTNIFLNLAIS 83
 QY 83 DILFVLTLPFWAVSHATGAWFSNATCKLLKGIYAINFCNGLMLTFCISMDRYIAIVQAT 142
 Db 84 DLLFETVPFWHYHVLWNEGFGHYMKMLSGFYLYALYSEIFFIILLTIDRYLAIVHAV 143
 QY 143 KSFRLSRITLPRSKILICLVWGLSVIISSTFVFNQKNTQSDVCEPKYQTVSEPIRWK 202
 Db 144 --FALRARTVTFATITSTITWGLAGLAALPEFIFHESQDSFGFCSPRYPE--GEEDSWK 200
 QY 203 LLMGLLELFGFFIFLPMFIFCYTIVKTLVQAQNSKRHKARIVIAVVLVFLACIAPHN 262
 Db 201 RFHALRMNIFGLALPLLVVVCYSGLIKTLRCPCPKKKHKAIRLIFVVMIVFIFWTPYN 260
 QY 263 MVLVTAANLGMNRSQCSEKLGITKTVTEVLAFLHCLNPLVYAFIQGKFRNY 317
 Db 261 LVLLFSAFHSTFLETSCEQSKHLDLMAQVTEVIATHCVCNPNVIAFVGERFRKH 315

RESULT 14

A23669
 N:Interleukin-8 receptor, high affinity - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 05-Nov-1999
 C:Accession: A23669
 R:Thomas, K.M.; Pyun, H.Y.; Navarro, J.
 J. Biol. Chem. 265, 20061-20064, 1990
 A:Title: Molecular cloning of the fMet-Leu-Phe receptor from neutrophils.
 A:Reference number: A23669; MUID:91056034
 A:Accession: A23669
 A:Molecule type: mRNA
 A:Residues: 1-354 <THO>
 A:Cross-references: GB:M58021; GB:J05705; NID:g165442; PIDN:AAA31377.1; PID:g165443
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein; neutrophil

Query Match 29.8%; Score 564.5; DB 2; Length 354;
 Best Local Similarity 37.7%; Pred. No. 4.6e-40;
 Matches 126; Conservative 65; Mismatches 108; Indels 35; Gaps 9;

QY 38 YLYRIAYSLICVLGNILVITFAFYKKARSMTDVYLLNMAIADILFVLTLPFWAVSH 97
 Db 45 YVWVYIYALVFLSLGNSLVMLVILYSRNSRSDTVYLLNLAMA-----PAPCPDH 96
 QY 98 A----TCGAWV-FSNATCKLLKGIYAINFCNGLMLTFCISMDRYIAIVQATKSFRLSRIT 151
 Db 97 AYLGKQKRDLDFRPLCKVSVLKEVNFYSGLILLACISVDRIYLAIVOSTRTLTQKRHL 156
 QY 152 LPRKIIICLVWGLSVIISSTFVFNQKYN-TQGSVCEPKYQTVS-EPIRWKLLMLGLE 209
 Db 157 V---KFCILGIWALSLLSLFFLEQVSPNNSPVC---YEDLGHNTAKCMVRLILP 210
 QY 210 LLFGFFILPMFIFCYTIVKTLVQAQNSKRHKARIVIAVVLVFLACIAPHNMVLLV-T 268
 Db 211 HTFGFIPLLVLMFCYGTTLRTLFQAHMGQKHRAMRVFAVVLIFLCLWLPYNLVLLADT 270
 QY 269 AANLGMNRSQCSEKLGITKTVTEVLAFLHCLNPLVYAFIQGKFRNYFLKILKDLWCV 328
 Db 271 LMRTHVIOETCORRNELDRALDATEILGLHCLNPIIYAFIQGKFRNYFLKILKDLWCV 330
 QY 329 RRYKSSGFCAGRYSENISROTSETADNDNASS 362
 Db 331 SKEFLTR-----HRVTSTSSSTNVPS 352

RESULT 15

A45177

chemokine (C-C) receptor 1 - human
 N:Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
 C:Accession: A45177; I55671
 R:Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.
 Cell 72, 415-425, 1993
 A:Title: Molecular cloning, functional expression, and signaling characteristics of a
 A:Reference number: A45177; MUID:93161416
 A:Accession: A45177
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-355 <NEO>
 A:Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
 A:Experimental source: HL60 cells
 A:Note: sequence extracted from NCBI backbone (NCBIP:124876)
 R:Gao, J.
 J. Exp. Med. 177, 1421-1427, 1993

A:Title: Structure and functional expression of the human macrophage inflammatory 1 a
 A:Reference number: I55671; MUID:93240122
 A:Accession: I55671
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-355 <RES>
 A:Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
 C:Genetics:
 A:Gene: GDB:CMKBR1; CMKR-1
 A:Cross-references: GDB:138446; OMIM:601159
 A:Map position: 3p21-3p21
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein;
 F:36-60/Domain: transmembrane #status predicted <TM1>
 F:71-91/Domain: transmembrane #status predicted <TM2>
 F:108-129/Domain: transmembrane #status predicted <TM3>
 F:147-171/Domain: transmembrane #status predicted <TM4>
 F:205-223/Domain: transmembrane #status predicted <TM5>
 F:240-264/Domain: transmembrane #status predicted <TM6>
 F:288-305/Domain: transmembrane #status predicted <TM7>
 F:5/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:24-273,106-183/Disulfide bonds: #status predicted
 F:345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 28.9%; Score 547.5; DB 2; Length 355;
 Best Local Similarity 36.4%; Pred. No. 1.2e-38;
 Matches 120; Conservative 69; Mismatches 116; Indels 25; Gaps 10;

QY 44 YSLICVLGLGNILVITFAFYKKARSMTDVYLLNMAIADILFVLTLPFWAVSHATGAW 103
 Db 41 YSLFVIGLVGNILVVLVLYVQYKRLKNTSIYLLNLALISDLFLFTLPFWIDYKLDQWV 100
 QY 104 FSNATCKLLKGIYAINFCNGLMLTFCISMDRYIAIVQATKSFRLSRITLPRSKITICLVW 163
 Db 101 FGDAMCKILSGFYTYGLYSEIFFIILLTIDRYLAIVHAV--FALRARTVTFGVITSI 158
 QY 164 GLSVIISSTFVFNQKNTQGSVCEPKYQTVS-----EPIR-WKLLMLGLEL-LFGFFI 216
 Db 159 ALAILASMPGLYFSK---TQ---WEFTHHTCSLHFPHESLRWKLFQ-ALKNLFLGLV 210
 QY 217 PLFMFIPCYTIVKTLVQAQNSKRHKARIVIAVVLVFLACIAPHNMVLLVTAANLGMN 276
 Db 211 PLLVMILCYTGILKILLRRPNEKSKAVRLIFVIMIFLFWTPYNTILISVQDFLFT 270
 QY 277 RSCQSEKLGITKTVTEVLAFLHCLNPLVYAFIQGKFRNYFLKILKDLWCVR---RRYK 333
 Db 271 HECEQSRHLDLAVQVTEVIATYTHCCVNPVIAFVGERFRKY---LQLPFRRVAVHLVK 326
 QY 334 SSGFSCAGRYSENISROTSETADNDNASSF 363
 Db 327 WLPFLSVDRIL-ERVSTSPSTGHELSAGF 355

Search completed: May 23, 2001, 15:31:57
Job time: 504 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:25:29 ; Search time 62.39 Seconds
(without alignments)
200.405 Million cell updates/sec

Title: US-08-887-977-10

Perfect score: 1894

Sequence: 1 MFSTPVKILQCISILHITQL.....NISQTSADNADNASFTM 365

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1670	88.2	374	1	CCR6_HUMAN
2	1375.5	72.6	367	1	CCR6_MOUSE
3	682	36.0	378	1	CCR7_HUMAN
4	682	36.0	378	1	CCR7_MOUSE
5	666.5	35.2	350	1	IL8A_PANTR
6	663.5	35.0	350	1	IL8A_GORGO
7	662	35.0	350	1	IL8A_HUMAN
8	654	34.5	355	1	IL8A_RABIT
9	645	34.1	356	1	IL8B_CANFA
10	644.5	34.0	360	1	IL8B_BOVIN
11	636.5	33.6	358	1	IL8B_RABIT
12	631.5	33.3	353	1	IL8B_PANTR
13	629.5	33.2	353	1	IL8B_MACMU
14	629.5	33.2	360	1	IL8B_HUMAN
15	623.5	32.9	353	1	IL8B_GORGO
16	613.5	32.4	369	1	CCR9_MOUSE
17	610.5	32.2	360	1	CCR4_HUMAN
18	610	32.2	349	1	IL8A_RAT
19	604.5	31.9	359	1	IL8B_RAT
20	598.5	31.6	342	1	BONZ_CERAE
21	595.5	31.4	343	1	BONZ_MACMU
22	594.5	31.4	342	1	BONZ_MACNE
23	593.5	31.3	357	1	CCR9_HUMAN
24	580.5	30.6	342	1	BONZ_HUMAN
25	580.5	30.6	359	1	IL8B_MOUSE
26	574.5	30.3	360	1	CCR4_MOUSE
27	571.5	30.2	359	1	CCR3_MOUSE
28	565.5	29.9	359	1	CCR3_RAT
29	558	29.5	358	1	CCR3_CAVPO
30	551	29.1	354	1	CCR5_RAT
31	548.5	29.0	373	1	CCR2_RAT
32	547.5	28.9	355	1	CCR1_HUMAN
33	546.5	28.9	352	1	CCR5_CERTO

34	546	28.8	373	1	CCR2_MOUSE	P51683 mus musculu
35	539.5	28.5	368	1	CCR3_HUMAN	P49682 homo sapien
36	538	28.4	354	1	C3X1_RAT	P35411 rattus norv
37	537.5	28.4	352	1	CCR5_CERAE	P56493 cercopithec
38	537.5	28.4	352	1	CCR5_MACMU	P79436 macaca mula
39	536.5	28.3	352	1	CCR5_PAPHA	P56441 papio hamad
40	536.5	28.3	374	1	CCR2_HUMAN	P41597 homo sapien
41	534	28.2	354	1	CCR5_MOUSE	P51682 mus musculu
42	533.5	28.2	352	1	CCR5_PYGNE	O97882 pygathrix n
43	532.5	28.1	352	1	CCR5_PYGBI	O97880 pygathrix b
44	532.5	28.1	352	1	CCR5_TRAFR	O97878 trachypithe
45	532.5	28.1	352	1	CCR5_TRAPH	O97879 trachypithe

ALIGNMENTS

RESULT 1

ID	CCR6_HUMAN	STANDARD:	PRT:	374 AA.
AC	P51684: Q92846; P78553;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CCR-6) (CCR-6) (LARC RECEPTOR) (GPR-CV4) (GPCRY4) (CHEMOKINE RECEPTOR-LIKE 3) (CCR-L3) (DRY6).			
DE	CCR6 OR CMKBR6 OR STRL22 OR GPR29 OR CKRL3.			
GN	Homo sapiens (Human).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. AND FUNCTION.			
RX	MEDLINE=97313465; PubMed=9169459;			
RA	Baba M., Imal T., Nishimura M., Kakizaki M., Takagi S., Hieshima K.,			
RA	Nomiyama H., Yoshie O.;			
RT	"Identification of CCR6, the specific receptor for a novel			
RT	lymphocyte-directed CC chemokine LARC.";			
RL	J. Biol. Chem. 272:14893-14898(1997).			
[2]				
RN	SEQUENCE FROM N.A.			
RP	SEQUENCE FROM N.A.			
RA	Lautens L.L., Modi W., Bonner T.I.;			
RL	Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.			
[3]				
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=97040707; PubMed=8886020;			
RX	Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G.;			
RA	"Molecular cloning and RNA expression of two new human chemokine			
RT	receptor-like genes.";			
RL	Biochem. Biophys. Res. Commun. 227:846-853(1996).			
[4]				
RN	SEQUENCE FROM N.A.			
RP	SEQUENCE FROM N.A.			
RA	McCoy R., Perlmutter D.H.;			
RL	Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.			
[5]				
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=97224503; PubMed=9070937;			
RA	Liao F., Lee H.-H., Farber J.M.;			
RT	"Cloning of STRL22, a new human gene encoding a G-protein-coupled			
RT	receptor related to chemokine receptors and located on chromosome			
RT	6q27.";			
RL	Genomics 40:175-180(1997).			
CC	-1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-			
CC	ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE			
CC	INTRACELLULAR CALCIUM IONS LEVEL.			
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	-1- TISSUE SPECIFICITY: SPLEEN, LYMPH NODES, APPENDIX, AND FETAL			
CC	NATURAL KILLER CELLS, MONOCYTES, OR GRANULOCYTES.			
CC	-1- INDUCTION: INTERLEUKIN-2.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-6 IS THE INITIATOR.			

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DR EMBL; U45984; AAB62714.1; -
DR EMBL; 279784; CAB02144.1; ALT_INIT.
DR EMBL; U60000; AAB06949.1; -
DR EMBL; U68030; AAC51124.1; -
DR EMBL; U68032; AAC51125.1; -
DR HSP; P34996; 1DDO.
DR GCRDB; GCR_1037; -
DR GCRDB; GCR_1075; -
DR GCRDB; GCR_1906; -
DR GCRDB; GCR_1919; -
DR GCRDB; GCR_1941; -
DR GCRDB; GCR_2110; -
DR MIM; 601835; -
DR InterPro; IPR000276; -
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 47 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 48 74 1 (POTENTIAL).
FT DOMAIN 75 83 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 84 104 2 (POTENTIAL).
FT DOMAIN 105 119 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 120 141 3 (POTENTIAL).
FT DOMAIN 142 159 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 160 180 4 (POTENTIAL).
FT DOMAIN 181 211 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 212 238 5 (POTENTIAL).
FT DOMAIN 239 254 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 255 279 6 (POTENTIAL).
FT DOMAIN 280 303 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 304 321 7 (POTENTIAL).
FT DOMAIN 322 374 CYTOPLASMIC (POTENTIAL).
FT DISULFID 118 197 BY SIMILARITY.
FT CARBOHYD 7 7 N-LINKED (GLCNAC... (POTENTIAL).
FT CONFLICT 23 23 N-LINKED (GLCNAC... (POTENTIAL).
FT CONFLICT 60 60 G -> A (IN REF. 4).
FT CONFLICT 74 74 Y -> N (IN REF. 4).
FT CONFLICT 86 86 L -> V (IN REF. 4).
FT CONFLICT 164 164 S -> T (IN REF. 5).
FT CONFLICT 182 182 T -> S (IN REF. 4).
FT CONFLICT 192 192 Q -> L (IN REF. 4).
FT CONFLICT 206 206 E -> V (IN REF. 4).
FT CONFLICT 225 225 I -> F (IN REF. 4).
FT CONFLICT 370 374 SSFTM -> VLVHVES (IN REF. 4).
SQ SEQUENCE 374 AA; 42494 MW; D7F963534E990BC4 CRC64;

Query Match 88.2%; Score 1670; DB 1; Length 374;
Best local Similarity 89.6%; Pred. No. 4.2e-99;
Matches 328; Conservative 8; Mismatches 10; Indels 20; Gaps 2;

QY 2 ESTPVKILC--QSILHITQILRCYCPCRRSSSPGYLYRTAYSICVLGLGNILW 59
DB 27 YSDSEMLCSLQEVRFSLFV-----PIAYSLICVFGLLGNILW 68
QY 60 ITFAFYKARSMTDVLNMAIADILVLTLPFAVSHATCAWVFSNATCKLLKGIYAIN 119
DB 69 ITFAFYKARSMTDVLNMAIADILVLTLPFAVSHATCAWVFSNATCKLLKGIYAIN 128
QY 120 FNCGMLLLTCISMDRYIAIVQATKSPFLRSRTLPKRSKICLVWGLSVIISSTFTVFNQK 179
DB 129 FNCGMLLLTCISMDRYIAIVQATKSPFLRSRTLPKRSKICLVWGLSVIISSTFTVFNQK 188

QY 180 YNTQSDVCEPKYQTVSEPIRWKLLMLGLELFGFFIPLMFICYTFIVKTLVQAQNSK 239
DB 189 YNTQSDVCEPKYQTVSEPIRWKLLMLGLELFGFFIPLMFICYTFIVKTLVQAQNSK 248
QY 240 RHKAIKRVIIAVLVFLACQIPHNMLLVTAANLGKNNRSCQSEKLGITYKTYTVEVLAFLH 299
DB 249 RHKAIKRVIIAVLVFLACQIPHNMLLVTAANLGKNNRSCQSEKLGITYKTYTVEVLAFLH 308
QY 300 CCLNPVLYAFIGOKFKNRYELKILKDLWCVRYYKYSKSGSCAGRYSENISQTSQTDNDN 359
DB 309 CCLNPVLYAFIGOKFKNRYELKILKDLWCVRYYKYSKSGSCAGRYSENISQTSQTDNDN 368
QY 360 ASSFTM 365
DB 369 ASSFTM 374

RESULT 2
CKR6_MOUSE
ID CKR6_MOUSE STANDARD; PRT; 367 AA.
AC 054689;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CC-CKR-6) (CCR-6) (KY411).
GN CCR6 OR CMKBR6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Yanagihara S., Komura E., Yamauchi Y.;
RT "Mouse G protein-coupled receptor KY411.";
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99077268; PubMed=9862452;
RA Varona R., Zaballos A., Gutierrez J., Martin P., Roncal F.,
RA Albar J.P., Ardavin C., Marquez G.;
RT "Molecular cloning, functional characterization and mRNA expression
analysis of the murine chemokine receptor CCR6 and its specific ligand
MIP-3alpha.";
RT FEBS Lett. 440:188-194(1998).
RL FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-
ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE
INTRACELLULAR CALCIUM IONS LEVEL.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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DR EMBL; AB009369; BAA23776.1; -
DR EMBL; AJ222714; CAA10956.1; -
DR MGD; MGI:1333797; Cmkbr6.
DR InterPro; IPR000276; -
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 39 1 (POTENTIAL).
FT TRANSMEM 40 66 2 (POTENTIAL).
FT DOMAIN 67 75 1 (POTENTIAL).
FT TRANSMEM 76 96 2 (POTENTIAL).
FT DOMAIN 97 111 EXTRACELLULAR (POTENTIAL);

FT	TRANSMEM	112	133	3 (POTENTIAL).
FT	DOMAIN	134	151	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	152	172	4 (POTENTIAL).
FT	DOMAIN	173	203	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	204	230	5 (POTENTIAL).
FT	DOMAIN	231	246	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	247	271	6 (POTENTIAL).
FT	DOMAIN	272	295	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	296	313	7 (POTENTIAL).
FT	DOMAIN	314	367	CYTOPLASMIC (POTENTIAL).
FT	DLSULFID	110	189	BY SIMILARITY.
FT	CARBOHYD	2	2	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	35	35	N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQ	SEQUENCE	367 AA;	42102 MW;	6A309AF833B1117E CRC64;

Query Match	72.6%;	Score	1375.5;	DB 1;	Length	367;
Best Local Similarity	78.8%;	Pred	No.1.6e-80;			
Matches	256;	Conservative	33;	Mismatches	35;	Indels
						1; Gaps

QY	42	IAYSLLICVLGLGNILWITFAFYKKARSMTDVLNMAIADILFVLTLPFWAVSHATGA	101
Db	43	IAYSLLICVFLGNIMVMTFAFYKKARSMTDVLNMAITDILFVLTLPFWAVTHATNT	102
QY	102	WVFSNATCKLLKGIYAINFCNGMLLTICISMDRYTAIVQATKSFRLSRSTLPKSLICLV	161
Db	103	WVFSALCKLMKGTAYVNFNCGMLLIACISMDRYTAIVQATKSFVRSSTLTHSKVICVA	162
QY	162	VGLSLVSIISSTVFVNOKYNTQSDVCEPKYQTVSEPIRWKLLMLGLELLFGFFIPLMF	221
Db	163	VWFSIIISSTPIFNKKVLEQDRDVCPEPRYSVSEPTWKLGLGLELFGFFIPLMF	222
QY	222	IFCYTFIVKTLVQAQNSKRHAIIRVIAVVLVFLACQIPHNNVLLVTAANLGKMNRSQS	281
Db	223	VFCYLFIKTLVQAQNSKRHAIIRVIAVVLVFLACQIPHNNVLLVTAVENTKVGSRSCST	282
QY	282	EKLIIGTKVTEVLAFLHCLNPLVYAFIQGFERNYFLKILDKLVCVRKRYKSSGFSCAG	341
Db	283	EKYLAVTRNVAEYLAFLHCLNPLVYAFIQGFERNYFMKIMKDVCMRKRKNMPGLFCAR	342
QY	342	RYSEN-1SROTSETADNDNASSFTM	365
Db	343	VISESIISROTSETVENDNASSFTM	367

RESULT	3
CKR7_HUMAN	STANDARD;
ID	CKR7_HUMAN
AC	P32248;
DT	01-OCT-1993 (Rel. 27, Created)
DT	01-FEB-1996 (Rel. 33, Last sequence update)
DT	01-OCT-2000 (Rel. 40, Last annotation update)
DE	C-CHEMOKINE RECEPTOR TYPE 7 PRECURSOR (C-C CKR-7) (CCR-7)
DE	(MIP-3 BETA RECEPTOR) (EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 1)
DE	(EB11) (BLR2).
DE	CKR7 OR CMKB7 OR EB11 OR EVIL.
GN	OS Homo sapiens (Human).
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_Taxid=9606;
ON	[1]
RP	SEQUENCE FROM N.A.
RP	MEDLINE=93188173; PubMed=8383238;
RA	Birkenbach M.P., Josefsen K., Yalamanchili R.R., Lenoir G.M.,
RA	Elliot K.;
RT	"Epstein-Barr virus-induced genes: first lymphocyte-specific G
RL	protein-coupled peptide receptors.";
RL	J. Virol. 67:2209-2220(1993).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Placenta;
RX	MEDLINE=95154835; PubMed=7851893;
RX	Schweickart V.L., Raport C.J., Godiska R., Byers M.G., Eddy R.L. Jr.,

Db 63 IMYSIIICFVGLLNGVWLTYYIFKRLKMTDTYLLNLAVALADILFLTLFPWYS-AAKS 121
 QY 102 WYFSNATCKLLKGIYAINFCMGLLTCTISMDRYIAIVQATKFRSLRSTLPKSIICLV 161
 Db 122 WYFGVHFKLFIAYKMSFGSMLLLCISIDRYAIVQASVHRHARVLLSKLSCVG 181
 QY 162 VNGLSVIISSTFVFN--QKYNTPQSGDVCPEPKYQTVSEPIRWKLLMLGLLELFGFFIPLM 219
 Db 182 IWLATVLSIPELLYSLDQRSSEQAMR-----SLITEHVEAFITTIQVQMWIGFLVPLL 237
 QY 220 FMIFCYTFIVKTLVQAOQSKRHKRAIRVIAVLFVFLACQPHN-MVLLVTAANLGNKMR 278
 Db 238 AMSFCYLVIIIRTLQARNEFNRAIKAVIAVVVFIQVLPYNGVLAQTVANFNITSST 297
 QY 279 COSEKLGIVKTVTEVLAFLHCCNPVLAFAIGQKFRNYELKILDKLWCVRKRYKSSGFS 338
 Db 298 CELSQNLNTAYDVITYSLACVRCVNFVLAFAIGVGRNDLFLKFLKGLGCLSQSOLROWSS 357
 QY 339 C--AGRYSENISROTSET 354
 Db 358 CRHRRSSMSVEAETTT 375

RESULT 4

ID CKR7_MOUSE STANDARD; PRT; 378 AA.
 AC P47774;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 7 PRECURSOR (C-C CKR-7) (CCR-7)
 DE (MIP-3 BETA RECEPTOR) (EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 1)
 DE (EB1).
 GN CKR7 OR CMKBR7 OR EB1 OR EB1H.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B6/CBA; TISSUE=Thymus;
 RX MEDLINE=95154835; PubMed=7851893;
 RA Schweickart V.L., Raport C.J., Godiska R., Byers M.G., Eddy R.L. Jr.,
 RA Shows T.B., Gray P.W.;
 RT "Cloning of human and mouse EB1, a lymphoid-specific
 RT G-protein-coupled receptor encoded on human chromosome 17q12-q21.2.";
 RL Genomics 23:643-650(1994).
 CC -!- FUNCTION: RECEPTOR FOR THE MIP-3-BETA CHEMOKINE. PROBABLE MEDIATOR
 CC OF EBV EFFECTS ON B LYMPHOCYTES OR OF NORMAL LYMPHOCYTE FUNCTIONS.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 DR EMBL; L31580; AAA74232.1;
 DR MGD; MGI:103011; Cmkbr7.
 DR InterPro; IPR000276;
 DR InterPro; IPR001718;
 DR Pfam; PF00003; 7cm_1; 1.
 DR PRINTS; PR00237; GPCRHHODOPS.N.
 DR PRINTS; PR00641; CHEMOKINER7.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24 POTENTIAL.
 CHAIN 25 378 C-C CHEMOKINE RECEPTOR TYPE 7.

FT DOMAIN 25 59
 FT TRANSMEM 60 86
 FT DOMAIN 87 95
 FT TRANSMEM 96 116
 FT TRANSMEM 117 130
 FT TRANSMEM 131 152
 FT TRANSMEM 153 170
 FT TRANSMEM 171 191
 FT DOMAIN 192 219
 FT TRANSMEM 220 247
 FT TRANSMEM 248 263
 FT TRANSMEM 264 289
 FT TRANSMEM 290 313
 FT TRANSMEM 314 331
 FT TRANSMEM 332 378
 FT CARBOHYD 36 36
 FT DISULFID 129 210
 SQ SEQUENCE 378 AA; 42941 MW; ACBIA422CF54AA54 CRC64;

Query Match 36.0%; Score 682; DB 1; Length 378;

Best Local Similarity 38.8%; Pred. No. 9.9e-37;

Matches 145; Conservative 76; Mismatches 123; Indels 30; Gaps 6;

QY 5 PVKIIQCSTLHITQLILRCYC-----APCRSG--SSPGYLYR 41
 Db 6 PRKNVLVALLVIFQV---CFQDEVTDDYIGENTTVDTLVESVCFKKDVRNFKAWFLP 62
 QY 42 IAYSLICVLGLGNILVVITFAFKKARSMTDVLNNMAIDILFVLTLPFWANSHATGA 101
 Db 63 LMYSVIGFVGLLNGVLVITAYIFKRLKMTDTYLLNLAVALADILFLTLFPWYSEAK-S 121
 QY 102 WYFSNATCKLLKGIYAINFCMGLLTCTISMDRYIAIVQATKFRSLRSTLPKSIICLV 161
 Db 122 WYFGVHFKLFIAYKMSFGSMLLLCISIDRYAIVQASVHRHARVLLSKLSCVG 181
 QY 162 VNGLSVIISSTFVFNQKYNTPQSGDVCPEPKYQTVSEPIRWKLLMLGLLELFGFFIPLMFM 221
 Db 182 IWLALFSLIPELLYSLGKNSGEDTL--RCSLSVAQAEALITTIQVQMWIGFLVPLMAM 239
 QY 222 IFCTYTFIVKTLVQAOQSKRHKRAIRVIAVLFVFLACQPHN-MVLLVTAANLGNKMRSCQ 280
 Db 240 SFCYLVIIIRTLQARNEFNRAIKAVIAVVVFIQVLPYNGVLAQTVANFNITSNCSCE 299
 QY 281 SEKLGIVKTVTEVLAFLHCCNPVLAFAIGQKFRNYELKILDKLWCVRKRYKSSGFSGA 340
 Db 300 TSKQLNTAYDVITYSLASVRCVNFVLAFAIGVGRNDLFLKFLKGLGCLSQRLHWSR 359
 QY 341 GRYSENISROTSET 354
 Db 360 HVRNASVMEAEET 373

RESULT 5

ID IL8A_PANTR STANDARD; PRT; 350 AA.
 AC P55920;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR A (IL-8R A) (IL-8 RECEPTOR TYPE
 DE 1) (CXCR-1) (CDW128).
 GN IL8RA OR CXCR1.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96175151; PubMed=9110929;
 RA Alvarez V., Coto E., Setien F., Gonzalez S., Gonzalez-Roces S.,
 RA Lopez-Larrea C.;
 RT "Characterization of interleukin-8 receptors in non-human primates.";

```

Immunogenetics 43:261-267(1996).
-!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
      NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
      CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
      G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
      MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
      AND TO MGSA (GRO) WITH A LOW AFFINITY.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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EMBL; X91109; ; NOT_ANNOTATED_CDS.
HSSP; P34996; IIDD.
InterPro; IPR000174; -.
InterPro; IPR000276; -.
InterPro; IPR001355; -.
Pfam; PR00001; 7tm_1; 1.
PRINTS; PR00237; GPCRHHODOPSN.
PRINTS; PR00427; INTRLEUKIN8R.
PRINTS; PR00572; INTRLEUKIN8A.
PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.
PROSITE; PS0362; G_PROTEIN_RECEP_FL_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
Chemoaxis.
KW DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
   FT TRANSMEM 40 66 1 (POTENTIAL).
   FT DOMAIN 67 75 CYTOPLASMIC (POTENTIAL).
   FT TRANSMEM 76 96 2 (POTENTIAL).
   FT DOMAIN 97 111 EXTRACELLULAR (POTENTIAL).
   FT TRANSMEM 112 133 3 (POTENTIAL).
   FT DOMAIN 134 154 CYTOPLASMIC (POTENTIAL).
   FT TRANSMEM 155 174 4 (POTENTIAL).
   FT DOMAIN 175 199 EXTRACELLULAR (POTENTIAL).
   FT TRANSMEM 200 220 5 (POTENTIAL).
   FT DOMAIN 221 242 CYTOPLASMIC (POTENTIAL).
   FT TRANSMEM 243 264 6 (POTENTIAL).
   FT DOMAIN 265 285 EXTRACELLULAR (POTENTIAL).
   FT TRANSMEM 286 308 7 (POTENTIAL).
   FT DOMAIN 309 350 CYTOPLASMIC (POTENTIAL).
   FT CARBOHYD 3 3 N-LINKED (GLCNAC. . ) (POTENTIAL).
   FT CARBOHYD 16 16 N-LINKED (GLCNAC. . ) (POTENTIAL).
   FT DISULFID 110 187 BY SIMILARITY.
SEQUENCE 350 AA; 39818 MW; A56PD0246AID440 CRC64;
Query Match 35.2%; Score 666.5; DB 1; Length 350;
Best Local Similarity 41.5%; Pred. No. 8.9e-36;
Matches 141; Conservative 66; Mismatches 110; Indels 23; Gaps 8;
QY 27 APCR-RSGSPGVLYRIAYSLICVLGLNLIVVIFAFYKKARSMTDVLLNNAIADIL 85
DB :||| : | : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
28 SPCRELETETLNKVIITVALVELLSLGNLMVLIYSRGSRVDVLLNALADLL 87
QY 86 FVLTLPFAVSHATGAWFSNATCKLKLGIIYAINFNCMLLLFCISMDRYIAIVQATKSF 145
DB :||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
88 FALTLPWAASKVNG-WIGFTFLCKVVSVLLKEVNFSGILLACISVDRLAIVHAHRTL 146
QY 146 RLRSRTLPRSKIICLVWGSLVISSTFFVNKGYN-TQSDDVCEPKYQTIV-SEPTRWL 203
DB : : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
147 TQKRHLV---KFVCLCGWGLSNMNSLPFFLFRAQYHPNNSSPYC---YEVLGNDTAWRM 200
QY 204 LMLGLELLFGFFPLPMFMICYTFIVTKTLVQAQNSRRHKRAIRVIIAVLLFLACQIPHNM 263
DB : : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
201 VLRIPLHTGFIVPLFMVLCYGYFTLRTLFKAHMGRAMRVIFAIVLLFLCWLPYNL 260
QY 264 VLLIV-TAAALGKNMRSCQSEKLIGYTKTVTEVLAFLHCCINPLVLYAFIGOKFRNYELKIL 322

```

[illegible]

FT TRANSMEM 286 308 7 (POTENTIAL)
 FT DOMAIN 309 350 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 16 16 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 110 187 BY SIMILARITY.
 SQ SEQUENCE 350 AA; 39790 MW; DB99591CD6C10757 CRC64;
 Query Match 35.0%; Score 663.5; DB 1; Length 350;
 Best Local Similarity 41.2%; Pred. No. 1.4e-35;
 Matches 140; Conservative 66; Mismatches 111; Indels 23; Caps 8;
 QY 27 APCR-BSGSPGYLYRAYSLICVLGLNGLVITFAFYKARSMYDVYLLNMAJADIL 85
 DB 28 SPCRLTETLNKVVIIITATALLLSLLGSLVNLVLYSRGGRSVYDVYLLNLAADLL 87
 QY 86 FVLTLPFAVSHATGAWFNATCKLLKGIYAINFNCGMLLLTICISMDRYIAIVQATKSF 145
 DB 88 FALTLPWAASKYNG-WIFGTFLCKVSVLLKEVNFYSGILLACISVDYRLAIVHATFTL 146
 QY 146 RURSRTLPRSKICLVVWGLSVIISSTFVNOKYN-TQSDVCEPKYQTV-SEPIRWKL 203
 DB 147 TOKRHLY--KFVCLGCGWGLSMILSPFLFRQAYHPNNSPVC---YEVLGNDTAKWRM 200
 QY 204 LMLGLELLEFFFLPMFIFCYTFIVKTLVQAQNSKRHRKAIKRVIIAVLVFLACQIPHM 263
 DB 201 VLRLPHTGTFVPLVFLMFLCYGFTLRTLFKAHMGOKHRAMRVIFAVLVFLCWLDPYNL 260
 QY 264 VLIV-TAANLGNKRNRCQSEKLGTYKTVTFLAFLHCLNPLVYAFIGOKFRNYFLKIL 322
 DB 261 VLLADFLMTQVIOESCERNVNSLADATEILGFLHCLNPLIYAFIGQFRIGFLKIL 320
 QY 323 KDLWCVRKYSGFGSCAGRYSENISQTSADNDNASS 362
 DB 321 AMHGLVSKFEFLAR-----HRVTSYTSSSVNVSS 348

RESULT 7
 IL8A_HUMAN
 ID IL8A_HUMAN STANDARD; PRT; 350 AA.
 AC P25024;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR A (IL-8R A) (IL-8 RECEPTOR TYPE
 1) (CXCR-1) (CDW128A).
 GN IL8A OR CXCR1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91368199; PubMed=1840701;
 RA Holmes W.E., Lee J., Kuang W.-J., Rice G.C., Wood W.I.;
 RT "Structure and functional expression of a human interleukin-8
 receptor.";
 RL Science 253:1278-1280(1991).
 RN [2]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RX MEDLINE=93205012; PubMed=8384312;
 RA Cerretti D.P., Kozlosky C.J., Vanden Bos T., Nelson N., Gearing D.P.,
 RA Beckmann M.P.;
 RT "Molecular characterization of receptors for human interleukin-8,
 GRO/melanoma growth-stimulatory activity and neutrophil activating
 peptide-2.";
 RL Mol. Immunol. 30:359-367(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93252387; PubMed=8486366;
 RA Mollereau C., Passage E., Mattei M.-G., Vassart G., Parmentier M.;
 RT "The high-affinity interleukin 8 receptor gene (IL8RA) maps to the
 2q33-q36 region of the human genome: cloning of a pseudogene

(IL8RBP) for the low-affinity receptor.";
 Genomics 16:248-251(1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95014476; PubMed=7929358;
 RA Ahuja S.K., Shetty A., Tiffany H.L., Murphy P.M.;
 RT "Comparison of the genomic organization and promoter function for
 human interleukin-8 receptors A and B.";
 J. Biol. Chem. 269:26381-26389(1994).
 RN [5]
 RP CHARACTERIZATION.
 RX MEDLINE=92355587; PubMed=1379593;
 RA Lee J., Horuk R., Rice G.C., Bennett G.L., Camerato T., Wood W.I.;
 RT "Characterization of two high affinity human interleukin-8
 receptors.";
 J. Biol. Chem. 267:16283-16287(1992).
 RN [6]
 RP STRUCTURE BY NMR OF 9-29 IN COMPLEX WITH IL-8.
 RX MEDLINE=99148123; PubMed=10368283;
 RA Skelton N.J., Quan C., Reilly D., Lowman H.;
 RT "Structure of a CXCR chemokine-receptor fragment in complex with
 interleukin-8.";
 Structure 7:157-168(1999).
 CC -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
 NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
 CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
 G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
 AND TO MSGA (GRO) WITH A LOW AFFINITY.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -!- DATABASE: NAME=PROW; NOTE=CD guide CDW128a entry;
 WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cdw128a.htm".
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 CC -----
 CC EMBL; L19591; AAB59436.1; -
 CC EMBL; L19592; AAA59160.1; -
 CC EMBL; M68932; AAA59159.1; -
 CC EMBL; X65858; CAA46688.1; -
 CC EMBL; U11870; AAA64378.1; -
 CC PIR; A39445; A39445.
 CC PDB; 1ILP; 23-DEC-98.
 CC PDB; 1ILQ; 23-DEC-98.
 CC GCRDb; GCR_0175; -
 CC GCRDb; GCR_0696; -
 CC GCRDb; GCR_1832; -
 CC GCRDb; GCR_1833; -
 CC GCRDb; GCR_2052; -
 CC MIM; 146929; -
 CC InterPro; IPR000174; -
 CC InterPro; IPR000276; -
 CC InterPro; IPR001355; -
 CC Pfam; PF00001; 7tm_1; 1.
 CC PRINTS; PR00237; GPCRHHODOPSN.
 CC PRINTS; PR00427; INTRLEUKIN8R.
 CC PRINTS; PR00572; INTRLEUKIN8R.
 CC PROSITE; PS00237; G_PROTEIN_RECEPT_F1_1; 1.
 CC PROSITE; PS00262; G_PROTEIN_RECEPT_F1_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein;
 CC Chemotaxis; Polymorphism; 3D-structure.
 FT DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 40 66 1 (POTENTIAL).
 FT DOMAIN 67 75 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 76 96 2 (POTENTIAL).
 FT DOMAIN 97 111 EXTRACELLULAR (POTENTIAL).

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FT TRANSMEM 112 133 3 (POTENTIAL).
FT DOMAIN 134 154 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 155 174 4 (POTENTIAL).
FT DOMAIN 175 199 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 200 220 5 (POTENTIAL).
FT DOMAIN 221 240 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 243 264 6 (POTENTIAL).
FT DOMAIN 265 285 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 286 308 7 (POTENTIAL).
FT DOMAIN 309 350 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 16 16 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 110 187 BY SIMILARITY.
FT VARIANT 276 T -> S.
FT SEQUENCE 350 AA; 39805 MW; 2463EEB51BEDD039 CRC64;
Query Match 35.0%; Score 662; DB 1; Length 350;
Best Local Similarity 42.1%; Pred. No. 1.7e-35;
Matches 138; Conservative 64; Mismatches 104; Indels 22; Gaps 7;
QY 38 YLYRIAYSLICVLGLLNILVITFAFYKAKRSMTDVLNMAIDILVLPFWAVSH 97
D 1: |||: : |||: ||: : : ||: |||: ||: ||: |||: |||: |||: |||:
Db 40 YVYIAYALVFLSLGSLNVLVLYGRVGRSVTDVYLLNALADLLFALPLPIWAASK 99
QY 98 ATGAWFESNATCKLLGLIYAINFNGCMLLLTICISMDRYIAIVQATKSPFLRSRTLPKSI 157
D 1: |||: : |||: ||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
Db 100 VNG-WIFGTFLCKVSLKVENFYSGILLACISVDRIALVHATRLTKORHLV---KF 155
QY 158 ICLVWGLSVIISSTFFVFNQYN-TGSDVCEPKYQTV-SEPIRWKLMGLGLELFGPF 215
D 1: |||: : |||: ||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
Db 156 VCLGCGLSMNLSPFLFRQAYHNSSPVC---YEVLGNDTAKRMVLRILPHTFEGFI 212
QY 216 IPLMFIFCYFYIKTLVQAKSRKHKAIRVILIAVLFLACQIPHNVMVLV-TRANLCK 274
D 1: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
Db 213 VPLEVMLFCYGTFTLTKFAHMGOKRAMRVIFAVLFLCWLDPYNLVLLADTLMRTOV 272
QY 275 MNRCSOSEKLGYKTVTEVLAFHCLLPVLYAFYIGOKFRNYFLKILKDLQVCVRKYKS 334
D 1: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
Db 273 IQTCERNRNLGRALDATEILGFLHSLNPIIYAFIGNFRHGFLKILAHGLVSKFELA 332
QY 335 SGFSCAGRYSENISQKTSADNDNASS 362
Db 333 R-----HRVTSYTSNNVSS 348
RESULT 8
IL8A_RABIT STANDARD; PRT; 355 AA.
AC P21109;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR A (IL-8R A) (CXCR-1).
GN IL8RA OR CXCR1.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP MEDLINE=91378994; PubMed=1898400;
RA Beckmann M.P., Munger W.E., Kozlosky C., Vandenbos T., Price V.,
RA Lyman S., Gerard N.P., Gerard C., Cerretti D.P.;
RA "Molecular characterization of the interleukin-8 receptor.";
RL Biochem. Biophys. Res. Commun. 179:784-789(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ALBINO; TISSUE=Neutrophils;
RX MEDLINE=91056034; PubMed=1700779;
RA Thomas K.M., Pyun H.Y., Navarro J.;
RT "Molecular cloning of the fMet-Leu-Phe receptor from neutrophils.";

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J. Biol. Chem. 265:20061-20064(1990).
[3]
RN SEQUENCE FROM N.A.
RP TISSUE=Neutrophils;
RX MEDLINE=92148149; PubMed=1737938;
RA Lee J., Kuang W.-J., Rice G.C., Wood W.I.;
RT "Characterization of complementary DNA clones encoding the rabbit
IL-8 receptor.";
RL J. Immunol. 148:1261-1264(1992).
CC 1- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC MESSENGER SYSTEM.
CC 1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC 1- TISSUE SPECIFICITY: NEUTROPHILS.
CC 1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC 1- CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE THE RECEPTOR FOR
CC FMET-LEU-PHE (N-FORMYL PEPTIDE RECEPTOR).
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CC -----
CC EMBL; M74240; AAA31375.1; -
CC EMBL; M58021; AAA31377.1; -
CC EMBL; M82873; AAA31376.1; -
CC PIR; A23669; A23669.
CC PIR; A46483; A46483.
CC PIR; JQ1231; JQ1231.
CC GCRDB; GCR_0107; -
CC GCRDB; GCR_0108; -
CC GCRDB; GCR_0298; -
CC InterPro: IPR000174; -
CC InterPro: IPR000276; -
CC InterPro: IPR001355; -
CC Pfam: PF00001; 7tm1.1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PRINTS; PR00427; INTRLEUKIN8R.
CC PRINTS; PR00572; INTRLEUKIN8R.
CC PROSITE; PS00237; G_PROTEIN_RECP_FL_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECP_FL_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Chemotaxis.
KW DOMAIN 1 40 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 41 67 1 (POTENTIAL).
FT DOMAIN 68 73 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 74 92 2 (POTENTIAL).
FT DOMAIN 93 114 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 115 138 3 (POTENTIAL).
FT DOMAIN 139 159 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 160 184 4 (POTENTIAL).
FT DOMAIN 185 204 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 205 232 5 (POTENTIAL).
FT DOMAIN 233 247 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 248 270 6 (POTENTIAL).
FT DOMAIN 271 290 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 291 313 7 (POTENTIAL).
FT DOMAIN 314 355 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 7 7 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 21 21 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 115 192 BY SIMILARITY.
FT CONFLICT 90 111 DALLFALTPWAVSKKGVIFG ->
FT CONFLICT 146 147 HA -> QS (IN REF. 2).
FT CONFLICT 204 204 R -> C (IN REF. 2).
FT CONFLICT 287 288 DI -> EL (IN REF. 2).
SQ SEQUENCE 355 AA; 40622 MW; EFE49ACB9D1E0F21 CRC64;

```


OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN
 RA Li Y., Feng J., Templeton J.W.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
 CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
 CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
 CC G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
 CC AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC EMBL; U19947; AAA84996.1;
 CC GCRDB; GCR_1224;
 CC InterPro; IPR000174;
 CC InterPro; IPR000276;
 CC Pfam; PF00001; 7tm.1; 1.
 CC PRINTS; PR00237; GPCRHHODOPS.
 CC PRINTS; PR00427; INTRLEUKIN8.
 CC PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
 CC PROSITE; PS0262; G_PROTEIN_RECEPTOR_F1_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein;
 CC Chemotaxis.
 CC DOMAIN 1 48 EXTRACELLULAR (POTENTIAL).
 CC TRANSSEM 49 75 1 (POTENTIAL).
 CC DOMAIN 76 84 2 (POTENTIAL).
 CC TRANSSEM 85 105 2 (POTENTIAL).
 CC DOMAIN 106 120 3 (POTENTIAL).
 CC TRANSSEM 121 142 3 (POTENTIAL).
 CC DOMAIN 143 163 3 (POTENTIAL).
 CC TRANSSEM 164 183 4 (POTENTIAL).
 CC DOMAIN 184 208 5 (POTENTIAL).
 CC TRANSSEM 209 231 5 (POTENTIAL).
 CC DOMAIN 232 251 6 (POTENTIAL).
 CC TRANSSEM 252 273 6 (POTENTIAL).
 CC DOMAIN 274 294 7 (POTENTIAL).
 CC TRANSSEM 295 315 7 (POTENTIAL).
 CC DOMAIN 316 360 7 (POTENTIAL).
 CC DISULFID 119 196 BY SIMILARITY.
 CC CARBOHYD 10 10 N-LINKED (GLCNAC...) (POTENTIAL).
 CC CARBOHYD 24 24 N-LINKED (GLCNAC...) (POTENTIAL).
 CC SEQUENCE 360 AA; 40625 MW; 9A7F70C982A632D1 CRC64;
 Query Match 34.0%; Score 644.5; DB 1; Length 360;
 Best Local Similarity 42.8%; Pred. No. 2.2e-34;
 Matches 142; Conservative 57; Mismatches 112; Indels 21; Gaps 9;
 QY 27 APCRRSSSPG-YLYRTIAYSLICVLGLNLIIVITFAFYKKARSMTDYYLLNMAIADIL 85
 DB 37 SPCEISTETLNKAYVWVIDALVFLSLGSLVLLVILYSRIGRSVTDYLLNMAIADIL 96
 QY 86 FVLTLFWANSHATGAWFVSNATKLLKGIYAINFCGMLLITCTISMDYIAIVQATKSF 145
 DB 97 FAMLPLIWTASKARG-WVFGTPLCKVWSLLKEVNFYSIGILLACISMDRYLAIVHAT--- 152
 QY 146 RLRSRTLPSS---KIICLVWGLSVIISSSTFVFNQKYNTOGSD-VCEPKQTV-SEPI 199
 DB 153 ----RTLTQKWHWVKFICGLWALSIVILALPIFIREAYPPYSDLVC---YEDLGANTT 205
 QY 200 RWKLLMLGLELFGFFIPLMFMIFCYTFIVKTLVQAQNSKRHKAIKRVIAVAVLVFLACQI 259

DB 206 KWRIMRVLPOTFGFLLPLLVMLFCYGTFLTLFSAQMGHKKRAMRVIFAVVVLFCWL 265
 QY 260 PHNMVLLV-TAANLGKMRSCSEKLYCTKTVTVEVLAFHLHCLLPVLYAFTGQKERNYF 318
 DB 266 PYNLVLIADTLMRAHVIAETCORRNDIGRALDATEILFLHSCLNPLIYVFIGQKFRHGL 325
 QY 319 LKILKDLWCVRKY--KSSGFCAGRYSGENIS 348
 DB 326 LKIMAIHGLISKEFLAKDGRFSFVSSSGNS 357
 RESULT 11
 IL8B_RABIT STANDARD; PRT; 358 AA.
 ID IL8B_RABIT
 AC P35344;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GRO/MGSA
 DE RECEPTOR).
 GN IL8RB OR CXCR2.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ALBINO; TISSUE=Blood;
 RX MEDLINE=94230294; PubMed=8175642;
 RA Prado G.N., Thomas K.M., Suzuki H., Larosa G.J., Wilkinson N.C.,
 RA Folco E., Navarro J.;
 RT "Molecular characterization of a novel rabbit interleukin-8 receptor
 RT isotype".
 RL J. Biol. Chem. 269:12391-12394(1994).
 CC -1- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
 CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
 CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
 CC G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER SYSTEM. THE AFFINITY OF THIS RECEPTOR IS IL-8 >> NAP-2 >
 CC MGSA (GRO).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREFERENTIALLY IN NEUTROPHILS.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC EMBL; L24445; AAA31378.1;
 CC PIR; A53752; A53752.
 CC GCRDB; GCR_0861;
 CC InterPro; IPR000057;
 CC InterPro; IPR000174;
 CC InterPro; IPR000276;
 CC Pfam; PF00001; 7tm.1; 1.
 CC PRINTS; PR00237; GPCRHHODOPS.
 CC PRINTS; PR00427; INTRLEUKIN8.
 CC PRINTS; PR00573; INTRLEUKIN8R.
 CC PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
 CC PROSITE; PS0262; G_PROTEIN_RECEPTOR_F1_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein;
 CC Chemotaxis.
 CC DOMAIN 1 46 EXTRACELLULAR (POTENTIAL).
 CC TRANSSEM 47 73 1 (POTENTIAL).
 CC DOMAIN 74 82 2 (POTENTIAL).
 CC TRANSSEM 83 103 2 (POTENTIAL).
 CC DOMAIN 104 118 3 (POTENTIAL).
 CC TRANSSEM 119 140 3 (POTENTIAL).

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DR      EMBL; X91113; CAA62563.1;
DR      HSP; P34996; 1DDD;
DR      InterPro; IPR000276;
DR      Pfam; PF00001; 7tm1; 1;
DR      PROSITE; PS00237; G_PROTEIN_RECF_F1_1; 1;
DR      PROSITE; PS0262; G_PROTEIN_RECF_F1_2; 1;
KW      G-protein coupled receptor; Transmembrane; Glycoprotein;
KW      Chemotaxis.
FT      NON_TER      1      1
FT      DOMAIN      <1      45      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM      46      72      1 (POTENTIAL).
FT      DOMAIN      73      81      CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM      82      102      2 (POTENTIAL).
FT      DOMAIN      103      117      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM      118      139      3 (POTENTIAL).
FT      DOMAIN      140      160      CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM      161      180      4 (POTENTIAL).
FT      DOMAIN      181      205      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM      206      228      5 (POTENTIAL).
FT      DOMAIN      229      248      CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM      249      270      6 (POTENTIAL).
FT      DOMAIN      271      291      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM      292      312      7 (POTENTIAL).
FT      DOMAIN      313      >353      CYTOPLASMIC (POTENTIAL).
FT      DISULFID      116      193      BY SIMILARITY.
FT      CARBOHYD      19      19      N-LINKED (GLCNAC. .) (POTENTIAL).
FT      NON_TER      353      353
FT      SEQUENCE      353 AA; 39998 MW; E745ACD9EC10C1E2 CRC64;

Query Match      33.6%; Score 636.5; DB 1; Length 358;
Best Local Similarity      42.7%; Pred. No. 7.1e-34;
Matches 140; Conservative 59; Mismatches 116; Indels 13; Gaps 9;

QY      27 APCR-RSGSPGYLYRIAYSLICVLGLNGLVITFAFYKARSMTDVYLLNMAIADIL 85
DB      35 APCRSLETSYVLLITVILFLLSLGNSLVMLVILYSRSTCSVTDVYLLNLAIDL 94
QY      86 FVLTPFWAVSHATGAWFSNATCKLLKGIYAINFCGMLLLTCISMDRYIAIVQATKSF 145
DB      95 FATLPIWAASKVHG-WTEGTPLCCKVSVLVKEVNFYSGILLACISVDRLAIVHATRM 153
QY      146 RLRSRTLPKSKICLVWGLSVIISSTVFV-NQNTQGSDDVCEPKYQTV-SEPIRWKL 203
DB      154 -IOKRHL--VKFICLSMWGVSILSLPILLFRNAIPPPNSPVC---YEDMGNSTAKRM 207
QY      204 LMLGLELFGFFIPLMFIMFYCTFIVKTLVQAQNSKRHRAIRVIAVVLVFLACQIPHNH 263
DB      208 VLRLPQTEGFILPLVLMFCYVFTLRTLFAHMGQKHRAIRVIAVVLVFLCWLPLYNL 267
QY      264 VLLV-TAANLGMNRSQCEKLGITYTKTVTEVLAFHCLNPLVYAFIGQKFRNYFKIL 322
DB      268 VLLTDTLMRTHVIOETCERRNDIDRALDATEILGFLHCLNPLIYAFIGQKFRYGLKIL 327
QY      323 KDLWCVRKY--KSGFCAGRYSENIS 348
DB      328 AAHGLISKEFLAKESRPSVASSSGNTS 355

RESULT 12
IL8B_PANTR      STANDARD;      PRT;      353 AA.
AC      Q28807;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DE      HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (FRAGMENT).
GN      IL8RB OR CXCR2.
OS      Pan troglodytes (Chimpanzee).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX      NCBI_TaxID=9598;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=96175151; PubMed=9110929;
RA      Alvarez V., Coto E., Setien F., Gonzalez S., Gonzalez-Roces S.,
RA      Lopez-Larrea C.;
RT      "Characterization of interleukin-8 receptors in non-human primates.";
RL      Immunogenetics 43:261-267(1996).
CC      -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC      NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC      CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC      G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC      MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
CC      AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
CC      -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC      -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
-----

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CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
 CC AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide Cdw128b entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw128b.htm".
 CC -----
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 CC -----

DR EMBL; M73969; AA83148.1; -
 DR EMBL; M94582; AAA36108.1; -
 DR EMBL; M99412; AAC14460.1; -
 DR EMBL; L19593; AAB59437.1; -
 DR EMBL; U11869; AAB60656.1; -
 DR PIR; A39446; A39446
 DR PIR; A53611; A53611.
 DR HSP; P34996; IDDD.
 DR GCRDB; GCR_0077; -
 DR GCRDB; GCR_0610; -
 DR GCRDB; GCR_1001; -
 DR GCRDB; GCR_1339; -
 DR GCRDB; GCR_1831; -
 DR MIM; 146928; -
 DR InterPro; IPR000057; -
 DR InterPro; IPR000174; -
 DR InterPro; IPR000276; -
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GCRRHODPSN.
 DR PRINTS; PR00427; INTRLEUKIN8R.
 DR PRINTS; PR00573; INTRLEUKIN8R.
 DR PROSITE; PS00237; G-PROTEIN_RECEPTOR_F1.1; 1.
 DR PROSITE; PS0262; G-PROTEIN_RECEPTOR_F1.2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Chemotaxis.
 FT DOMAIN 1 48 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 49 75 1 (POTENTIAL).
 FT DOMAIN 76 84 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 85 105 2 (POTENTIAL).
 FT DOMAIN 106 120 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 121 142 3 (POTENTIAL).
 FT DOMAIN 143 163 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 164 183 4 (POTENTIAL).
 FT DOMAIN 184 208 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 209 231 5 (POTENTIAL).
 FT DOMAIN 232 251 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 252 273 6 (POTENTIAL).
 FT DOMAIN 274 294 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 295 315 7 (POTENTIAL).
 FT DOMAIN 316 360 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 22 22 N-LINKED (GLUCNA... (POTENTIAL).
 FT DISULFID 119 196 BY SIMILARITY.
 SQ SEQUENCE 360 AA; 40759 MW; 564F04A8BCC0A197 CRC64;

Query Match 33.2%; Score 629.5; DB 1; Length 360;
 Best Local Similarity 43.4%; Pred. No. 2e-33;
 Matches 132; Conservative 56; Mismatches 97; Indels 19; Gaps 8;
 Qy 27 APCR-RSGSSPGYVRIAYSLICVGLGNILVITFAFYKARSMTDVLNMAIADIL 85
 Db 37 APCPESELEINKYFVVIYVFLSLGSLVMLVILYSRVSVTDVLLNLAADLL 96
 Qy 86 FVLTLPFWAVSHATCAWFSNATKLLKGIYAINFCNGLMLLTICISMDRYAIQVATKSF 145
 Db 97 FALTLPWAASKVNG-WIFGTPLCKVWSLLKEVNFYSGILLACISVDRYLAIVHAT--- 152

Qy 146 RLRSRTLPSS-----KIICLVVWGLSVIISSTTFVFNQK-YNTQGSDDVCERKYQTV-SPEI 199
 Db 153 ----RTLQKRYLVKFCICLSIWGLSLLALPVLFRRTVYSSNVPAC---YEDMGNTA 205
 Qy 200 RWKLLMLGLELLFGFFPLPMFICFYFVTKVLVQAQNSKHKAIKRVIIIVVFLACQI 259
 Db 206 NWRMLRLIFQSGFIVPLFMFCYGTFLTRTFKAHMGOKHRAMRVIFAIVLFLCWL 265
 Qy 260 PHNVLLV-TAANLGNKMRSCSEKLIGYTKVTVEFLAFLHCLNPLVLYAFIGOKRNYF 318
 Db 266 PYNVLVADTLMTQVTOETCERRNHDRLADTEILGILHCLNPLIYAFIGOKFRHGL 325
 Qy 319 LKIL 322
 Db 326 LKIL 329
 RESULT 15
 IL8B_GORGO
 ID IL8B_GORGO STANDARD; PRT; 353 AA.
 AC Q28422;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (FRAGMENT).
 GN IL8RB OR CXCR2.
 OS Gorilla gorilla gorilla (Lowland gorilla).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Gorilla.
 OC NCBI_TaxID=9595;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=96175151; PubMed=9110929;
 RA Alvarez V., Coto E., Setien F., Gonzalez S., Gonzalez-Roces S.,
 RA Lopez-Larrea C.;
 RA "Characterization of Interleukin-8 receptors in non-human primates";
 RL Immunogenetics 43:261-267(1996).
 CC -1- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
 CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
 CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
 CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
 CC AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 CC EMBL; X91114; CAA62564.1; -
 CC HSP; P34996; IDDD.
 DR InterPro; IPR000276; -
 DR Pfam; PF00001; 7tm_1; 1.
 DR PROSITE; PS00237; G-PROTEIN_RECEPTOR_F1.1; 1.
 DR PROSITE; PS0262; G-PROTEIN_RECEPTOR_F1.2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Chemotaxis.
 FT DOMAIN 1 45 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM <1 45 1 (POTENTIAL).
 FT DOMAIN 76 72 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 73 81 2 (POTENTIAL).
 FT DOMAIN 82 102 3 (POTENTIAL).
 FT TRANSMEM 103 117 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 118 139 3 (POTENTIAL).
 FT DOMAIN 140 160 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 161 180 4 (POTENTIAL).
 FT DOMAIN 181 205 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 206 228 5 (POTENTIAL).

FT	DOMAIN	229	248	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	249	270	6 (POTENTIAL).
FT	DOMAIN	271	291	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	292	312	7 (POTENTIAL).
FT	DOMAIN	313	>353	CYTOPLASMIC (POTENTIAL).
FT	DISULFID	116	193	BY SIMILARITY.
FT	CARBOHYD	19	19	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	NON_TER	353	353	
SQ	SEQUENCE	353 AA;	39919 MW;	1FF04E31A7E825E4 CRC64;
Query Match 32.9%; Score 623.5; DB 1; Length 353;				
Best Local Similarity 43.1%; Pred. No. 4.6e-33;				
Matches 131; Conservative 56; Mismatches 98; Indels 19; Gaps 8;				
Qy	27	APCR-RSGSSPGYRIAYSLICVLGLNIIWITFAFYKKARSTDDVYLLNMAIADIL	85	
Db	34	SPCEPESLEINKYFVYIIYALVFLLSLLGNSLVILYRSVGRSVTDVYLLNLALADLL	93	
Qy	86	FVLTLPFWAVSHATGAWFESNATCKLLKGIYAINFNCMLLLTCISMDRYIAIVQATKSF	145	
Db	94	FALTLPWAASKVNG-WIFGTCLCKVWSLLKEVNFYSGILLACISVDRYLAIVHAT---	149	
Qy	146	RLRSTLPRS----KIICLVWGLSVIISSTFVFNQK-YNTQGSVDCEPKYQTV-SEPI	199	
Db	150	---RTLQKRYLVKRFICLSINGLSLLALPVLFRRTIYPSNVSPVC---YEDMGNTA	202	
Qy	200	RWKLMLGLELFGFPIPLMFIFCYTFIVKTIVQAQNSKRHKAIRVIAVVLVFLACQI	259	
Db	203	NWRMLRLPQSGFGFIVPLIIMLFYCGFTLTLFKAHMGOKHRAMRVIFAVWLIFLLCWL	262	
Qy	260	PHNMVLLV-TAANLGKMRSCOSEKLGITKTVTVEFLAFHCLNPVLYAFIGOKERNYF	318	
Db	263	PYNVLLADTLMTQVIQETCERRNHINOALDATEILGILHSCLNPLIYAFIGOKFCHGL	322	
Qy	319	LKIL	322	
Db	323	LKIL	326	

Search completed: May 23, 2001, 15:36:16
Job time: 647 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:24:54 ; Search time 189.03 Seconds
(without alignments)
226.318 Million cell updates/sec

Title: US-08-887-977-10
Perfect score: 1894
Sequence: 1 MFSTPVKILQCILHITOL.....NISQTSERANDNASSFTM 365

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPTREMBL_15:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_unclassified:*
 - 13: sp_vertebrate:*
 - 14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1365.5	72.1	367	11 Q9R1V0	Q9R1V0 mus musculus
2	613.5	32.4	360	4 Q9ULY6	Q9ULY6 homo sapien
3	610.5	32.2	360	4 Q9ULY7	Q9ULY7 homo sapien
4	599.5	31.7	343	6 Q9N0Z0	Q9N0Z0 cercocebus
5	595.5	31.4	343	6 Q9XT45	Q9XT45 macaca mula
6	593.5	31.3	369	4 Q9U0Q6	Q9U0Q6 homo sapien
7	583.5	30.8	342	6 Q9TW16	Q9TW16 pan troglod
8	578.5	30.5	368	13 Q42444	Q42444 oncorhynch
9	556	29.4	360	6 Q18793	Q18793 macaca mula
10	548.5	29.0	373	11 Q55193	Q55193 rattus norv
11	547.5	28.9	352	6 Q77776	Q77776 cercocebus
12	547	28.9	352	6 Q9TV44	Q9TV44 cercoptithec
13	546.5	28.9	339	6 Q9TUS4	Q9TUS4 lemur varie
14	545.5	28.8	339	6 Q9TUS3	Q9TUS3 lemur catia
15	545.5	28.8	339	6 Q9TUS5	Q9TUS5 erythrocebu
16	543.5	28.7	339	6 Q9TUS6	Q9TUS6 erythrocebu
17	542.5	28.6	339	6 Q9TUS7	Q9TUS7 erythrocebu
18	542.5	28.6	352	6 Q9TV47	Q9TV47 cercoptithec
19	541.5	28.6	339	6 Q9TUS6	Q9TUS6 papio cynoc

20	541.5	28.6	339	6	Q9TQX2	Q9TQX2 erythrocebu
21	541.5	28.6	339	6	Q9TQV7	Q9TQV7 cercoptithec
22	541.5	28.6	352	6	Q9MZA1	Q9MZA1 lagotrix 1
23	540.5	28.5	352	6	Q9XT76	Q9XT76 cercoptithec
24	540	28.5	339	6	Q9TUV8	Q9TUV8 saguinus sp
25	539.5	28.5	334	6	Q9TUV7	Q9TUV7 erythrocebu
26	539.5	28.5	352	6	Q9XT12	Q9XT12 cercoptithec
27	539.5	28.5	352	6	Q9TV49	Q9TV49 cercocebus
28	539.5	28.5	352	6	Q9TSQ7	Q9TSQ7 cercoptithec
29	538.5	28.4	339	6	Q9TUV3	Q9TUV3 callitrix
30	538.5	28.4	339	6	Q9TUV4	Q9TUV4 mandrillus
31	538.5	28.4	340	6	Q9TUV2	Q9TUV2 macaca mula
32	538.5	28.4	352	6	Q9TV48	Q9TV48 cercoptithec
33	537.5	28.4	339	6	Q9TUV7	Q9TUV7 macaca fusc
34	537.5	28.4	339	6	Q9TUV6	Q9TUV6 macaca fusc
35	537.5	28.4	339	6	Q9TUV5	Q9TUV5 macaca mula
36	537.5	28.4	339	6	Q9TUV1	Q9TUV1 macaca mula
37	537.5	28.4	339	6	Q9TUV9	Q9TUV9 macaca mula
38	537.5	28.4	339	6	Q9TUV7	Q9TUV7 macaca mula
39	537.5	28.4	339	6	Q9TUV6	Q9TUV6 macaca neme
40	537.5	28.4	339	6	Q9TUT1	Q9TUT1 macaca neme
41	537.5	28.4	339	6	Q9TUT7	Q9TUT7 cercoptithec
42	537.5	28.4	339	6	Q9TUT3	Q9TUT3 erythrocebu
43	537.5	28.4	339	6	Q9TUT2	Q9TUT2 erythrocebu
44	537.5	28.4	339	6	Q9TSQ2	Q9TSQ2 cercoptithec
45	537.5	28.4	339	6	Q9TSN3	Q9TSN3 macaca fusc

ALIGNMENTS

RESULT	1
Q9R1V0	
ID	Q9R1V0 PRELIMINARY; PRT; 367 AA.
AC	Q9R1V0
DT	01-MAY-2000 (TREMREL. 13, Created)
DT	01-MAY-2000 (TREMREL. 13, Last sequence update)
DE	01-JUN-2000 (TREMREL. 14, Last annotation update)
DE	CC CHEMOKINE LARC SPECIFIC RECEPTOR.
GN	MCCR6.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Tanaka Y.;
RT	"Molecular Cloning of Murine Homologue of CCR6, the Specific Receptor for CC Chemokine LARC."
RL	Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AB016031; BAA82443.1;
DR	INTERPRO; IPR000190;
DR	INTERPRO; IPR000276;
DR	INTERPRO; IPR000355;
DR	PFAM; PF00001; 7tm_1; 1.
DR	PRINTS; PR00237; GPCRHHODOPSN.
DR	PRINTS; PR00635; ANGIOTENSINR.
DR	PRINTS; PR00657; CCHEMOKINER.
DR	PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW	Receptor.
SK	SEQUENCE 367 AA; 42082 MW; 207FD98B2F7A6DD3 CRC64;

Query Match	72.1%; Score 1365.5; DB 11; Length 367;
Best Local Similarity	78.8%; Pred. No. 4.8e-104;
Matches 256; Conservative	32; Mismatches 36; Indels 1; Gaps 1;
Oy	42 TAYSLICVLGLGNLTIVITFAFYKARSMTDYLNNMAIADILFVLTLPFWAVSHATCA 101
Db	43 TAYSLICVFLGLGNLMVMTVITFAFYKARSMTDYLNNMAITDILFVLTLPFWAVTHATNT 102
Oy	102 WYFSNATCKLLGIYAINFCNGLMLTCTISMDRYIAVQATKSFRRSRTLPKRIICLV 161

```

Db 103 WYFSDALCKLMKGTAVNFCNCGMLLACISMDRYIAIVQATKSFRVRSRTLTHSKVICVA 162
QY 162 VWGLSVIISSTFVFNQKYNTOGSDVCEPKYQTVSEPIRWKLLMLGLELFGFFIPLMF 221
Db 163 VWFISIISSPTFIENKVELQDQDCEPRYSVSEPIWKLLGLGLELFGFFIPLMF 222
QY 222 IFCYTFIVKTLVQAQNSKRHKAIRVIAIVLVFLACIQIPHNWVLLVTAANLGMKNSCQS 281
Db 223 VFCYLFIIKTLVQAQNSKRHKAIRVIAIVLVFLACIQIPHNWVLLVTAANTGKVARSCST 282
QY 282 EKLIGYTVTVTEVLAFLHCLAPLVYAFIGOKFRNRYFLAKLDLWCVRRKYKSSGFSACG 341
Db 283 EKVLATYRNAEVLAFHLSCLAPLVYAFIGOKFRNRYFLAKLDLWCVRRKYKSSGFSACG 342
QY 342 RYSEN-ISQTSSETADNDNASSFTM 365
Db 343 VYSESYISQTSSETVENDNASSFTM 367

RESULT 2
QY 09ULY6 PRELIMINARY; PRT; 360 AA.
AC 09ULY6;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TremBLrel. 14, Last annotation update)
DE B-CHEMOKINE RECEPTOR CCR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kato H., Tsuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki H.,
RA Hirai K., Tokunaga K.;
RT "New variations of human CC-chemokine receptors CCR3 and CCR4.";
RL Genes Immun. 1:97-104(1999).
DR EMBL; AB023891; BAA86968.1; -
DR INTERPRO; IPR000190; -
DR INTERPRO; IPR000248; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR000355; -
DR INTERPRO; IPR001277; -
DR INTERPRO; IPR002236; -
DR INTERPRO; IPR002239; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00241; ANGIOTENSINR.
DR PRINTS; PR00635; ANGIOTENSINR.
DR PRINTS; PR00645; LCR1ORPHANR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01106; CHEMOKINER1.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT VARIANT 178 178 S -> C.
SQ SEQUENCE 360 AA; 41386 MW; AAF0EA3AD1EAF6D2 CRC64;

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Query Match 32.4%; Score 613.5; DB 4; Length 360;
Best Local Similarity 38.8%; Pred. No. 1.3e-42;
Matches 135; Conservative 61; Mismatches 115; Indels 37; Gaps 10;

QY 28 PCRRSG-SSPCYLY-RIAYSLICVLGLNLIIVITFAFYKKARSMTDYYLLNMAIADIL 85
Db 28 PCTKEGKAFGELFPLPYLSLVFVGLGNSVVLVLFKYKRLRSMTDYYLLNLAISDL 87

QY 86 FVLTLPEWAVSHATGAWVFSNATCKLLKGIYAINFCNCGMLLTCISMDRYIAIVQATKSF 145
Db 88 FVFSLPFWGY-YAADOWVFGGLCKRMISWMYLVGVGSIFFVWMLSIDRYLAIVHAV--F 144

QY 146 RLRSRTLPKRSKIICLVWGLSVIISSTFVFNQKYNTOGSDVCEPKYQTVSEPIRWKLLM 205

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Db 145 SLRARTITYGVITSLATWSAVFASLPGLFLESTSYTERNHTYCKTKYSLNS--TTWKVLS 202
QY 206 LGLEL-LFGFFIPLMFIFCYTFIVKTLVQAQNSKRHKAIRVIAIVLVFLACIQIPHNW 264
Db 203 -SLEINILGLVPLIGIMLCYCSMIIRTLQHCNKKKNAKVMIAVAVVFLGFWPTYNIV 261
QY 265 LLVTAANLGMKNSRCSQSEKLGITYTKTVTEVLAFLHCLNPNVLYAFIGOKFRNRYFLKLD 324
Db 262 LFLTELVELEVLDQCTERVLDYAQATETELAFVHCCLNPIIYFFLGEKFKYILQLFK- 320
QY 325 LMCVRRKYKSSGFSACG-----YSENI--SRQTSSETADND 358
Db 321 -----TCRGLVLCQYGLLIQIYSADTPSSSYTQSTMDHD 355

RESULT 3
QY 09ULY7 PRELIMINARY; PRT; 360 AA.
AC 09ULY7;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TremBLrel. 14, Last annotation update)
DE B-CHEMOKINE RECEPTOR CCR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kato H., Tsuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki H.,
RA Hirai K., Tokunaga K.;
RT "New variations of human CC-chemokine receptors CCR3 and CCR4.";
RL Genes Immun. 1:97-104(1999).
DR EMBL; AB023889; BAA86966.1; -
DR INTERPRO; IPR000190; -
DR INTERPRO; IPR000248; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR000355; -
DR INTERPRO; IPR001277; -
DR INTERPRO; IPR002236; -
DR INTERPRO; IPR002239; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00241; ANGIOTENSINR.
DR PRINTS; PR00635; ANGIOTENSINR.
DR PRINTS; PR00645; LCR1ORPHANR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01106; CHEMOKINER1.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT VARIANT 130 130 V -> L.
SQ SEQUENCE 360 AA; 41388 MW; F52DA1A8D9DA7DDB CRC64;

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Query Match 32.2%; Score 610.5; DB 4; Length 360;
Best Local Similarity 38.8%; Pred. No. 2.3e-42;
Matches 135; Conservative 61; Mismatches 115; Indels 37; Gaps 10;

QY 28 PCRRSG-SSPCYLY-RIAYSLICVLGLNLIIVITFAFYKKARSMTDYYLLNMAIADIL 85
Db 28 PCTKEGKAFGELFPLPYLSLVFVGLGNSVVLVLFKYKRLRSMTDYYLLNLAISDL 87

QY 86 FVLTLPEWAVSHATGAWVFSNATCKLLKGIYAINFCNCGMLLTCISMDRYIAIVQATKSF 145
Db 88 FVFSLPFWGY-YAADOWVFGGLCKRMISWMYLVGVGSIFFVWMLSIDRYLAIVHAV--F 144

QY 146 RLRSRTLPKRSKIICLVWGLSVIISSTFVFNQKYNTOGSDVCEPKYQTVSEPIRWKLLM 205
Db 145 SLRARTITYGVITSLATWSAVFASLPGLFLESTSYTERNHTYCKTKYSLNS--TTWKVLS 202

QY 206 LGLEL-LFGFFIPLMFIFCYTFIVKTLVQAQNSKRHKAIRVIAIVLVFLACIQIPHNW 264

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Db 203 -SLEINILGLVPLGIMLCFCYSMIITLQHCNKKNAVKMIFAVVVLFLGFWTPTNIV 261
 Qy 265 LLVTAANLGMNRSGQSEKLGITKVTVEFLAPLHCLNPLVYAFYQKERNYFLKLKD 324
 Db 262 LFLTEIVLELVQDCTFERYLDAIOATETLAFVHCLNPLIIFFLGKFRKYLQLFK- 320
 Qy 325 LMCVRRYKSGSFSCAGR-----YSNII--SROTSETADND 358
 Db 321 -----TCRGLFVLCQCGLLQLIYSADTPSSSYTQSTMDHD 355

RESULT 4
 Q9N020 ID Q9N020 PRELIMINARY; PRT; 343 AA.
 AC Q9N020
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE STRL33.
 OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Cercopithecus.
 OX NCBI_TaxID=9531;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20261727; PubMed=10799581;
 RA Pohlmann S., Lee B., Melster S., Krumbiegel M., Leslie G., Doms R.W.,
 RA Kirchhoff F.;
 RT "Simian immunodeficiency virus utilizes human and sooty mangabey but
 RT not rhesus macaque STRL33 for efficient entry.";
 RL J. Virol. 74:5075-5082(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Pohlmann S., Lee B., Meister S., Krumbiegel M., Leslie G., Doms R.W.,
 RA Kirchhoff F.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF237559; AAF68392.1;
 SQ SEQUENCE 343 AA; 39588 MW; A75B7A0751C13455 CRC64;

Query Match 31.7%; Score 599.5; DB 6; Length 343;
 Best Local Similarity 34.7%; Pred. No. 1.8e-41;
 Matches 126; Conservative 77; Mismatches 107; Indels 53; Gaps 8;
 Qy 12 QSILHITOLILRCYCPCRRSGSPGYLYRIAYSLICVLGLNGLNVLWITFAFYKKARM 71
 Db 25 QDFLQFRKVFLLPC-----MYLVFVCGLVGNSLVLSIFHYHKLQSL 66
 Qy 72 TDVYLNNMAIADILFVLTPFWAVSHATGAWVFSNATCKLLKGIAINFCGMLLTCTIS 131
 Db 67 TDVFLVNLPLADLVFVCTLPFWAYA-GIHEWIFGVQVCKTLGIVTYNFTYMLTCTIT 125
 Qy 132 MDRIYTAIVOATKSFRLSRSTLPRSKIIICLVWGLSVIISSTVFVNQKYNQTSQDVCEPK 191
 Db 126 VDRFVIVVVKATRAYNQAKRWGKVIKLLIWIISLVSLPQIIYGNVFNLD-KLICRYH 184
 Qy 192 YQTVSEPIRWKLLMLGLELFFGLFPLMFIMFYCTFIKTLVQAQNSKRHKAIRVIAV 251
 Db 126 VDRFVIVVVKATRAYNQAKRWGKVIKLLIWIISLVSLPQIIYGNVFNLD-KLICRYH 184
 Qy 192 YQTVSEPIRWKLLMLGLELFFGLFPLMFIMFYCTFIKTLVQAQNSKRHKAIRVIAV 251
 Db 185 DEEIS-----TVLATQMTLGFLLPMLMIVCYSVIITLLHAGGFQKHSRLKIIFLVM 238
 Qy 252 LVFLACQIHPHNVLLVTAANLGMNRSCQSE-----KLIGYTKVTVEFLAFLHCLNPLV 307
 Db 239 AVFLTQTPFNVLKLI-----RSTHWEYIAMSFTHTIIVTAIYLAIRACLNPLV 289
 Qy 308 AFIGOKFRNYFLKILKDLWC-----VRRYKSGSFCAGRYSENI SROTSETADNDNASS 362
 Db 290 AFVSLKFRKFWKLVKIDICLPYLGVSQWKS-----SEDNKTFSASHNVEATSM 340
 Qy 363 FTM 365
 Db 341 FOL 343

RESULT 6
 Q9U0Q6 ID Q9U0Q6 PRELIMINARY; PRT; 369 AA.

RESULT 5
 Q9XT45 ID Q9XT45 PRELIMINARY; PRT; 343 AA.
 AC Q9XT45
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE CHEMOKINE RECEPTOR BONZO.
 GN STRL33
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Margulies B.J., Hauer D.A., Clements J.E.;
 RT "Identification of Thirteen Rhesus Macaque Chemokine Receptors.";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF124380; AAD31419.1;
 DR INTERPRO; IPR000248;
 DR INTERPRO; IPR000276;
 DR INTERPRO; IPR000355;
 DR INTERPRO; IPR001277;
 DR INTERPRO; IPR002235;
 DR PFAM; PF00001; 7tm.1.1;
 DR PRINTS; PR00237; GPCRHDODPSN.
 DR PRINTS; PR00241; ANGIOTENSINR.
 DR PRINTS; PR00645; LCRIORPHANR.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01105; BONZOORPHANR.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 KW Receptor.
 SQ SEQUENCE 343 AA; 39423 MW; 48DB2544949EB83F CRC64;

Query Match 31.4%; Score 595.5; DB 6; Length 343;
 Best Local Similarity 34.7%; Pred. No. 3.7e-41;
 Matches 126; Conservative 76; Mismatches 108; Indels 53; Gaps 8;
 Qy 12 QSILHITOLILRCYCPCRRSGSPGYLYRIAYSLICVLGLNGLNVLWITFAFYKKARM 71
 Db 25 QDFLQFRKVFLLPC-----MYLVFVCGLVGNSLVLSIFHYHKLQSL 66
 Qy 72 TDVYLNNMAIADILFVLTPFWAVSHATGAWVFSNATCKLLKGIAINFCGMLLTCTIS 131
 Db 67 TDVFLVNLPLADLVFVCTLPFWAYA-GIHEWIFGVQVCKTLGIVTYNFTYMLTCTIT 125
 Qy 132 MDRIYTAIVOATKSFRLSRSTLPRSKIIICLVWGLSVIISSTVFVNQKYNQTSQDVCEPK 191
 Db 126 VDRFVIVVVKATRAYNQAKRWGKVIKLLIWIISLVSLPQIIYGNVFNLD-KLICRYH 184
 Qy 192 YQTVSEPIRWKLLMLGLELFFGLFPLMFIMFYCTFIKTLVQAQNSKRHKAIRVIAV 251
 Db 185 DEEIS-----TVLATQMTLGFLLPMLMIVCYSVIITLLHAGGFQKHSRLKIIFLVM 238
 Qy 252 LVFLACQIHPHNVLLVTAANLGMNRSCQSE-----KLIGYTKVTVEFLAFLHCLNPLV 307
 Db 239 AVFLTQTPFNVLKLI-----RSTHWEYIAMSFTHTIIVTAIYLAIRACLNPLV 289
 Qy 308 AFIGOKFRNYFLKILKDLWC-----VRRYKSGSFCAGRYSENI SROTSETADNDNASS 362
 Db 290 AFVSLKFRKFWKLVKIDICLPYLGVSQWKS-----SEDNKTFSASHNVEATSM 340
 Qy 363 FTM 365
 Db 341 FOL 343

AC Q9U0Q6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE CHEMOKINE RECEPTOR CCR9 (CC CHEMOKINE RECEPTOR 9A).
 GN CCR9.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zaballos A., Gutierrez J., Varona R., Ardavin C., Marquez G.;
 RT "Identification of the orphan chemokine receptor GPR-9-6 as CCR9, the
 RT receptor for the chemokine TECK.";
 RL J. Immunol. 162:5671-5675(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yu C.-R., Peden K.W.C., Farber J.M.;
 RT "CCR9A and CCR9B, Two Receptors for the Chemokine CCL25 (TECK/Ckbeta-
 RT 15).";
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ132337; CAB43477.1;
 DR EMBL: AF145439; AAF66699.1;
 DR INTERPRO: IPR000248;
 DR INTERPRO: IPR000276;
 DR INTERPRO: IPR000355;
 DR INTERPRO: IPR001277;
 DR INTERPRO: IPR001718;
 DR PFAM: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHHODOPSN.
 DR PRINTS: PR00241; ANGIOTENSINR.
 DR PRINTS: PR00641; CHEMOKINER.
 DR PRINTS: PR00645; LCRIORPHANR.
 DR PRINTS: PR00657; CCHEMOKINER.
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 KW Receptor.
 SQ SEQUENCE 369 AA; 42015 MW; F27CEA0CFB66844C CRC64;

Query Match 31.3%; Score 593.5; DB 4; Length 369;
 Best Local Similarity 40.2%; Pred. No. 5.9e-41;
 Matches 115; Conservative 64; Mismatches 104; Indels 3; Gaps 3;

QY 44 YSLICVLGILGILNLTAFYKARSMIDVLLNMAIADILEVLTLFPWAVSHATCAW 103
 DB 55 YWLIVGALNSLVILVYCTRYKVTMDMLLNIAIADLLEVLTLFPWAVIA-AAQWK 113
 QY 104 FSNATCKLKGIIYAINFCGMILLTICISMDRYIAIQAATKSFRLSRTLPRSKIIICLVVW 163
 DB 114 FQTEWCKVNSMYKNFYSCVLLIMCISVDRIYIAQAAMRAHWREKRLLYSKWVCFTIW 173
 QY 164 GLSVIISSTFFVFNQYNTQGSVCEPKYQTVSEPTRWKLLMLGLELLFGFFIPLMPNIF 223
 DB 174 VLAALAIPEILYISQKEESGIAICTMVPYS-DESKLKSAVLTLLKVLGFFLPFVVMAC 232
 QY 224 CYTFIVKTLVQAQNSKRRAIRVIAVVELACQIPHNMVLLVTAANLGKMNRS-CQSE 282
 DB 233 CYTIIHTLIQAKSKKALKKATITVLVFLVSQPFICILLVQITIDAYAMFISCAVS 292
 QY 283 KLIGYTKTVEVLAFHCLCNPLVYAFIGQKFRNYFLKILKDLWCV 328
 DB 293 TNIDICFQVQTIAFHSCLNPLVYVFGFRDLVKTLKNLGCI 338

RESULT 7
 ID Q9TV16 PRELIMINARY; PRT; 342 AA.
 AC Q9TV16;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE G PROTEIN-COUPLED RECEPTOR STRL33.

OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=STRL33(BONZO);
 RC Brussel A., Pretet J.L., Girard M., Butor C.;
 RT "Sequences and Predicted Structures of Chimpanzee STRL33 (Bonzo) and
 RT gp15 (BOB).";
 RL AIDS Res. Hum. Retroviruses 15:0-0(1999).
 DR EMBL: AF084229; AAD52041.1;
 DR INTERPRO: IPR000248;
 DR INTERPRO: IPR000276;
 DR INTERPRO: IPR000355;
 DR INTERPRO: IPR001277;
 DR INTERPRO: IPR002235;
 DR PFAM: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHHODOPSN.
 DR PRINTS: PR00241; ANGIOTENSINR.
 DR PRINTS: PR00645; LCRIORPHANR.
 DR PRINTS: PR00657; CCHEMOKINER.
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 KW Receptor.
 SQ SEQUENCE 342 AA; 39273 MW; 5B58003797806B2A CRC64;

Query Match 30.8%; Score 593.5; DB 6; Length 342;
 Best Local Similarity 34.4%; Pred. No. 3.6e-40;
 Matches 125; Conservative 77; Mismatches 108; Indels 53; Gaps 8;

QY 12 QSLIHITOLILRCYCPCRRSGSPGYLYRIAYSLICVLGILGILNLTAFYKARSM 71
 DB 24 QDFLOFSKVFLPC-----MYLVFVCGLVGNSLVLVISIFYHKLQSL 65
 QY 72 TDVYLLNMAIADILEVLTLFPWAVSHATCAWVFSNATCKLKGIIYAINFCGMILLTICIS 131
 DB 66 TDVFLVNLPLADLVFVCTLPFWAYA-GIHEWVFGVGMCKSLGIVTINFTYTSMLITCIT 124
 QY 132 MDRIYIAVQATKSFRLSRTLPRSKIIICLVVWGLSVIISSTFFVFNQYNTQGSVCEPK 191
 DB 125 VDREIVVYKATKAYNQAKRTGWKVTSLLIWISLVSLPQIIYGNVFNLD-KLICGYH 183
 QY 192 YQTVSEPTRWKLLMLGLELLFGFFIPLMPNIFVYKTLVQAQNSKRRAIRVIAV 251
 DB 184 DEATIS-----TVVLATQMTGLFFIPLMTMVCYVIKTLHAGGQFKHSLKILFLVM 237
 QY 252 LVFLACQIPHNMVLLVTAANLGKMNRCQSE----KLIGYTKTVEVLAFHCLCNPLVLY 307
 DB 238 AVFLLTQMPFNLMKLI-----RSTHWEYVYAMTSFHYTMTVTEATYLRACLNPVLY 288
 QY 308 AFIGQKFRNYFLKILKDLWC-----VRRKYKSGFSGACGRYSENISROTSETADNDNASS 362
 DB 289 AFVSLKFRKFNKLVKIDIGCLPYLGVSQHWKS-----SEDSKTSFASHHNVEATSM 339
 QY 363 FTM 365
 DB 340 FOL 342

RESULT 8
 ID O42444 PRELIMINARY; PRT; 368 AA.
 AC O42444;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE INTERLEUKIN-8-LIKE RECEPTOR.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

```
OX NCBI_TaxID=8022;
RN SEQUENCE FROM N.A.
RA Zou J., Daniels G.D., Cunningham C., Secombes C.J.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR ENBL: AJ003159; CAA05917.1; -
DR INTERPRO: IPR000276; -
DR PFAM: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G-PROTEIN RECEPTOR; UNKNOWN.1.
SQ SEQUENCE 368 AA; 41523 MW; BE28E2D4C47E821A CRC64;

Query Match 30.5%; Score 578.5; DB 13; Length 368;
Best Local Similarity 38.0%; Pred. No. 9.8e-40;
Matches 123; Conservative 65; Mismatches 125; Indels 11; Gaps 5;

QY 44 YSLICVLGLGNILVW-ITFAFYKARSKMTDVTYLLNMAIDLVLTPFWAVSHATGAW 102
DB 54 YWSIVILGGGLNLTWVWYHLYHFQRKLTMTDIYLLNLAVALDFLGLTLPMAV-EANQGW 112
QY 103 VFSNATCKLKGIAINFCNCGMLLTCTISMDRYIAIVQATKFRSLRSLPRSKIIICLVV 162
DB 113 SFGGLCKVTSFAFYKINFEFSSMLLTCTISVDYVIVQVTHMAQNSKQRLSCSKFVCACV 172
QY 163 WGLSVIISSTVFVNQKYNQTSQSDVEPKYQTVSEPIRKWLMGLGLFGLFPIPLMFMI 222
DB 173 WLLAVLLALPEFMFANVKELDQGYCTVWYWS-NQNNRTKIVVLGLQICMGFCPLPLVNV 231
QY 223 FCYTFIVKTLVQAOANSKRHKAIRVIAIVLFLACIQIPHNWVLLVTAANLGMNRS-COS 281
DB 232 FCYAGIIITLTKTSFQKHAKRLVILVVAVFVLSQLPNSVNLVMEATQAANSTQTDCA 291
QY 282 EKLIGYKTVTEVLAFLHCLNPLVLYAFIGOKFRNVLKILKDLACVRRKYSKSGFSCAG 341
DB 292 AKRNVVSVLKSAYTHACLNPFLYVGVFRFRDILKLLRIYHCWPAKGL----- 344

RESULT 9
O18793 ID O18793 PRELIMINARY; PRT; 360 AA.
AC O18793
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE C-C CHEMOKINE RECEPTOR.
GN CCR2B.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Hauer D.A., Margulies B.J., Clements J.E.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR ENBL: AF013958; AAD11572.1; -
DR INTERPRO: IPR000248; -
DR INTERPRO: IPR000276; -
DR INTERPRO: IPR000355; -
DR INTERPRO: IPR001277; -
DR INTERPRO: IPR002236; -
DR INTERPRO: IPR002237; -
DR INTERPRO: IPR002240; -
DR PFAM: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00241; ANGIOTENSINR.
DR PRINTS: PR00645; LCR1ORPHANR.
DR PRINTS: PR00657; CCHENOKINER.

DR PRINTS; PRO1106; CHEMOKINER1.
DR PRINTS; PRO1107; CHEMOKINER2.
DR PRINTS; PRO1110; CHEMOKINERS.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR; UNKNOWN.1.
SQ SEQUENCE 360 AA; 41139 MW; 4B2552BCE913F99F CRC64;

Query Match 29.4%; Score 556; DB 6; Length 360;
Best Local Similarity 34.8%; Pred. No. 6.6e-38;
Matches 120; Conservative 67; Mismatches 130; Indels 28; Gaps 10;

QY 25 YCAPCRSGSP--GYLYRIAYSLSICVLGLGNILVITFAFYKARSKMTDVTYLLNMAIA 82
DB 28 YGAPCHKFDVKQIGAQLPLPLYSLVIFFGVGNLMVLVLLINCKKLSLTDIYLLNLAIS 87
QY 83 DILFVLTLFPWAYSHATGAWFVSNAATCKLLKGIAINFCNCGMLLTCTISMDRYIAIVQAT 142
DB 88 DLLFLITLPLWAHS--AANWVFGNAMCKLFTGLYHIGYGLGFIILLTDIYLAIVHAV 146
QY 143 KSFRLRSRTLPKSKIIICLVVWGLSVIISSTVFVNQKYNQTSQSDVEPKYQTVSEPIRWK 202
DB 147 --FALKARTVTFGVSVITWLVAVFASVPGIIFTKQEDSVVYICGYPF-----PRGW 199
QY 203 LLMGLLELFGFFIPLMFIPCYTFIVKTLVQAOQNSKRHKAIRVIAIVLFLACQIPH 261
DB 200 NFHTIMRNILGLVPLIMVICYSGILKTLRCRNEKKRRAVRLIFTIMIVFLFWTPY 259
QY 262 NMVLLVTAAN--LGKMNRSQSEKLGITYKTVTEVLAFLHCLNPLVLYAFIGOKFRNYFL 319
DB 260 NIVILLNTFOEFGLSN--CESTRQLDQATQVTTGLMTHCCINPIIYAFVGEKFRYLS 317
QY 320 KILKDLWCVRKRYKSGF--SCAGRYSENT---SROTSETADND 358
DB 318 MFF-----RKYITRFCKQCPVFRVETVDGVTSTNTPSTAEOE 355

RESULT 10
O55193 ID O55193 PRELIMINARY; PRT; 373 AA.
AC O55193
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 2 (C-C CKR-2) (CCR-2) (CCR2).
GN CMKBR2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE DAWLEY;
RX MEDLINE=98318173; PubMed=9655467;
RA Jiang Y., Salafian M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
RA deFebre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
RT "Chemokine receptor expression in cultured glia and rat experimental
RT allergic encephalomyelitis";
RL J. Neuroimmunol. 86:1-12(1998).
CC -!- FUNCTION: RECEPTOR FOR THE MCP-1 (JE), MCP-3 (FIC) AND MCP-5
CC CHEMOKINES. TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR
CC CALCIUM IONS LEVEL (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -!- TISSUE SPECIFICITY: EXPRESSED IN LUNG, SPLEEN, KIDNEY, THYMUS AND
CC MACROPHAGES.
CC -!- INDUCTION: IN ANIMALS IN WHICH EXPERIMENTAL ALLERGIC
CC ENCEPHALOMYELITIS (EAE) HAS BEEN INDUCED.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR ENBL: U77349; AAC03242.1; -
DR INTERPRO: IPR000276; -
DR INTERPRO: IPR000355; -
DR INTERPRO: IPR00237; -
DR PFAM: PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
```

[1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN-1208;
RA
RA Chen Z., Kwon D., Jin Z., Monard S., Telfer P., Jones M., Lu C.,
RA Agullar R., Ho D.D., Marx P.A.;
RT "Natural infection of a homozygous delta 24 CR5 red-capped mangabey
RT with a R2b-tropic simian immunodeficiency virus.";

DR EMBL; AF035220; AAD4401
DR INTERPRO: IPR000248: -

RT "Natural infectio

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:28:24 ; Search time 184.73 Seconds
(without alignments)
11.759 Million cell updates/sec

Title: US-08-887-977-10_COPY_1_38
Perfect score: 206
Sequence: 1 MFSTPVKILQCSILHITQLILRCYCPCRRSGSPGY 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues
Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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12: /SID56/gcgdata/geneseq/geneseq/AA1991.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	206	100.0	365	19	W48086		Human dendritic ce
2	206	100.0	365	21	Y97077		Primate (human) ch
3	55.5	27.4	292	20	Y29255		Amino acid sequenc
4	56	27.2	219	21	B43512		Human cancer assoc
5	56	27.2	361	21	B03950		Human mesenchymal
6	56	27.2	643	21	B73347		Human signal pepti
7	56	27.2	874	21	B01431		Human TANGO 224 (f
8	55	26.7	122	12	R15123		hCG/hLH chimera, A
9	55	26.7	145	12	R15116		hCG/hLH chimera, A
10	55	26.7	145	12	R15118		hCG/hLH chimera, A
11	55	26.7	145	12	R15122		hCG/hLH chimera, A

12	55	26.7	145	12	R15124	hCG/hLH chimera, A
13	55	26.7	145	12	R15125	hCG/hLH chimera, A
14	54	26.2	106	20	Y32825	HTV chemokine gene
15	54	26.2	121	21	Y92001	Human luteinizing
16	54	26.2	122	20	Y29594	Human luteinizing
17	54	26.2	141	7	P60602	Sequence of human
18	54	26.2	141	20	W99548	hLH-beta analogue
19	54	26.2	141	20	W99547	hLH-beta analogue
20	54	26.2	141	20	W99520	Glycoprotein hormo
21	54	26.2	141	20	W99522	Glycoprotein hormo
22	54	26.2	141	20	W99523	Glycoprotein hormo
23	54	26.2	141	20	W99524	Glycoprotein hormo
24	54	26.2	141	20	W99525	Glycoprotein hormo
25	54	26.2	141	20	W99516	Glycoprotein hormo
26	54	26.2	141	20	W99517	Glycoprotein hormo
27	54	26.2	141	20	W99518	Glycoprotein hormo
28	54	26.2	141	20	W99519	Glycoprotein hormo
29	54	26.2	234	16	R86271	Single chain gonad
30	54	26.2	234	16	R86261	Partially deglycos
31	54	26.2	234	16	R86249	Single chain gonad
32	54	26.2	446	21	B43754	Human cancer assoc
33	53	25.7	62	20	Y19648	SEQ ID NO 366 from
34	53	25.7	147	19	W72404	Arabidopsis thalia
35	52.5	25.5	111	18	W21859	Leech protein caus
36	51	24.8	326	21	B18989	Amino acid sequenc
37	50	24.3	122	12	R15119	hCG/hLH chimera, A
38	50	24.3	145	12	R15106	hCG/hLH chimera, D
39	50	24.3	145	12	R15102	hCG/hLH chimera, D
40	50	24.3	218	22	B48600	Human oligodendroc
41	50	24.3	877	19	W23946	Porcine phosphoino
42	50	24.3	877	20	W90082	Porcine G-protein
43	50	24.3	877	21	Y76801	pig p101 regulator
44	50	24.3	1480	13	R25079	Drosophila SLIT pr
45	49	23.8	141	20	W99521	Glycoprotein hormo

ALIGNMENTS

RESULT 1
W48086
ID W48086 standard; Protein; 365 AA.
AC W48086;
XX
XX
DT 11-JUN-1998 (first entry)
XX
XX Human dendritic cell chemokine receptor.
DE
XX Human: thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta;
KW receptor; dendritic cell; macrophage; inflammation; asthma.
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT Misc-difference 193
FT /note= "encoded by CAN"
FT
XX
XX WO9801557-A2.
XX
XX
PD 15-JAN-1998.
XX
PF 02-JUL-1997; 97WO-US10819.
XX
PR 04-JUN-1997; 97US-0048593.
PR 05-JUL-1996; 96US-0675814.
PR 11-OCT-1996; 96US-0028329.
XX
XX (SCHE) SCHERING CORP.
XX
XX Gish KC, Schall TJ, Vicari A, Wang W, Zlotnik A;
XX WPI; 1998-101054/09.
DR

DR N-PSDB; V15418.
 XX Novel chemokines, e.g. thymus expressed chemokine - used for
 PT treating inflammatory conditions including asthma.
 XX
 PS Claim 3; Page 94-95; 202pp; English.
 XX
 CC The present sequence represents human dendritic cell chemokine receptor.
 CC Antibodies which bind to the protein can be used in detecting or
 CC diagnosing various immunological conditions related to expression
 CC of the protein. The nucleic acid can be used for screening and
 CC isolating DNA clones for the chemokines, especially from other
 CC species. The chemokine can be used in the treatment of conditions
 CC associated with abnormal physiology or development, including
 CC inflammatory conditions such as asthma.
 XX
 SQ Sequence 365 AA;

Query Match 100.0%; Score 206; DB 19; Length 365;
 Best Local Similarity 100.0%; Pred. No. 1.9e-19;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFSTPVKILCQSILHITQLILRCYCPCRRSGSSPGY 38
 |||||
 DB 1 mfstpvkllcqsilhitqlilrcycapcrrsgsspgy 38

RESULT 2
 Y97077
 ID Y97077 standard; Protein; 365 AA.
 AC Y97077;
 XX
 XX
 DT 04-DEC-2000 (first entry)
 XX
 DE Primate (human) chemokine receptor CCR6.
 XX
 KW MIP-3-alpha; chemokine; CCR6 receptor; ligand; cytostatic; agonist;
 KW antagonist; anti-psoriatic; dermatological; immunosuppressive;
 KW anti-inflammatory.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 193
 FT /note= "Encoded by CAN#"
 XX
 PN WO200046248-A1.
 XX
 PD 10-AUG-2000.
 XX
 PF 02-FEB-2000; 2000WO-US00511.
 XX
 PR 03-FEB-1999; 99US-0244281.
 XX
 PA (SCHE) SCHERING CORP.
 XX
 PI Oldham ER, Honey B, Dieu-Nosjean M, Caux C, Zlotnik A;
 XX
 DR WPI; 2000-543477/49.
 DR N-PSDB; A51971.
 XX
 PT Novel methods for modulating the migration of cells within or to the
 PT skin using MIP-3-alpha or CCR6 agonists or antagonists, useful for
 PT treating skin disorders, e.g. cancer
 XX
 PS Disclosure; Page 53-54; 61pp; English.
 XX
 CC The MIP-3-alpha chemokine is expressed in inflamed skin cells. This
 CC chemokine is the ligand for the CCR6 receptor. MIP-3-alpha or CCR6
 CC agonists or antagonists can be used to modulate the migration of a cell
 CC within or to the skin of a mammal. MIP-3-alpha can be used to purify a

CC population of cells expressing a MIP-3-alpha receptor. The methods are
 CC useful for treating a mammalian subject with a skin disease or condition,
 CC e.g. cancer, metastasis, psoriasis, atopic or contact dermatitis,
 CC systemic lupus erythematosus and lichen ruber planus, or for treating
 CC skin transplants or grafts.
 XX

SQ Sequence 365 AA;

Query Match 100.0%; Score 206; DB 21; Length 365;
 Best Local Similarity 100.0%; Pred. No. 1.9e-19;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFSTPVKILCQSILHITQLILRCYCPCRRSGSSPGY 38
 |||||
 DB 1 mfstpvkllcqsilhitqlilrcycapcrrsgsspgy 38

RESULT 3
 Y29255
 ID Y29255 standard; Protein; 292 AA.
 XX
 AC Y29255;
 XX
 DT 25-OCT-1999 (first entry)
 XX
 DE Amino acid sequence of a virulence factor encoded by ORF40238.
 XX
 KW Human pathogen; virulence polypeptide; virulence factor;
 KW pathogenic infection; Pseudomonas aeruginosa infection.
 XX
 OS Pseudomonas aeruginosa.
 XX
 PN WO9927129-A1.
 XX
 PD 03-JUN-1999.
 XX
 PF 25-NOV-1998; 98WO-US25247.
 XX
 PR 25-NOV-1997; 97US-0066517.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 XX
 PI Ausubel F, Cao H, Drenkard E, Goodman HM, Mahajan-Miklos S;
 PI Rahme LG, Tan M, Tsongalis J;
 XX
 DR WPI; 1999-357851/30.
 XX

Virulence factors useful in developing disease treatments

Disclosure; Fig 3; 228pp; English.

The present sequence represents a Pseudomonas aeruginosa polypeptide
 sequence. P. aeruginosa is an opportunistic human pathogen present in
 soil water and plants. The specification describes virulence polypeptides
 and nucleic acid sequence encoding such polypeptides. These sequences
 can be used to identify a compound which is capable of decreasing the
 expression of a pathogenic virulence factor. Compounds that inhibit
 the expression or activity of virulence factor polypeptides can be
 used to treat pathogenic infections, especially where the infection
 is a P. aeruginosa infection.
 CC note: the sequences given in the specification were poorly legible, and
 CC in some instances assumptions were made as to the identity of the
 CC residue; it is therefore possible that the sequence given below is
 CC not entirely correct.
 XX

SQ Sequence 292 AA;

Query Match 27.4%; Score 56.5; DB 20; Length 292;
 Best Local Similarity 36.1%; Pred. No. 7.9;
 Matches 13; Conservative 3; Mismatches 9; Indels 11; Gaps 1;

RESULT
R15116

PF 07-MAY-1991; 91WO-US03162.

XX 08-MAY-1990; 90US-0520703.

XX (UYNE-) UNIV MED NEW JERSEY.

XX Campbell RK, Moyle WR;

XX WPI; 1991-353528/48.

XX New glyco-protein hormone analogues - for inducing fertility as

XX immuno-castration agents, for suppressing reproductive system

XX development and as immuno-contragestive vaccines.

XX Table VI; Page 65; 94pp; English.

XX The sequence is an analogue of mature hCG beta subunit having

XX residues 89, 91, 92 and 99 replaced by the corresponding

XX residues in the human LH protein. The chimeric hormone may be

XX useful in the treatment of infertility in men and women and the

XX promotion of fertility in male and female animals.

XX See R15043, R15061-R15125 and R15161-R15198.

XX Sequence 145 AA;

XX Query Match 26.7%; Score 55; DB 12; Length 145;

XX Best Local Similarity 62.5%; Pred. No. 6;

XX Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

XX QY 22 LRCYCPCRRSGSSPG 37

XX | | | | | : | |

XX Db 86 lscrcgpcrrsttscg 101

XX RESULT 11

XX R15122

XX ID R15122 standard; Protein; 145 AA.

XX AC R15122;

XX DT 11-FEB-1992 (first entry)

XX DE hCG/hLH chimera, A7.

XX KW Glycoprotein hormone; immuno-castration;

XX immuno-contragestive; vaccine; human chorionic gonadotropin;

XX KW luteinising hormone; LH; CG.

XX OS Homo sapiens.

XX PN WO9116922-A.

XX PD 14-NOV-1991.

XX PF 07-MAY-1991; 91WO-US03162.

XX PR 08-MAY-1990; 90US-0520703.

XX PA (UYNE-) UNIV MED NEW JERSEY.

XX PI Campbell RK, Moyle WR;

XX WPI; 1991-353528/48.

XX New glyco-protein hormone analogues - for inducing fertility as

XX immuno-castration agents, for suppressing reproductive system

XX development and as immuno-contragestive vaccines.

XX Table VI; Page 65; 94pp; English.

XX The sequence is an analogue of mature hCG beta subunit having

XX residues 42, 47, 51, 77, 82, 83, 89, 91, 92 and 99 replaced by the

XX CC residues 89, 91, 92 and 99 replaced by the

XX CC residues 42, 47, 51, 77, 82, 83, 89, 91, 92 and 99 replaced by the

CC corresponding residues in the human LH protein. The chimeric

CC hormone may be useful in the treatment of infertility in men and

CC women and the promotion of fertility in male and female animals.

CC See R15043, R15061-R15125 and R15161-R15198.

XX Sequence 145 AA;

XX Query Match 26.7%; Score 55; DB 12; Length 145;

XX Best Local Similarity 62.5%; Pred. No. 6;

XX Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

XX QY 22 LRCYCPCRRSGSSPG 37

XX | | | | | : | |

XX Db 86 lscrcgpcrrsttscg 101

XX RESULT 12

XX R15124

XX ID R15124 standard; Protein; 145 AA.

XX AC R15124;

XX DT 11-FEB-1992 (first entry)

XX DE hCG/hLH chimera, A9.

XX KW Glycoprotein hormone; immuno-castration;

XX immuno-contragestive; vaccine; human chorionic gonadotropin;

XX KW luteinising hormone; LH; CG.

XX OS Homo sapiens.

XX PN WO9116922-A.

XX PD 14-NOV-1991.

XX PF 07-MAY-1991; 91WO-US03162.

XX PR 08-MAY-1990; 90US-0520703.

XX PA (UYNE-) UNIV MED NEW JERSEY.

XX PI Campbell RK, Moyle WR;

XX WPI; 1991-353528/48.

XX New glyco-protein hormone analogues - for inducing fertility as

XX immuno-castration agents, for suppressing reproductive system

XX development and as immuno-contragestive vaccines.

XX Table VI; Page 65; 94pp; English.

XX The sequence is an analogue of mature hCG beta subunit having

XX residues 2, 8, 10, 15, 77, 82, 83, 89, 91, 92 and 99 replaced by the

XX corresponding residues in the human LH protein. The chimeric

XX hormone may be useful in the treatment of infertility in men and

XX women and the promotion of fertility in male and female animals.

XX CC See R15043, R15061-R15125 and R15161-R15198.

XX Sequence 145 AA;

XX Query Match 26.7%; Score 55; DB 12; Length 145;

XX Best Local Similarity 62.5%; Pred. No. 6;

XX Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

XX QY 22 LRCYCPCRRSGSSPG 37

XX | | | | | : | |

XX Db 86 lscrcgpcrrsttscg 101

XX RESULT 13

R15125
ID R15125 standard; Protein: 145 AA.
XX AC R15125;
XX XX
DT 11-FEB-1992 (first entry)
XX DE hCG/hLH chimera, A10.
XX KW Glycoprotein hormone; immuno-castration;
KW immuno-contragestive; vaccine; human chorionic gonadotropin;
KW luteinizing hormone; LH; CG.
XX OS Homo sapiens.
XX XX WO9116922-A.
XX PN 14-NOV-1991.
XX PD
XX PF 07-MAY-1991; 91WO-US03162.
XX PR 08-MAY-1990; 90US-0520703.
XX PA (UYNE-) UNIV MED NEW JERSEY.
XX PI Campbell RK, Moyle WR;
XX DR WPI; 1991-353528/48.
XX XX New glyco-protein hormone analogues - for inducing fertility as
PT immuno-castration agents, for suppressing reproductive system
PT development and as immuno-contragestive vaccines.
XX XX
PS Table VI; Page 65; 94pp; English.
XX XX The sequence is an analogue of mature hCG beta subunit having
CC residues 42, 47, 51, 89, 91, 92 and 99 replaced by the
CC corresponding residues in the human LH protein. The chimeric
CC hormone may be useful in the treatment of infertility in men and
CC women and the promotion of fertility in male and female animals.
CC See R15043, R15061-R15125 and R15161-R15198.
XX XX
SQ Sequence 145 AA;

Query Match 26.7%; Score 55; DB 12; Length 145;
Best Local Similarity 62.5%; Pred. No. 6;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 22 LRCYCPCRRSGSSPG 37
DB 86 lscrcgpcrrstscg 101

RESULT 14
Y32825
ID Y32825 standard; Protein: 106 AA.
XX AC Y32825;
XX XX
DT 09-NOV-1999 (first entry)
XX DE HIV chemokine gene product from strain p896.
XX KW HIV; AIDS; chemokine; SDF-1; gp120; glycoprotein 120; antisense;
KW long terminal repeat; vaccine; detection; entry phase.
XX OS Human immunodeficiency virus.
XX XX
FH Key Location/Qualifiers
FT Misc-difference 28
FT /label= unknown
FT Misc-difference 38

FT Misc-difference 73 /label= Unknown
FT /label= Unknown
XX WO9941355-A2.
XX PD 19-AUG-1999.
XX PF 12-FEB-1999; 99WO-US03162.
XX PR 13-FEB-1998; 98US-0074640.
XX PA (UYNV) UNIV NEW YORK STATE RES FOUND.
XX XX Ambrus JL, Krawczyk KA, Ludwig LB;
XX DR WPI; 1999-518447/43.
XX XX New HIV gene, encoding chemokines useful for binding to the
PT chemokine receptor on human cells during the entry phase of HIV
PT infection,
XX PS Claim 3; Page 81; 87pp; English.
XX XX This sequence is the HIV strain p896 chemokine. The HIV chemokine protein
CC has similarity with chemokine SDF-1. It is thought that the HIV chemokine
CC may play a role as a cofactor with glycoprotein 120 (gp120) in the
CC binding and entry of HIV to a target cell. The HIV chemokine gene
CC was deduced from the known sequence of the minus strand. The peptides
CC derived from the HIV chemokine gene or variants or modified versions of
CC the HIV chemokine may be used to block entry of target cell during
CC various phases of HIV infection and AIDS. Also, chemokine receptors may
CC provide a method by which the HIV chemokine may be isolated and purified
CC from HIV. The HIV chemokine and variants may also be useful in the
CC development of a vaccine for AIDS prevention. Isolated and purified HIV
CC chemokine or derived peptides may be used to generate antibodies useful
CC in diagnostic assays for detection of HIV chemokine in clinical samples.
XX XX
SQ Sequence 106 AA;

Query Match 26.2%; Score 54; DB 20; Length 106;
Best Local Similarity 60.0%; Pred. No. 5.9;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 10 LCQSILHITQLILRC 24
DB 82 lccsilhiagivlac 96

RESULT 15
Y92001
ID Y92001 standard; Protein: 121 AA.
XX AC Y92001;
XX XX
DT 19-JUL-2000 (first entry)
XX DE Human luteinizing hormone beta subunit.
XX KW human luteinizing hormone; beta subunit; CKGF; mutant;
KW cysteine knot growth factor; hairpin loop; thyroid stimulating hormone;
KW TSH; hypothyroidism; thyroid cancer.
XX OS Homo sapiens.
XX XX
FH Key Location/Qualifiers
FT Domain 8..33
FT /label= beta_hairpin_loop_1
FT Misc-difference 1..33
FT /note= "mutant optionally comprises one or more
FT substitutions in these residues, preferably
FT a basic residue"

```

FT Domain 58..87
XX /label= beta_hairpin_loop_3
PN WO200017360-A1.
XX
XX 30-MAR-2000.
XX
XX 19-MAR-1999; 99WO-US05908.
XX
XX 22-SEP-1998; 98WO-US19772.
XX
XX (UYMA-) UNIV MARYLAND BALTIMORE.
XX
XX Weintraub BD, Szkudlinski MW;
XX
XX WPI; 2000-283585/24.
XX
XX New mutant cystine knot growth factor proteins comprising one or more
XX mutant subunits, useful for treating or preventing diseases e.g.
XX hypothyroidism and thyroid cancer
XX
XX Claim 73; Page 297; 320pp; English.
XX
XX This is the wild type human luteinizing hormone beta subunit. Mutants
XX comprise at least one electrostatic charge altering mutation in a beta
XX hairpin loop, resulting in increased bioactivity.
XX Mutant cystine knot growth factor (CKGF) proteins comprising one or more
XX mutant subunits and having novel properties or improved pharmacological
XX properties, compared to wild type CKGFs, are claimed. The CKGF
XX superfamily comprises at least four families of growth factors: the
XX glycoprotein hormones, the platelet-derived growth factor (PDGF) family,
XX the neurotrophins and the transforming growth factor-beta family; the
XX families are known to be structurally similar (especially comprising the
XX cystine knot topology) and it was shown that mutations at certain
XX positions in the CKGF hairpin loops of family members and other members
XX of the CKGF superfamily could significantly alter the biological
XX activities of the CKGF.
XX A mutant thyroid stimulating hormone (TSH) heterodimer or analogue
XX can be administered to treat or prevent hypothyroidism (claimed). They
XX are also useful to treat or diagnose thyroid cancer, by administering the
XX mutant heterodimer or analogue to stimulate iodine uptake, and
XX subsequently administering radiolabeled iodine to treat the cancer or
XX enable radiolabel detection (claimed).
XX
SQ Sequence 121 AA;

Query Match 26.2%; Score 54; DB 21; Length 121;
Best Local Similarity 62.5%; Pred. No. 6.8;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 22 LRCYCACPGRSGSSPG 37
Db 86 lscrcgpcrrstsdcg 101

Search completed: May 23, 2001, 15:28:25
Job time: 402 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:30:04 ; Search time 95.91 Seconds
(without alignments)
7.611 Million cell updates/sec

Title: US-08-887-977-10_COPY_1_38

Perfect score: 206
Sequence: 1 MFSTPVKILQCQILHITQLILRCYCPCRRSGSPG 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pap.*
- 5: /cgn2_6/ptodata/2/iaa/PT05_COMB.pap.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	24.3	218	4	US-08-084-079-5
2	50	24.3	877	2	US-08-916-917-2
3	50	24.3	877	2	US-08-972-631-2
4	50	24.3	877	2	US-08-972-629-2
5	50	24.3	877	2	US-08-972-630-2
6	50	24.3	877	2	US-08-672-211-2
7	50	24.3	877	3	US-09-225-170-2
8	49	23.8	207	1	US-08-557-917A-2
9	49	23.8	207	4	US-09-084-153-2
10	49	23.8	207	4	US-09-084-079-2
11	49	23.8	447	4	US-09-378-255-2
12	49	23.8	880	2	US-08-916-917-12
13	49	23.8	880	3	US-08-225-170-12
14	49	23.8	880	4	US-09-378-255-6
15	49	23.8	880	4	US-09-141-212-2
16	49	23.8	880	4	US-09-141-212-4
17	48.5	23.5	114	1	US-08-425-673-7
18	48	23.3	462	2	US-08-477-451-24
19	46	22.3	88	2	US-08-327-362-2
20	46	22.3	88	2	US-08-709-924-24
21	46	22.3	88	2	US-08-709-925-24
22	46	22.3	88	4	US-09-158-565-2
23	46	22.3	98	2	US-08-709-924-23
24	46	22.3	98	2	US-08-709-925-23
25	46	22.3	145	1	US-08-425-673-1
26	46	22.3	145	1	US-08-425-673-2
27	46	22.3	145	1	US-08-475-213-10

28	46	22.3	145	2	US-08-395-238-2
29	46	22.3	145	4	US-09-142-320-4
30	46	22.3	145	4	US-09-142-320-11
31	46	22.3	145	4	US-09-142-320-12
32	46	22.3	145	4	US-09-142-320-13
33	46	22.3	145	4	US-09-142-320-14
34	46	22.3	145	4	US-09-142-320-15
35	46	22.3	145	4	US-09-142-320-16
36	46	22.3	165	2	US-08-709-924-2
37	46	22.3	165	2	US-08-709-925-2
38	46	22.3	307	4	US-08-804-166-4
39	46	22.3	307	4	US-08-910-991-4
40	46	22.3	336	4	US-08-804-166-8
41	46	22.3	336	4	US-08-910-991-8
42	46	22.3	454	2	US-09-014-969-9
43	46	22.3	472	4	US-08-976-255-17
44	46	22.3	1040	2	US-08-254-989-2
45	45.5	22.1	771	4	US-09-188-930-183

ALIGNMENTS

RESULT 1

US-09-084-079-5

; Sequence 5, Application US/09084079

; Patent No. 6150136

; GENERAL INFORMATION:

; APPLICANT: Bronstein, Jeff M.

; APPLICANT: Seitz, Robert S.

; APPLICANT: Lallone, Roger L.

; TITLE OF INVENTION: Oligodendrocyte-specific Protein and Method for

; TITLE OF INVENTION: Diagnosing and Treating Disease

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sheldon & Mak

; STREET: 225 S. Lake Avenue, 9th Floor

; CITY: Pasadena

; STATE: California

; ZIP: 91101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage

; COMPUTER: IBM compatible

; OPERATING SYSTEM: Windows 95

; SOFTWARE: WordPerfect for Windows version 8.0.

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/084,079

; FILING DATE: 22-MAY-1998

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Farah, David A.

; REGISTRATION NUMBER: 38,134

; REFERENCE/DOCKET NUMBER: 11201-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (626)796-4000

; TELEFAX: (626)795-6321

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 218 amino acid residues

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-084-079-5

Query Match 24.3% Score 50; DB 4; Length 218;

Best Local Similarity 30.0%; Pred. No. 14;

Matches 9; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 8 IILCQSLHITQLILRCYCPCRRSGSPG 37

DB 84 LMTAASVLGLPAILLITLVLCIRMGQPG 113

RESULT 3
US-08-972-631-2
; Sequence 2, Application US/08972631
; Patent No. 5856133
; GENERAL INFORMATION:
; APPLICANT: Stephans, Len
; APPLICANT: Hawkins, Phillip T.
; TITLE OF INVENTION: G-BETA-GAMMA REGULATED
; TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3', KINASE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 2730 Sand Hill Road
; CITY: Menlo Park
; STATE: California

Query Match 24.3%; Score 50; DB 2; Length 877;
Best Local Similarity 33.3%; Pred. No. 64;
Matches 11; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)854-3660
TELEFAX: (415)854-3694
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 877 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-972-629-2

Query Match 24.3%; Score 50; DB 2; Length 877;
Best Local Similarity 33.3%; Pred. No. 64;
Matches 11; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY 3 STPVKILQCISILHTQLILRCYCPCRRSGSS 35
| | | | | : | | | | : | | : |
Db 809 SCFPAVCLDQDERKILQSVIRCEVSPCYKPKS 841

RESULT 5
US-08-972-630-2
Sequence 2, Application US/08972630
Patent No. 5869271
GENERAL INFORMATION:
APPLICANT: Stephens, Len
APPLICANT: Hawkins, Phillip T.
TITLE OF INVENTION: G-BETA-GAMMA REGULATED
TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 2730 Sand Hill Road
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/972,630
FILING DATE: 27-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 08/672,211
APPLICATION NUMBER: US 08/672,211
FILING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,277
REFERENCE/DOCKET NUMBER: 8549-0005-999
TELEPHONE: (415)854-3660
TELEFAX: (415)854-3694
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 877 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-972-630-2

Query Match 24.3%; Score 50; DB 2; Length 877;
Best Local Similarity 33.3%; Pred. No. 64;
Matches 11; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY 3 STPVKILQCISILHTQLILRCYCPCRRSGSS 35

Db 809 SCFPAVCLDQDERKILQSVIRCEVSPCYKPKS 841

RESULT 6
US-08-672-211-2
Sequence 2, Application US/08672211
Patent No. 5874273
GENERAL INFORMATION:
APPLICANT: Stephens, Len
APPLICANT: Hawkins, Phillip T.
TITLE OF INVENTION: G-BETA-GAMMA REGULATED
TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 2730 Sand Hill Road
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,211
FILING DATE: 27-JUN-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,277
REFERENCE/DOCKET NUMBER: 8549-0005-999
TELEPHONE: (415)854-3660
TELEFAX: (415)854-3694
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 877 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-672-211-2

Query Match 24.3%; Score 50; DB 2; Length 877;
Best Local Similarity 33.3%; Pred. No. 64;
Matches 11; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY 3 STPVKILQCISILHTQLILRCYCPCRRSGSS 35
| | | | | : | | | | : | | : |
Db 809 SCFPAVCLDQDERKILQSVIRCEVSPCYKPKS 841

RESULT 7
US-09-225-170-2
Sequence 2, Application US/09225170
Patent No. 6017763
GENERAL INFORMATION:
APPLICANT: Stephens, Len
APPLICANT: Hawkins, Phillip Thomas
APPLICANT: Braselmann, Sylvia
TITLE OF INVENTION: G-BETA-GAMMA REGULATED
TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA

ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,170
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: 08/916,917
APPLICATION NUMBER: 08/916,917
FILING DATE: 15-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Abrams, Samuel B
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 8549-0006-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 877 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6017763e
US-09-225-170-2

Query Match 24.3%; Score 50; DB 3; Length 877;
Best Local Similarity 33.3%; Pred. No. 64;
Matches 11; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

OY 3 STPVKILQCSILHITQILRCYCPCRRSGSS 35
DB 809 SCFVAVLQDQDKRILQSVIRCEVSPCKRPEKS 841

RESULT 8
US-08-557-917A-2
Sequence 2, Application US/08557917A
Patent No. 5756300
GENERAL INFORMATION:
APPLICANT: Bronstein, Jeff M.
APPLICANT: Seitz, Robert S.
APPLICANT: Lallone, Roger L.
TITLE OF INVENTION: Oligodendrocyte-specific Protein and Method for
TITLE OF INVENTION: Diagnosing and Treating Disease
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 S. Lake Avenue, 9th Floor
CITY: Pasadena
STATE: California
ZIP: 91101
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: WordPerfect for Windows version 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,917A
FILING DATE: 14-NOVEMBER-1995
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Farah, David A.
REGISTRATION NUMBER: 38,134
REFERENCE/DOCKET NUMBER: 11201
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818)796-4000
TELEFAX: (818)795-6321

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 207 amino acid residues
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-557-917A-2

Query Match 23.8%; Score 49; DB 1; Length 207;
Best Local Similarity 30.0%; Pred. No. 19;
Matches 9; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

OY 8 IILQCSILHITQILRCYCPCRRSGSSPG 37
DB 84 LMAASVLGLPAILLTLTLVPCIRMGHEPG 113

RESULT 9
US-09-084-153-2
Sequence 2, Application US/09084153
Patent No. 6147191
GENERAL INFORMATION:
APPLICANT: Bronstein, Jeff M.
TITLE OF INVENTION: Oligodendrocyte-specific Protein
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 S. Lake Avenue, 9th Floor
CITY: Pasadena
STATE: California
ZIP: 91101
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows version 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/084,153
FILING DATE: 26-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Farah, David A.
REGISTRATION NUMBER: 38,134
REFERENCE/DOCKET NUMBER: 11201-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (626)796-4000
TELEFAX: (626)795-6321
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 207 amino acid residues
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-084-153-2

Query Match 23.8%; Score 49; DB 4; Length 207;
Best Local Similarity 30.0%; Pred. No. 19;
Matches 9; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

OY 8 IILQCSILHITQILRCYCPCRRSGSSPG 37
DB 84 LMAASVLGLPAILLTLTLVPCIRMGHEPG 113

RESULT 10
US-09-084-079-2
Sequence 2, Application US/09084079
Patent No. 6150136
GENERAL INFORMATION:
APPLICANT: Bronstein, Jeff M.
APPLICANT: Seitz, Robert S.

APPLICANT: Lallone, Roger L.
TITLE OF INVENTION: Oligodendrocyte-specific Protein and Method for
Diagnosing and Treating Disease
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 S. Lake Avenue, 9th Floor
CITY: Pasadena
STATE: California
ZIP: 91101
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows version 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/084,079
FILING DATE: 22-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Farah, David A.
REGISTRATION NUMBER: 38,134
REFERENCE/DOCKET NUMBER: 11201-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (626)796-4000
TELEFAX: (626)795-6321
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 207 amino acid residues
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-084-079-2

Query Match 23.8%; Score 49; DB 4; Length 207;
Best Local Similarity 30.0%; Pred. No. 19;
Matches 9; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 8 IILCOSILHITQILRCYCPCRRSGSSPG 37
::: ||| : :|| ||| ||| |||

DB 84 LMAASVLGLPAILLTLLVLPICIRMGHEPG 113

RESULT 11
US-09-378-255-2
Sequence 2, Application US/09378255
Patent No. 6174716
GENERAL INFORMATION:
APPLICANT: MACPHEE, COLIN HOUSTON
APPLICANT: PATEL, LISA
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30173
CURRENT APPLICATION NUMBER: US/09/378,255
CURRENT FILING DATE: 1999-08-20
EARLIER APPLICATION NUMBER: UK 9818435.1
EARLIER FILING DATE: 1998-08-24
EARLIER APPLICATION NUMBER: UK 9903414.2
EARLIER FILING DATE: 1999-02-15
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 447
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-378-255-2

Query Match 23.8%; Score 49; DB 4; Length 447;
Best Local Similarity 33.3%; Pred. No. 42;
Matches 11; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY 3 STPVKILQCOSILHITQILRCYCPCRRSGSS 35

DB 379 SCPPFAVLQDQDERKILQSVRCVSPCYKPKS 411
::: ||| : :|| ||| ||| |||

RESULT 12
US-08-916-917-12
Sequence 12, Application US/08916917
Patent No. 5856132
GENERAL INFORMATION:
APPLICANT: Stephens, Len
APPLICANT: Hawkins, Phillip Thomas
APPLICANT: Braselmann, Sylvia
TITLE OF INVENTION: G-BETA-GAMMA REGULATED
OPERATING SYSTEM: PHOSPHATIDYLINOSITOL-3', KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM-Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,917
FILING DATE: 15-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/672,211
FILING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Abrams, Samuel B
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 8549-0006-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 880 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 5856132e
US-08-916-917-12

Query Match 23.8%; Score 49; DB 2; Length 880;
Best Local Similarity 33.3%; Pred. No. 87;
Matches 11; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY 3 STPVKILQCOSILHITQILRCYCPCRRSGSS 35
::: ||| : :|| ||| ||| |||

DB 812 SCPPFAVLQDQDERKILQSVRCVSPCYKPKS 844

RESULT 13
US-09-225-170-12
Sequence 12, Application US/09225170
Patent No. 6017763
GENERAL INFORMATION:
APPLICANT: Stephens, Len
APPLICANT: Hawkins, Phillip Thomas
APPLICANT: Braselmann, Sylvia
TITLE OF INVENTION: G-BETA-GAMMA REGULATED
OPERATING SYSTEM: PHOSPHATIDYLINOSITOL-3', KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,170
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/916,917
FILING DATE: 15-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Abrams, Samuel B
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 8549-0006-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 880 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6017763e
US-09-225-170-12

Query Match 23.8%; Score 49; DB 3; Length 880;
Best Local Similarity 33.3%; Pred. No. 87;
Matches 11; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY 3 STPVKILQCSILHITQILRLCYCAPCRRSGSS 35
DB 812 SCPPFAVCLDQDERKILQSVRCVSPCYKPEKS 844

RESULT 14
US-09-378-255-6
Sequence 6, Application US/09378255
Patent No. 6174716
GENERAL INFORMATION:
APPLICANT: NACPHEE, COLIN HOUSTON
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30173
CURRENT APPLICATION NUMBER: US/09/378,255
EARLIER FILING DATE: 1999-08-20
EARLIER APPLICATION NUMBER: UK 9818435.1
EARLIER FILING DATE: 1998-08-24
EARLIER APPLICATION NUMBER: UK 9903414.2
EARLIER FILING DATE: 1999-02-15
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 880
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-378-255-6

Query Match 23.8%; Score 49; DB 4; Length 880;
Best Local Similarity 33.3%; Pred. No. 87;
Matches 11; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY 3 STPVKILQCSILHITQILRLCYCAPCRRSGSS 35
DB 812 SCPPFAVCLDQDERKILQSVRCVSPCYKPEKS 844
RESULT 15
US-09-141-212-2
Sequence 2, Application US/09141212
Patent No. 6200777
GENERAL INFORMATION:
APPLICANT: NACPHEE, COLIN
APPLICANT: PATEL, LISA
TITLE OF INVENTION: NOVEL COMPOUNDS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/141,212
FILING DATE: 27-AUG-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 97306807.5
FILING DATE: 01-SEP-1997
APPLICATION NUMBER: EP 98300687.5
FILING DATE: 30-JAN-1998
APPLICATION NUMBER: GB 9807720.9
FILING DATE: 08-APR-1998
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-30012
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0700
TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 880 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-141-212-2

Query Match 23.8%; Score 49; DB 4; Length 880;
Best Local Similarity 33.3%; Pred. No. 87;
Matches 11; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY 3 STPVKILQCSILHITQILRLCYCAPCRRSGSS 35
DB 812 SCPPFAVCLDQDERKILQSVRCVSPCYKPEKS 844

Search completed: May 23, 2001, 15:30:04
Job time: 411 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:31:57 ; Search time 110.15 Seconds
(without alignments)
23.708 Million cell updates/sec

Title: US-08-887-977-10_COPY_1_38
Perfect score: 206
Sequence: 1 MFSTPVKIILQCSILHITQLILRCYCPCRRSGSSPGY 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues
Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_67:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	56.5	27.4	120	2 C72504	hypothetical prote
2	55	26.7	412	2 A31995	nicotinic acetylch
3	55	26.7	412	2 S45064	nicotinic acetylch
4	54	26.2	141	1 UTHUB	lutropin beta chai
5	54	26.2	279	2 D70684	hypothetical prote
6	54	26.2	591	1 C8HUB	complement C8 beta
7	54	26.2	9376	2 T14593	syringomycin synth
8	53	25.7	118	2 PN0141	lutropin beta chai
9	53	25.7	118	2 PN0139	lutropin beta chai
10	53	25.7	141	1 UTPGB	lutropin beta chai
11	52.5	25.5	111	2 JG0177	LEP precursor - Ko
12	51.5	25.0	154	2 T27983	hypothetical prote
13	51.5	25.0	924	2 T21738	hypothetical prote
14	51	24.8	383	2 S55594	G protein-coupled
15	51	24.8	405	2 A28009	43K postsynaptic m
16	51	24.8	444	2 I39294	McLeod syndrome-as
17	50.5	24.5	1880	2 T18531	tractin - medicina
18	50	24.3	141	1 UTSOB	lutropin beta chai
19	50	24.3	141	1 UTSBB	lutropin beta chai
20	50	24.3	141	2 I46949	lutinizng hormon
21	49	23.8	80	2 I65235	testicular luteini
22	49	23.8	119	2 A61465	lutropin beta chai
23	49	23.8	129	2 T16394	hypothetical prote
24	49	23.8	138	2 S00512	lutropin beta chai
25	49	23.8	139	2 I52320	testicular luteini
26	49	23.8	141	1 UTRTB	lutropin beta chai
27	49	23.8	141	2 JCA527	lutinizng hormon
28	49	23.8	157	2 S57999	probable olfactory
29	49	23.8	165	1 KTBAB	choriogonadotropin

30	49	23.8	260	2 JC5826	hydroxycacylgutath
31	49	23.8	430	2 T42951	hypothetical prote
32	49	23.8	431	2 G36809	hypothetical prote
33	49	23.8	590	2 I46687	complement compone
34	49	23.8	687	2 T39838	hypothetical prote
35	48.5	23.5	123	2 B72548	hypothetical prote
36	48.5	23.5	131	1 KRSHA3	keratin high-sulfu
37	48.5	23.5	297	2 E83194	polyamine transpor
38	48.5	23.5	413	2 JC4862	activin beta-A cha
39	48.5	23.5	710	2 T41352	probable transcrip
40	48	23.3	219	2 A35650	Sur protein - chic
41	48	23.3	511	1 B64850	probable virulence
42	48	23.3	568	2 T28041	hypothetical prote
43	48	23.3	658	2 T19487	hypothetical prote
44	48	23.3	682	2 JC7385	multispecific orga
45	47.5	23.1	299	2 JC4374	sterol uptake prot

ALIGNMENTS

RESULT 1

C72504
Hypothetical protein APE2009 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000
C:Accession: C72504
R:Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Ta
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero
A:Reference number: A72450; MUID:99310339
A:Accession: C72504
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-120 <KAW>
A:Cross-references: DDBJ:AP000063; NID:g5105654; PIDN:BAA81019.1; PID:di044805; PID:g
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE2009
C:Superfamily: Aeropyrum pernix hypothetical protein APE2009

Query Match

Best Local Similarity 27.4%; Score 56.5; DB 2; Length 120;
Matches 15; Conservative 5; Mismatches 11; Indels 7; Gaps 1;

Oy 6 VKIILQCSILHITQLILRC-----YCAPCRRSGSSP 36

Db 19 VLLILSSLLILTSLLRLCLRYWSAAYIPGRKPGYSP 56

RESULT 2

A31995
nicotinic acetylcholine receptor-associated 46K protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 01-Dec-2000
C:Accession: A31995; S04488
R:Frail, D.E.; McLaughlin, L.L.; Mudd, J.; Merlie, J.P.
J. Biol. Chem. 263, 15602-15607, 1988
A:Title: Identification of the mouse muscle 43,000-dalton acetylcholine receptor-asso
A:Reference number: A31995; MUID:89008468
A:Accession: A31995
A:Molecule type: mRNA
A:Residues: 1-412 <FRA>
A:Cross-references: GB:J03962; NID:g200652; PIDN:AAA40030.1; PID:g200653
R:Frøehner, S.C. 249, 229-233, 1989
FEBS Lett. 249, 229-233, 1989
A:Title: Expression of RNA transcripts for the postsynaptic 43 kDa protein in innerva
A:Reference number: S04488; MUID:89289985
A:Accession: S04488
A:Molecule type: mRNA
A:Residues: 1-343, 'DV', 346-412 <FRO>

Db 174 VQDFVHLSLWLRSMGIPCR 194

RESULT 6

C8HUB
complement C8 beta chain precursor [validated] - human
C:Species: Homo sapiens (man)
C:Date: 28-Dec-1987 #sequence_revision 15-Oct-1994 #text_change 17-Nov-2000
C:Accession: A43071; A94618; A90517; A27208; A26705
R:Sodetz, J.M.
submitted to GenBank, June 1988
A:Reference number: A43071
A:Accession: A43071
A:Molecule type: mRNA
A:Residues: 1-591 <SOD1>
A:Cross-references: GB:M16973; NID:g179719; PIDN:AAA51862.1; PID:g179720
R:Sodetz, J.M.
submitted to the Protein Sequence Database, August 1987
A:Reference number: A94618
A:Accession: A94618
A:Molecule type: mRNA
A:Residues: 'SOD', 5-591 <SOD2>
R:Howard, O.M.Z.; Rao, A.G.; Sodetz, J.M.
Biochemistry 26, 3565-3570, 1987
A:Title: Complementary DNA and derived amino acid sequence of the beta subunit of human C9.
A:Reference number: A90517; MUID:88000561
A:Accession: A90517
A:Molecule type: mRNA
A:Residues: 'SQCD', 5-436, 'PGIPGAAD', 446-591 <HOW>
A:Cross-references: GB:M16973; NID:g179719
A:Note: parts of this sequence, including the amino and carboxyl ends of the mature protein
R:Haefliger, J.A.; Tschopp, J.; Nardelli, D.; Wahli, W.; Koehler, H.P.; Tosi, M.; Stanley
Biochemistry 26, 3551-3556, 1987
A:Title: Complementary DNA cloning of complement C8-beta and its sequence homology to C9
A:Reference number: A27208; MUID:88000559
A:Accession: A27208
A:Molecule type: mRNA
A:Residues: 47-116, 'R', 118-591 <HAE>
A:Cross-references: GB:X04393; NID:g29574; PIDN:CAA27981.1; PID:g29575
R:Forsteege, J.; Blommers, M.; Hess, D.; Furmanek, A.; Miroshnichenko, O.
J. Biol. Chem. 274, 32786-32794, 1999
A:Title: The four terminal components of the complement system are C-mannosylated on multiple sites
A:Reference number: A59362; MUID:20020247
A:Contents: annotation
A:Note: Identification and location of C-mannosylation sites by mass-spectroscopy
C:Genetics:
A:Gene: GDB:C8B
A:Cross-references: GDB:119736; OMIM:120960
A:Map position: lp32-lp32
C:Complex: heterotrimer of C8 alpha chain (PIR:C8HUA), C8 beta chain (PIR:C8HUB), and C8 gamma chain (PIR:C8HUG)
C:Function:
A:Description: combines with complement C5b-7 complex to polymerize complement component C5b-9
A:Pathway: complement pathway
C:Superfamily: complement C9; EGF homology; LDL receptor ligand-binding repeat homology; N:Alternate names: complement C9; complement pathway; cytolysis; glycoprotein; m
C:Keywords: complement alternate pathway; complement pathway; cytolysis; glycoprotein; m
F:1-32/Domain: signal sequence #status predicted <SIG>
F:33-54/Domain: propeptide #status predicted <PRO>
F:55-591/Product: complement C8 beta chain #status experimental <MPT>
F:63-117/Domain: thrombospondin type 1 repeat homology <THR1>
F:122-155/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F:503-534/Domain: EGF homology <EGF>
F:544-591/Domain: thrombospondin type 1 repeat homology <THR2>
F:70,73,551,554/Modified site: 2'-mannosyl-tryptophan (Trp) #status experimental
F:243/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:553/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 26.2%; Score 54; DB 1; Length 591;
Best Local Similarity 28.1%; Pred. No. 19;
Matches 9; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 2 FSTPVKILCOILHITQILILRCYCPCRRSG 33

Db 481 YSSTVRQNMKQALEFOKEVSSCHCAPCQNG 512

RESULT 7

TI4593
syringomycin synthetase - Pseudomonas syringae pv. syringae
C:Species: Pseudomonas syringae pv. syringae
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 01-Dec-2000
C:Accession: TI4593
R:Guenzi, E.; Galli, G.; Grgurina, I.; Gross, D.C.; Grandi, G.
J. Biol. Chem. 273, 32857-32863, 1998
A:Title: Characterization of the syringomycin synthetase gene cluster. A link between
A:Reference number: Z18153; MUID:99047670
A:Accession: TI4593
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-9376 <GUE>
A:Cross-references: EMBL:AF047828; NID:g3510628; PID:g3510629; PIDN:AAC80285.1
C:Genetics:
A:Gene: syre
C:Superfamily: acetate--CoA ligase homology; acyl carrier protein homology
C:Keywords: carrier protein; phosphopantetheine; phosphoprotein
F:441-896/Domain: acetate--CoA ligase homology <ACL1>
F:914-981/Domain: acyl carrier protein homology <ACP1>
F:1529-1984/Domain: acetate--CoA ligase homology <ACL2>
F:2002-2069/Domain: acyl carrier protein homology <ACP2>
F:2613-3071/Domain: acetate--CoA ligase homology <ACL3>
F:3089-3156/Domain: acyl carrier protein homology <ACP3>
F:3700-4158/Domain: acetate--CoA ligase homology <ACL4>
F:4176-4244/Domain: acyl carrier protein homology <ACP4>
F:4768-5224/Domain: acetate--CoA ligase homology <ACL5>
F:5242-5310/Domain: acyl carrier protein homology <ACP5>
F:5834-6280/Domain: acetate--CoA ligase homology <ACL6>
F:6298-6366/Domain: acyl carrier protein homology <ACP6>
F:6892-7352/Domain: acetate--CoA ligase homology <ACL7>
F:7370-7437/Domain: acyl carrier protein homology <ACP7>
F:7990-8440/Domain: acetate--CoA ligase homology <ACL8>
F:8458-8526/Domain: acyl carrier protein homology <ACP8>
F:9015-9083/Domain: acyl carrier protein homology <ACP9>
F:946,2034,3121,4208,5274,6330/Binding site: phosphopantetheine (Ser) (covalent) #sta

Query Match 26.2%; Score 54; DB 2; Length 9376;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 5 PVKILCOILHITQILIL 22

Db 1099 PQQVLRQALHVTLELL 1116

RESULT 8

PN0141
lutropin beta chain - sperm whale
N:Alternate names: lutinizing hormone, beta chain
C:Species: Physeter catodon (sperm whale)
C:Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 07-May-1999
C:Accession: PN0141
R:Pankov, Y.A.; Karasev, V.S.
Biochimia 49, 1004-1018, 1984
A:Title: Lutinizing hormone of the sperm-whale: amino acid sequence of reduced and c
A:Reference number: PN0141; MUID:84281133
A:Accession: PN0141
A:Molecule type: protein
A:Residues: 1-118 <PAN>
A:Note: article in Russian with English abstract
C:Superfamily: pituitary glycoprotein hormone beta chain
C:Keywords: glycoprotein; hormone
F:9-34,23-57,26-88,38-110,72-100,90-93/Disulfide bonds: #status predicted
F:13/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 26.2%; Score 54; DB 1; Length 591;
Best Local Similarity 28.1%; Pred. No. 19;
Matches 9; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

Query Match 25.7%; Score 53; DB 2; Length 118;
Best Local Similarity 56.2%; Pred. No. 7.3;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 22 LRCYCPCRRSGSPG 37
| | | | | | | | | |
Db 86 LSCGCGPCRLSSDCG 101

RESULT 9
PN0139
lutropin beta chain - minke whale
N:Alternate names: luteinizing hormone beta chain
C:Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
C>Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 08-Dec-1995
C:Accession: PN0139
R:Karasev, V.S.; Pankov, Y.A.
Biochimica 50, 1972-1986, 1985
A:Title: Amino acid sequence of reduced and carboxymethylated alpha- and beta-subunits of
A:Reference number: PN0138
A:Accession: PN0139
A:Molecule type: protein
A:Residues: 1-118 <KAR>
A:Note: article in Russian with English abstract
C:Superfamily: pituitary glycoprotein hormone beta chain
C:Keywords: glycoprotein; hormone
F:9-34,23-57,26-88,38-110,72-100,90-93/Disulfide bonds: #status predicted
F:13/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 25.7%; Score 53; DB 2; Length 118;
Best Local Similarity 56.2%; Pred. No. 7.3;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 22 LRCYCPCRRSGSPG 37
| | | | | | | | | |
Db 86 LSCGCGPCRLSSBCG 101

RESULT 10
UTPG8
lutropin beta chain precursor - pig
N:Alternate names: interstitial cell-stimulating hormone (ICSH) beta chain; luteinizing
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 24-Apr-1984 #sequence_revision 30-Jun-1993 #text_change 16-Jun-2000
C:Accession: A48170; A30322; A01501; A60584
R:Ezashi, T.; Hirai, T.; Kato, T.; Wakabayashi, K.; Kato, Y.
J. Mol. Endocrinol. 5, 137-146, 1990
A:Title: The gene for the beta subunit of porcine LH: clusters of GC boxes and CACCC ele
A:Reference number: A48170; MUID:91063934
A:Accession: A48170
A:Molecule type: DNA
A:Residues: 1-141 <EZA>
A:Cross-references: GB:D00579; NID:g217693; PIDN:BAA00457.1; PID:g217694
R:Kato, Y.; Hirai, T.
Mol. Cell. Endocrinol. 62, 47-53, 1989
A:Title: Cloning and DNA sequence analysis of the cDNA for the precursor of porcine lute
A:Reference number: A30322; MUID:89306142
A:Accession: A30322
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-141 <KAT>
R:Maguain-Rogister, G.; Hennen, G.
Eur. J. Biochem. 39, 235-253, 1973
A:Title: Luteinizing hormone. The primary structures of the beta-subunit from bovine and
A:Reference number: A91212; MUID:74075724
A:Accession: A01501
A:Molecule type: protein
A:Residues: 21-29, 'Z', 31-39, 'D', 41-61, 'R', 63-82, 'I', 84-86, 'S', 88-121, 'PG', 124-133, 'P', 13
A:Note: 30-Arg was also found
A:Note: about half the chains lack one or both carboxyl-terminal leucines
R:Nomura, K.; Ohmura, K.; Nakamura, Y.; Horiba, N.; Shirakura, Y.; Sato, Y.; Ujihara, M.
Endocrinology 124, 712-719, 1989

A:Title: Porcine luteinizing hormone isoform(s): relationship between their molecular
A:Reference number: A60584; MUID:89107050
A:Accession: A60584
A:Molecule type: protein
A:Residues: 21-31;137-139 <NOM>
A:Note: the lutropin beta chain is heterogeneous at the carboxyl end; this form lacks
C:Genetics:
A:Introns: 5/3; 61/3
C:Superfamily: pituitary glycoprotein hormone beta chain
C:Keywords: blocked amino end; glycoprotein; hormone
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-141/Product: lutropin beta chain #status experimental <MAT>
F:21/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #
F:29-54,43-77,46-108,58-130,92-120,110-113/Disulfide bonds: #status predicted
F:33/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 25.7%; Score 53; DB 1; Length 141;
Best Local Similarity 56.2%; Pred. No. 8.4;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 22 LRCYCPCRRSGSPG 37
| | | | | | | | | |
Db 106 LSCGCGPCRLSSDCG 121

RESULT 11
JG0177
LHP precursor - Korean leech
C:Species: Hirudo nipponia (Korean leech)
C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 19-May-2000
C:Accession: JG0177
R:Minakata, H.; Ikeda, T.; Nagahama, T.; Oumi, T.; Ukena, K.; Matsushima, O.; Kawano,
Biosci. Biotechnol. Biochem. 63, 443-445, 1999
A:Title: Comparison of precursor structures of the GGNG peptides derived from the ear
A:Reference number: JG0176; MUID:99209006
A:Accession: JG0177
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-111 <MIN>
A:Cross-references: DDBJ:D63651
C:Superfamily: leech LEP precursor

Query Match 25.5%; Score 52.5; DB 2; Length 111;
Best Local Similarity 40.0%; Pred. No. 8.1;
Matches 12; Conservative 6; Mismatches 7; Indels 5; Gaps 1;

QY 8 ILQCQSLHITQLILRCYCPCRRSGSPG 37
: | | | | | | | | | | | | | |
Db 6 LVLCLSLHVTGVERRY-----RLGSDEG 30

RESULT 12
T27983
hypothetical protein ZK721.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C:Accession: T27983
R:Miller, N.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid ZK721.
A:Reference number: Z20450
A:Accession: T27983
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-154 <MIL>
A:Cross-references: EMBL:U40951; PIDN:AAA81733.1; CESP:ZK721.4
C:Genetics:
A:Gene: CESP:ZK721.4
A:Introns: 30/3; 80/2
C:Superfamily: Caenorhabditis elegans hypothetical protein ZK721.4

Qy 1 MFSTPVKII LCQSILHITQLLRC 24

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:36:16 ; Search time 62.39 seconds
(without alignments)
20.864 Million cell updates/sec

Title: US-08-887-977-10_COPY_1_38
Perfect score: 206
Sequence: 1 MFSTPVKILLQCSILHQLILRCYCPCRRSGSPGY 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	55	26.7	140	1	CO8B_RAT
2	55	26.7	411	1	RAPS_HUMAN
3	55	26.7	411	1	RAPS_MOUSE
4	54	26.2	141	1	LSHB_HUMAN
5	54	26.2	591	1	CO8B_HUMAN
6	53	25.7	118	1	LSHB_BALAC
7	53	25.7	118	1	LSHB_PHYCA
8	53	25.7	141	1	LSHB_PIG
9	52	25.2	315	1	VN35_ROT1
10	51	24.8	411	1	RAPS_TORCA
11	51	24.8	444	1	XK_HUMAN
12	50	24.3	141	1	LSHB_BOVIN
13	50	24.3	141	1	LSHB_SHEEP
14	50	24.3	207	1	CLDB_HUMAN
15	50	24.3	877	1	P101_PIG
16	49	23.8	138	1	LSHB_CANFA
17	49	23.8	141	1	LSHB_CERSI
18	49	23.8	141	1	LSHB_MOUSE
19	49	23.8	141	1	LSHB_RAT
20	49	23.8	143	1	LSHB_FELCA
21	49	23.8	165	1	CGHB_PAPAN
22	49	23.8	207	1	CLDB_MOUSE
23	49	23.8	260	1	GLO2_HUMAN
24	49	23.8	260	1	GLO2_RAT
25	49	23.8	431	1	CGVK_HSVSA
26	49	23.8	590	1	CO8B_RABIT
27	48.5	23.5	131	1	KRA3_SHEEP
28	48.5	23.5	511	1	MVIN_ECOLI
29	47.5	23.1	48	1	RL33_MTCGA
30	47.5	23.1	299	1	SUTL_YEAST
31	47	22.8	128	1	LSHB_PHOSU
32	47	22.8	254	1	UL79_HSV7J
33	46.5	22.6	1896	1	RPB1_DROME

34	46	22.3	74	1	SGS7_DROME
35	46	22.3	165	1	CGHB_HUMAN
36	46	22.3	252	1	PHNP_ECOLI
37	46	22.3	328	1	YLM8_CAEEL
38	46	22.3	336	1	UL16_EBV
39	46	22.3	484	1	US15_HCMVA
40	46	22.3	524	1	MVIN_SALTU
41	46	22.3	971	1	Y029_HUMAN
42	46	22.3	1040	1	RAG1_MOUSE
43	46	22.3	1043	1	RAG1_HUMAN
44	46	22.3	1406	1	CPBX_DROME
45	45.5	22.1	183	1	KITH_FOWPV

ALIGNMENTS

RESULT 1
CO8B_RAT STANDARD; PRT; 140 AA.
AC P55314:
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE COMPLEMENT COMPONENT C8 BETA CHAIN (FRAGMENT).
GN C8B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BN/CRL; TISSUE=Liver;
RX MEDLINE=95394451; PubMed=7665162;
RA Kershaw E.E., Chua S.C., Williams J.A., Murphy E.M., Leibel R.L.;
RT "Molecular mapping of SSRs for Pgml and C8b in the vicinity of the
rat fatty locus".
RL Genomics 27:149-154(1995).

CC -!- FUNCTION: C8 IS A CONSTITUENT OF THE MEMBRANE ATTACK COMPLEX.
CC C8 BINDS TO THE C5B-7 COMPLEX, FORMING THE C5B-8 COMPLEX. C5-B8
CC BINDS C9 AND ACTS AS A CATALYST IN THE POLYMERIZATION OF C9.
CC -!- SUBUNIT: C8 IS COMPOSED OF THREE CHAINS: ALPHA, BETA AND GAMMA.
CC THE BETA CHAIN BINDS TO THE C8 ALPHA CHAIN AND TO THE C5B-C7
CC COMPLEX, PRESUMABLY TO C5B. IT IS ESSENTIAL TO THE INCORPORATION
CC OF C8 INTO THE C5B-C8 COMPLEX.
CC -!- SIMILARITY: TO COMPLEMENT FACTORS C6, C7, C9, AND TO PERFORIN.
CC -!- SIMILARITY: CONTAINS 2 TSP TYPE-1 DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 LDL-RECEPTOR CLASS A DOMAIN.
CC -----
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CC -----
CC EMBL; U20194; AAA82890.1; -
CC InterPro; IPR000561; -
CC InterPro; IPR000884; -
CC InterPro; IPR001862; -
CC InterPro; IPR002172; -
CC Pfam; PF00090; tsp_1; 1.
CC PROSITE; PS00022; EGF_1; 1.
CC PROSITE; PS01186; EGF_2; FALSE NEG.
CC PROSITE; PS01209; LDLRA_1; PARTIAL.
CC PROSITE; PS00068; LDLRA_2; PARTIAL.
CC PROSITE; PS00279; MAC_PERFORIN; PARTIAL.
CC PROSITE; PS00092; TSP1; 1.
CC Complement pathway; Complement alternate pathway; Glycoprotein;
CC Plasma; Membrane attack complex; Cytolysis; EGF-like domain;
CC Repeat.

FT NON_TER 1 1
 FT DOMAIN 49 85 EGF-LIKE.
 FT DOMAIN 92 140 TYPE-1 TSP 2.
 SQ SEQUENCE 140 AA; 15331 MW; F7FDE36325EC0488 CRC64;

Query Match 26.7%; Score 55; DB 1; Length 140;
 Best Local Similarity 31.2%; Pred. No. 1.2;
 Matches 10; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 2 FSTPVKILQCSILHITQILRLCYCAPCRSSG 33
 Db 31 YSTVKQNMKALEEFOKEVSSCRAPCRNNG 62

RESULT 2

AC Q13702; DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE 43 KDA RECEPTOR-ASSOCIATED PROTEIN OF THE SYNAPSE (RAPSYN)
 DE (ACETYLCHOLINE RECEPTOR-ASSOCIATED 43 KDA PROTEIN) (43 KDA
 DE POSTSYNAPTIC PROTEIN).
 GN RAPSN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle;
 RX MEDLINE=97001170; PubMed=8812503;
 RA Buckel A., Beeson D., James M., Vincent A.;
 RT "Cloning of cDNA encoding human rapsyn and mapping of the RAPSN gene
 RT locus to chromosome 11p11.2-pl1.1.";
 RL Genomics 35:613-616(1996).
 CC -!- FUNCTION: THOUGHT TO PLAY SOME ROLE IN ANCHORING OR STABILIZING
 CC THE NICOTINIC ACETYLCHOLINE RECEPTOR AT SYNAPTIC SITES. IT MAY
 CC LINK THE RECEPTOR TO THE UNDERLYING POSTSYNAPTIC CYTOSKELETON,
 CC POSSIBLY BY DIRECT ASSOCIATION WITH ACTIN OR SPECTRIN.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF POSTSYNAPTIC
 CC MEMBRANES.
 CC -!- DOMAIN: A CYSTEINE-RICH REGION HOMOLOGOUS TO PART OF THE
 CC REGULATORY DOMAIN OF PROTEIN KINASE C MAY BE IMPORTANT IN
 CC INTERACTIONS OF THIS PROTEIN WITH THE LIPID BILAYER.
 CC -!- SIMILARITY: BELONGS TO THE RAPSN FAMILY.

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CC EMBL; Z33905; CAA83954.1;
 CC MIM; 601592;
 DR InterPro: IPR001237;
 DR PRINTS; PR00217; POSTSYNAPTIC.
 DR PROSITE; PS00405; 43_KD_POSTSYNAPTIC; 1.
 KW Synapse; Postsynaptic membrane; Cytoskeleton; Phosphorylation;
 KW Myristate.
 FT INIT_MET 0 0 BY SIMILARITY.
 FT LIPID 1 1 MYRISTATE (BY SIMILARITY).
 FT MOD_RES 195 195 PHOSPHORYLATION (POTENTIAL).
 FT MOD_RES 404 404 PHOSPHORYLATION (POTENTIAL).
 FT DOMAIN 362 398 INVOLVED IN MEMBRANE ASSOCIATION
 FT FT (POTENTIAL).
 SQ SEQUENCE 411 AA; 46199 MW; 6A9FBA4B95E58C8C CRC64;

Query Match 26.7%; Score 55; DB 1; Length 411;
 Best Local Similarity 37.1%; Pred. No. 3.2;
 Matches 13; Conservative 1; Mismatches 9; Indels 12; Gaps 2;

QY 11 CQSILHITQILRLCY-----CAPCRSSGSSPCY 38
 Db 381 CSHIFH-----LRCLQNNGTRSCNCRSSMKPGF 410

RESULT 3

AC P12672; DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE 43 KDA RECEPTOR-ASSOCIATED PROTEIN OF THE SYNAPSE (RAPSYN)
 DE (ACETYLCHOLINE RECEPTOR-ASSOCIATED 43 KDA PROTEIN) (43 KDA
 DE POSTSYNAPTIC PROTEIN).
 GN RAPSN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle;
 RX MEDLINE=89289985; PubMed=2737281;
 RA Froehner S.C.;
 RT "Expression of RNA transcripts for the postsynaptic 43 kDa protein in
 RT innervated and denervated rat skeletal muscle.";
 RL FEBS Lett. 249:229-233(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle;
 RX MEDLINE=89008468; PubMed=3170600;
 RA Fraill D.E., McLaughlin L.L., Mudd J., Merlie J.P.;
 RT "Identification of the mouse muscle 43,000-dalton acetylcholine
 RT receptor-associated protein (RAPSN) by cDNA cloning.";
 RL J. Biol. Chem. 263:15602-15607(1988).
 CC -!- FUNCTION: THOUGHT TO PLAY SOME ROLE IN ANCHORING OR STABILIZING
 CC THE NICOTINIC ACETYLCHOLINE RECEPTOR AT SYNAPTIC SITES. IT MAY
 CC LINK THE RECEPTOR TO THE UNDERLYING POSTSYNAPTIC CYTOSKELETON,
 CC POSSIBLY BY DIRECT ASSOCIATION WITH ACTIN OR SPECTRIN.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF POSTSYNAPTIC
 CC MEMBRANES.
 CC -!- DOMAIN: A CYSTEINE-RICH REGION HOMOLOGOUS TO PART OF THE
 CC REGULATORY DOMAIN OF PROTEIN KINASE C MAY BE IMPORTANT IN
 CC INTERACTIONS OF THIS PROTEIN WITH THE LIPID BILAYER.
 CC -!- SIMILARITY: BELONGS TO THE RAPSN FAMILY.

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CC EMBL; X15788; CAA33789.1;
 CC EMBL; J03962; AAA40030.1;
 DR PIR; S04488; S04488.
 DR PIR; A31995; A31995.
 DR MGI; MGI:99422; Rapsn.
 DR InterPro: IPR001237;
 DR PRINTS; PR00217; POSTSYNAPTIC.
 DR PROSITE; PS00405; 43_KD_POSTSYNAPTIC; 1.
 KW Synapse; Postsynaptic membrane; Cytoskeleton; Phosphorylation;
 KW Myristate.
 FT INIT_MET 0 0
 FT LIPID 1 1 MYRISTATE.
 FT MOD_RES 195 195 PHOSPHORYLATION (POTENTIAL).
 FT MOD_RES 404 404 PHOSPHORYLATION (POTENTIAL).

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FT DOMAIN 362 398 INVOLVED IN MEMBRANE ASSOCIATION
FT CONFLICT 343 344 (POTENTIAL).
FT SEQUENCE 411 AA; 46233 MW; 1085A5C709FDIE56 CRC64;
SQ

Query Match 26.7%; Score 55; DB 1; Length 411;
Best Local Similarity 37.1%; Pred. No. 3.2;
Matches 13; Conservative 1; Mismatches 9; Indels 12; Gaps 2;

QY 11 COSILHITLILRCY-----CAPCRSGSSPGY 38
Db 381 CSHIFH-----LRCLONNGTRSCPNCRSSMKPGF 410

RESULT 4
LSHB_HUMAN
ID LSHB_HUMAN STANDARD; PRT; 141 AA.
AC P01229;
DT 21-JUL-1986 (Rel. 01, Created)
DE 01-NOV-1995 (Rel. 32, Last sequence update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
DE LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HORMONE BETA SUBUNIT) (LSH-
DE BETA) (LSH-B) (LH-B).
GN LHB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84093590; PubMed=6690982;
RA Talmadge K., Vamvakopoulos N.C., Fiddes J.C.;
RT "Evolution of the genes for the beta subunits of human chorionic
RT gonadotropin and luteinizing hormone."
RL Nature 307:37-40(1984).
RN [2]
RP SEQUENCE OF 21-141.
RX MEDLINE=76062547; PubMed=1191677;
RA Sairam M.R., Li C.H.;
RT "Human pituitary lutropin. Isolation, properties, and the complete
RT amino acid sequence of the beta-subunit."
RL Biochim. Biophys. Acta 412:70-81(1975).
RN [3]
RP PRELIMINARY SEQUENCE OF 21-141.
RX MEDLINE=73090987; PubMed=4685398;
RA Shome B., Parlow A.F.;
RT "The primary structure of the hormone-specific, beta subunit of human
RT pituitary luteinizing hormone (hLH)."
RL J. Clin. Endocrinol. Metab. 36:618-621(1973).
RN [4]
RP PRELIMINARY PARTIAL SEQUENCE.
RX MEDLINE=73221227; PubMed=4719207;
RA Closset J., Hennen G., Lequin R.M.;
RT "Human luteinizing hormone. The amino acid sequence of the
RT subunit."
RL FEBS Lett. 29:97-100(1973).
RN [5]
RP STRUCTURE OF CARBOHYDRATE.
RX MEDLINE=91122088; PubMed=1991473;
RA Weisshaar G., Hiyama J., Renwick A.G.C., Nimitz M.;
RT "NMR investigations of the N-linked oligosaccharides at individual
RT glycosylation sites of human lutropin."
RL Eur. J. Biochem. 195:257-268(1991).
RN [6]
RP STRUCTURE BY NMR OF 58-77.
RX MEDLINE=92357029; PubMed=1495492;
RA Keutmann H.T., Hua Q.-X., Weiss M.A.;
RT "Structure of a receptor-binding fragment from human luteinizing
RT hormone beta-subunit determined by [1H]- and [15N]nuclear magnetic
RT resonance spectroscopy."
RL Mol. Endocrinol. 6:904-913(1992).
RN [7]

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RP VARIANT ARG-74.
RX MEDLINE=92085985; PubMed=1727547;
RA Weiss J., Axelrod L., Whitcomb R.W., Harris P.E., Crowley W.F.,
RA Jameson J.L.;
RT "Hypogonadism caused by a single amino acid substitution in the beta
RT subunit of luteinizing hormone."
RL New Engl. J. Med. 326:179-183(1992).
CC -1- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC -1- TISSUE SPECIFICITY: PITUITARY.
CC -1- DISEASE: DEFECTS IN LHB ARE A CAUSE OF HYPOGONADISM WHICH IS
CC CHARACTERIZED BY INFERTILITY AND PSEUDOPHERMAPRODITISM.
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.
CC -----
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CC -----
DR EMBL; X00264; CAA25067.1;
DR EMBL; S71273; AAD14960.1; ALT_SEQ.
DR PIR; A01497; UTHUB.
DR HSSP; P01233; IHRP.
DR GlycoSuiteDB; P01229;
DR MIM; 152780;
DR InterPro; IPR000359;
DR InterPro; IPR001545;
DR InterPro; IPR002400;
DR Pfam; PF00007; Cys_knot; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW Hormone; Glycoprotein; Signal; Pseudohermaphroditism;
KW Disease mutation.
FT SIGNAL 1 20
FT CHAIN 21 141 LUTROPIN BETA CHAIN.
FT DISULFID 29 77 BY SIMILARITY.
FT DISULFID 43 92 BY SIMILARITY.
FT DISULFID 46 130 BY SIMILARITY.
FT DISULFID 54 108 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 113 120 BY SIMILARITY.
FT CARBOHYD 50 50 N-LINKED (GLCNAC...).
FT VARIANT 74 74 Q -> R (IN HYPOGONADISM; LACK OF
FT RECEPTOR-BINDING).
FT CONFLICT 39 39 /FTID=VAR_003189.
FT CONFLICT 76 76 E -> O (IN REF. 2).
FT CONFLICT 132 135 MISSING (IN REF. 2).
SQ SEQUENCE 141 AA; 15345 MW; E411766253113F7C CRC64;

Query Match 26.2%; Score 54; DB 1; Length 141;
Best Local Similarity 62.5%; Pred. No. 1.7;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 22 LRCYCPCRRSGSSPG 37
Db 106 LSCRCGPCRRSTSDCG 121

RESULT 5
CO8B_HUMAN STANDARD; PRT; 591 AA.
AC P07358;
DT 01-APR-1988 (Rel. 07, Created)

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DR	PROSITE; PS01186; EGF_2; FALSE_NEG.
DR	PROSITE; PS01209; LDLRA_1; 1.
DR	PROSITE; PS00068; LDLRA_2; 1.
DR	PROSITE; PS00279; MAC_PERFORIN; 1.
DR	PROSITE; PS0092; TSP1; 2.
KW	Complement pathway; Complement alternate pathway; Glycoprotein;
KW	Signal; Plasma; Membrane attack complex; Cytolysis; EGF-like domain;
KW	Repeat; Transmembrane.
FT	SIGNAL 1 26
FT	PROPEP 27 54
FT	CHAIN 55 591
FT	DOMAIN 64 119
FT	DOMAIN 120 157
FT	TRANSMEM 312 328
FT	TRANSMEM 333 352
FT	DOMAIN 499 535
FT	DOMAIN 542 591
FT	DISULFID 122 133
FT	DISULFID 127 146
FT	DISULFID 140 155
FT	DISULFID 378 403
FT	CARBOHYD 70 70
FT	CARBOHYD 73 73
FT	CARBOHYD 101 101
FT	CARBOHYD 243 243
FT	CARBOHYD 551 551
FT	CARBOHYD 554 554
FT	CONFLICT 117 117
SQ	SEQUENCE 591 AA; 66947 MW; 1DBC54FF83AF6BF CRC64;

Query Match 26.2%; Score 54; DB 1; Length 591;
 Best Local Similarity 28.1%; Pred. No. 5.9;
 Matches 9; Conservative 11; Mismatches 12; Indels 0; Gaps

QY	2 FSTPVKIILQSILHITQLRLCYCAPRRSG 33
DB	481 YSSTVRQNKKALEEFQEVSSCHAPCGNG 512

RESULT 6
 LSHB_BALAC STANDARD; PRT; 118 AA.
 AC P33088;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE LUTROPIN BETA CHAIN (LUTEINIZING HORMONE BETA SUBUNIT) (LSH-BETA)
 DE (LSH-B) (LH-B).
 GN LHB.
 OS Balaenoptera acutorostrata (Minke whale) (Lesser rorqual).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
 OC Balaenopteridae; Balaenoptera.
 ON NCBI_TaxID=9767;
 RX [1]
 RP SEQUENCE.
 RA Karasev V.S., Pankov Y.A.;
 RT "Amino acid sequence of reduced and carboxymethylated alpha- and beta
 subunits of the little picked whale luteinizing hormone.";
 RL Biochimica 50:1972-1986(1985).
 CC -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
 THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
 CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
 CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTRPIN,
 LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
 CC -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
 FAMILY.
 DR PIR: PN0139;
 DR HSP; P01233; IHRP.
 DR InterPro: IPR000359;
 DR InterPro: IPR001545;
 DR InterPro: IPR002400;

DR Pfam; PF00007; Cys_knot; 1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
 DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; FALSE_NEG.
 KW Hormone; Glycoprotein.
 FT DISULFID 9 57 BY SIMILARITY.
 FT DISULFID 23 72 BY SIMILARITY.
 FT DISULFID 26 110 BY SIMILARITY.
 FT DISULFID 34 88 BY SIMILARITY.
 FT DISULFID 38 90 BY SIMILARITY.
 FT DISULFID 93 100 BY SIMILARITY.
 FT CARBOHYD 13 13 N-LINKED (GLCNAC...).
 SQ SEQUENCE 118 AA; 12414 MW; 039F229EFC480F5D CRC64;

Query Match 25.7%; Score 53; DB 1; Length 118;
 Best Local Similarity 56.2%; Pred. No. 2;
 Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 22 LRCYCAPCRRSGSSPG 37
 I I I I I I I I
 DB 86 LSCGCGPCLSSBSCG 101

RESULT 7

LSHB_PHYCA STANDARD; PRT; 118 AA.
 AC P25330;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE LUTROPIN BETA CHAIN (LUTEINIZING HORMONE BETA SUBUNIT) (LSH-BETA)
 DN (LSH-B) (LH-B).
 GN LHB.
 OS Physeter catodon (Sperm whale) (Physeter macrocephalus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
 OC Physeteridae; Physeter.
 OX NCBI_TaxID=9755;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=87032654; PubMed=3771098;
 RA Pankov Y.A., Karasov V.S.;
 RT "Primary structure of sperm whale luteinizing hormone.";
 RL Int. J. Pept. Protein Res. 28:124-129(1986).
 RN [2]
 RP SEQUENCE.
 RX MEDLINE=84281133; PubMed=6466737;
 RA Pankov Y.A., Karasev V.S.;
 RT "Luteinizing hormone of the sperm whale. Amino acid sequences of reduced and carboxymethylated beta-subunits.";
 RL Biochimica 49:1004-1018(1984).
 CC -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
 CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN, LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
 CC -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN FAMILY.
 CC PIR; P01411; P01411.
 DR HSP; P01233; 1HRP.
 DR InterPro; IPR000359; -
 DR InterPro; IPR001545; -
 DR InterPro; IPR002400; -
 DR Pfam; PF00007; Cys_knot; 1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
 DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
 KW Hormone; Glycoprotein.
 FT DISULFID 9 57 BY SIMILARITY.
 FT DISULFID 23 72 BY SIMILARITY.
 FT DISULFID 26 110 BY SIMILARITY.
 FT DISULFID 34 88 BY SIMILARITY.

FT DISULFID 38 90 BY SIMILARITY.
 FT DISULFID 93 100 BY SIMILARITY.
 FT CARBOHYD 13 13 N-LINKED (GLCNAC...).
 SQ SEQUENCE 118 AA; 12412 MW; 81177A56382F15E7 CRC64;

Query Match 25.7%; Score 53; DB 1; Length 118;
 Best Local Similarity 56.2%; Pred. No. 2;
 Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 22 LRCYCAPCRRSGSSPG 37
 I I I I I I I I
 DB 86 LSCGCGPCLSSDCG 101

RESULT 8

LSHB_PIG STANDARD; PRT; 141 AA.
 AC P01232;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HORMONE BETA SUBUNIT) (LSH-BETA) (LSH-B).
 DN LHB.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91063934; PubMed=1701088;
 RA Ezashi T., Hirai T., Kato T., Wakabayashi K., Kato Y.;
 RT "The gene for the beta subunit of porcine LH: clusters of GC boxes and CACC elements.";
 RL J. Mol. Endocrinol. 5:137-146(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89306142; PubMed=2744222;
 RA Kato Y., Hirai T.;
 RT "Cloning and DNA sequence analysis of the cDNA for the precursor of porcine luteinizing hormone (LH) beta subunit.";
 RL Mol. Cell. Endocrinol. 62:47-53(1989).
 RN [3]
 RP SEQUENCE OF 21-139.
 RX MEDLINE=74075724; PubMed=4770795;
 RA Maghain-Rogister G., Hennen G.;
 RT "Luteinizing hormone. The primary structures of the beta-subunit from bovine and porcine species.";
 RL Eur. J. Biochem. 39:235-253(1973).
 CC -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
 CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN, LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
 CC -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN FAMILY.
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 CC EMBL; D00579; BAA00457.1; -
 DR PIR; A30322; UTEGB.
 DR PIR; A48170; A48170.
 DR HSP; P01233; 1HRP.
 DR InterPro; IPR000359; -
 DR InterPro; IPR001545; -
 DR InterPro; IPR002400; -

DR Pfam: PF00007; Cys_knot; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PROSITE; PS00261; GLYCO.HORMONE.BETA_1; 1.
DR PROSITE; PS00689; GLYCO.HORMONE.BETA_2; 1.
KW Hormone; Signal; Glycoprotein.
FT SIGNAL 1 20
FT CHAIN 21 141 LUTROPIN BETA CHAIN.
FT DISULFID 29 77 BY SIMILARITY.
FT DISULFID 43 92 BY SIMILARITY.
FT DISULFID 46 130 BY SIMILARITY.
FT DISULFID 54 108 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 113 120 BY SIMILARITY.
FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .).
FT MOD_RES 21 21 BLOCKED.
FT VARIANT 30 30 R -> Z.
FT VARIANT 40 40 N -> D (IN REF. 3).
FT CONFLICT 62 62 V -> R (IN REF. 3).
FT CONFLICT 83 83 S -> I (IN REF. 3).
FT CONFLICT 87 87 I -> S (IN REF. 3).
FT CONFLICT 122 123 GP -> PG (IN REF. 3).
SQ SEQUENCE 141 AA; 14889 MW; 803E8E7C59F3C2CF CRC64;

Query Match 25.7%; Score 53; DB 1; Length 141;
Best Local Similarity 56.2%; Pred. No. 2.3;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 22 LRCYCPCRRSGSPG 37
| : | | | | | | | |
DB 106 LSCHCPCRLSSDCG 121

RESULT 9
VN35_ROT1 STANDARD; PRT; 315 AA.
AC Q03244;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE NONSTRUCTURAL RNA-BINDING PROTEIN 35 (NS35) (NCVP3).
GN S7.
OS Turkey rotavirus (serotype 7 / strain Ty-1).
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
OX NCBI_TaxID=36445;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93134787; PubMed=8380660;
RA Patton J.T., Salter-Cid L., Kalbach A., Mansell E.A., Kattoura M.;
RT "Nucleotide and amino acid sequence analysis of the rotavirus
nonstructural RNA-binding protein NS35.";
RL Virology 192:438-446(1993).
CC -!- FUNCTION: ESSENTIAL FOR GENOME REPLICATION AND FOR THE FORMATION
OF THE VIROPLASM. IT MAY ALSO BE IMPORTANT IN VIRAL RNA PACKAGING.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL; L04533; AAA47300.1; .
KW Nonstructural protein; RNA-binding.
FT DOMAIN 204 240 RNA-BINDING (POTENTIAL).
SQ SEQUENCE 315 AA; 35930 MW; B4FB84AB69EA65C6 CRC64;

Query Match 25.2%; Score 52; DB 1; Length 315;
Best Local Similarity 57.1%; Pred. No. 6.3;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 22 LRCYCPCRRSGSS 35
| : | | | | | | | |
DB 4 LACFCVPCDREGAS 17

RESULT 10
RAPS_TORCA STANDARD; PRT; 411 AA.
AC P09108;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE 43 KDA RECEPTOR-ASSOCIATED PROTEIN OF THE SYNAPSE (RAPSYN)
DE (ACETYLCHOLINE RECEPTOR-ASSOCIATED 43 KDA PROTEIN) (43 KDA
POSTSYNAPTIC PROTEIN).
GN RAPSIN.
OS Torpedo californica (Pacific electric ray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalia; Hymnosqualea; Pristiorajae; Batoidae;
OC Torpediniformes; Torpedinoidei; Torpedinidae; Torpedo.
OX NCBI_TaxID=7787;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87317641; PubMed=3476945;
RA Fraill D.E., Mudd J., Shah V., Carr C., Cohen J.B., Merlie J.P.;
RT "cDNAs for the postsynaptic 43-kDa protein of Torpedo electric organ
encode two proteins with different carboxyl termini.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:6302-6306(1987).
RN [2]
RP SEQUENCE OF 8-412.
RX MEDLINE=88107644; PubMed=3427060;
RA Carr C., McCourt D., Cohen J.B.;
RT "The 43-kilodalton protein of Torpedo nicotinic postsynaptic
membranes: purification and determination of primary structure.";
RL Biochemistry 26:7090-7102(1987).
RN [3]
RP MYRISTOYLATION.
RX MEDLINE=88331095; PubMed=3417776;
RA Musil L.S., Carr C., Cohen J.B., Merlie J.P.;
RT "Acetylcholine receptor-associated 43K protein contains covalently
bound myristate.";
RL J. Cell Biol. 107:1113-1121(1988).
CC -!- FUNCTION: THOUGHT TO PLAY SOME ROLE IN ANCHORING OR STABILIZING
THE NICOTINIC ACETYLCHOLINE RECEPTOR AT SYNAPTIC SITES. IT MAY
LINK THE RECEPTOR TO THE UNDERLYING POSTSYNAPTIC CYTOSKELETON,
POSSIBLY BY DIRECT ASSOCIATION WITH ACTIN OR SPECTRIN.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF POSTSYNAPTIC
MEMBRANES.
CC -!- ALTERNATIVE PRODUCTS: THERE ARE AT LEAST TWO DISTINCT PROTEINS
EXPRESSED, WHICH DIFFER IN THEIR C-TERMINUS.
CC -!- DOMAIN: A CYSTEINE-RICH REGION HOMOLOGOUS TO PART OF THE
REGULATORY DOMAIN OF PROTEIN KINASE C MAY BE IMPORTANT IN
INTERACTIONS OF THIS PROTEIN WITH THE LIPID BILAYER.
CC -!- SIMILARITY: BELONGS TO THE RAPSIN FAMILY.
CC
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CC
CC EMBL; J02952; AAA49282.1; .
DR EMBL; J02953; AAA49283.1; .
DR PIR; A28009; A28009.
DR InterPro; IPR001237; .
DR InterPro; IPR001841; .
DR Pfam; PF00097; zf-C3HC4; 1.
DR PRINTS; PS00217; POSTSYNAPTIC.
DR PROSITE; PS00405; 43 KD POSTSYNAPTIC; 1.
KW Synapse; Postsynaptic membrane; Cytoskeleton; Phosphorylation;
Myristate; Alternative splicing.

FT INTL_MET 0 0 MYRISTATE.
 FT LIPID 1 1
 FT MOD_RES 195 195 PHOSPHORYLATION (POTENTIAL).
 FT MOD_RES 404 404 PHOSPHORYLATION (POTENTIAL).
 FT DOMAIN 362 398 INVOLVED IN MEMBRANE ASSOCIATION
 (POTENTIAL).
 FT VARSPLIC 399 411 MISSING (IN SHORT ISOFORM).
 FT CONFLICT 361 361 Y -> T (IN REF. 2).
 FT CONFLICT 393 393 N -> D (IN REF. 2).
 FT CONFLICT 410 410 Y -> T (IN REF. 2).
 SQ SEQUENCE 411 AA; 46321 MW; 4D26262679C9B4D CRC64;

Query Match 24.8%; Score 51; DB 1; Length 411;
 Best Local Similarity 25.6%; Pred. No. 11;
 Matches 11; Conservative 8; Mismatches 12; Indels 12; Gaps 2;

Qy 3 STPVKIIICQSLHITQILRCY-----CAPCRSSGSPGY 38
 Db 373 NSQALPCSHLFH-----LKQLTNGRCPCNKRSSVKPGY 410

RESULT 11
 XK_HUMAN STANDARD; PRT; 444 AA.
 AC P51811;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE MEMBRANE TRANSPORT PROTEIN XK (KX ANTIGEN).
 GN XK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=94273191; PubMed=8004674;
 RX Ho M., Chelly J., Carter N., Danek A., Crocker P., Monaco A.P.;
 RT "Isolation of the gene for McLeod syndrome that encodes a novel
 membrane transport protein.";
 RL Cell 77:869-880(1994).
 RN [2]
 RP REVISIONS TO 204-205.
 RA Ho M.F.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: MAY BE INVOLVED IN SODIUM-DEPENDENT TRANSPORT OF NEUTRAL
 AMINO ACIDS OR OLIGOPEPTIDES.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -!- TISSUE SPECIFICITY: HIGH LEVELS IN SKELETAL MUSCLE, HEART, BRAIN,
 AND PANCREAS; LOW LEVELS IN PLACENTA, LUNG, LIVER, AND KIDNEY.
 CC -!- POLYMORPHISM: XK IS RESPONSIBLE FOR THE KX BLOOD GROUP SYSTEM.
 CC -!- DISEASE: DEFECTS IN XK ARE THE CAUSE OF MCLEOD SYNDROME, AN X-
 LINKED MULTISYSTEM DISORDER CHARACTERIZED BY ABNORMALITIES IN THE
 NEUROMUSCULAR AND HEMATOPOIETIC SYSTEMS.
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 CC
 CC EMBL; 232684; CAA83632.1;
 DR MIR; 314850;
 DR KW Transmembrane; Transport; Amino-acid transport; Blood group antigen.
 FT DOMAIN 1 2 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 3 23 POTENTIAL.
 FT DOMAIN 24 37 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 38 58 POTENTIAL.
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 POTENTIAL.

FT DOMAIN 90 140 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 141 161 POTENTIAL.
 FT DOMAIN 162 171 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 172 192 POTENTIAL.
 FT DOMAIN 193 208 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 209 229 POTENTIAL.
 FT DOMAIN 230 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 256 POTENTIAL.
 FT DOMAIN 257 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 298 POTENTIAL.
 FT DOMAIN 299 317 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 318 338 POTENTIAL.
 FT DOMAIN 339 349 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 350 370 POTENTIAL.
 FT DOMAIN 371 444 CYTOPLASMIC (POTENTIAL).
 SQ SEQUENCE 444 AA; 50876 MW; E94BDD0E3BEF7AB2 CRC64;

Query Match 24.8%; Score 51; DB 1; Length 444;
 Best Local Similarity 36.7%; Pred. No. 12;
 Matches 11; Conservative 4; Mismatches 15; Indels 0; Gaps 0;

Qy 2 FSTPVKIIICQSLHITQILRCYCAPCR 31
 Db 372 FFHCKKLFSSVSEGFQWLRFCWCACRQ 401

RESULT 12
 LSHB_BOVIN STANDARD; PRT; 141 AA.
 AC P04651;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HORMONE BETA SUBUNIT) (LSH-
 BETA) (LSH-B) (LH-B).
 GN LHB.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=85207729; PubMed=2987241;
 RX Virgin J.B., Silver B.J., Thomson A.R., Nilson J.H.;
 RT "The gene for the beta subunit of bovine luteinizing hormone encodes
 a gonadotropin mRNA with an unusually short 5'-untranslated region.";
 RL J. Biol. Chem. 260:7072-7077(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85182575; PubMed=3838746;
 RA Maurer R.A.;
 RT "Analysis of several bovine lutropin beta subunit cDNAs reveals
 heterogeneity in nucleotide sequence.";
 RL J. Biol. Chem. 260:4684-4687(1985).
 RN [3]
 RP SEQUENCE OF 21-139.
 RX MEDLINE=74075724; PubMed=4770795;
 RA Maghuln-Rogister G., Hennen G.;
 RT "Luteinizing hormone. The primary structures of the beta-subunit from
 bovine and porcine species.";
 RL Eur. J. Biochem. 39:235-253(1973).
 CC -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
 THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
 CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
 CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
 LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
 CC -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
 FAMILY.
 CC
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DR EMBL; M10077; AAA30623.1; -;
 DR EMBL; M11506; AAB59267.1; -;
 DR PIR; A01499; UTBOB.
 DR HSP; P01233; LHRP.
 DR GlycoSuiteDB; P04651; -;
 DR InterPro; IPR000359; -;
 DR InterPro; IPR001545; -;
 DR InterPro; IPR002400; -;
 DR Pfam; PF00007; Cys_knot; 1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
 DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
 KW Hormone; Signal; Glycoprotein.
 FT SIGNAL 1 20
 FT CHAIN 21 141 LUTROPIN BETA CHAIN.
 FT DISULFID 29 77 BY SIMILARITY.
 FT DISULFID 43 92 BY SIMILARITY.
 FT DISULFID 46 130 BY SIMILARITY.
 FT DISULFID 54 108 BY SIMILARITY.
 FT DISULFID 58 110 BY SIMILARITY.
 FT DISULFID 113 120 BY SIMILARITY.
 FT CARBOHYD 33 33 N-LINKED (GLCNAC...).
 FT CONFLICT 1 2 MISSING (IN REF. 2).
 FT CONFLICT 74 74 Q -> E (IN REF. 3).
 FT CONFLICT 112 112 P -> S (IN REF. 2).
 FT CONFLICT 122 123 GP -> PG (IN REF. 3).
 FT CONFLICT 126 126 Q -> E (IN REF. 3).
 SQ SEQUENCE 141 AA; 15202 MW; 44Pb1CBD4901BC95 CRC64;

Query Match 24.3%; Score 50; DB 1; Length 141;
 Best Local Similarity 50.0%; Pred. No. 5.8;
 Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 22 LRCYCAPCRSSGSPG 37
 | : | | | | : |
 DB 106 LSCHCPCRLSSTDCG 121

RESULT 13

LSHB_SHEEP STANDARD; PRT; 141 AA.
 AC P01231;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HORMONE BETA SUBUNIT) (LSH-
 DE BETA) (LSH-B) (INTERSTITIAL CELL STIMULATING HORMONE).
 GN LHB.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxId=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93351742; PubMed=8349025;
 RA Brown P., McNeilly J.R., Wallace R.M., McNeilly A.S., Clark A.J.;
 FT "Characterization of the ovine LH beta-subunit gene: the promoter
 FT directs gonadotrope-specific expression in transgenic mice.";
 RL Mol. Cell. Endocrinol. 93:157-165(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pituitary;
 RX MEDLINE=90245669; PubMed=2336396;
 RA D'Angelo-Bernard G., Mounni M., Jutisz M., Counis R.;
 FT "Cloning and sequence analysis of the cDNA for the precursor of the

RT beta subunit of ovine luteinizing hormone.";
 RL Nucleic Acids Res. 18:2175-2175(1990).
 RN [3]
 RX SEQUENCE OF 21-139.
 RA MEDLINE=72211145; PubMed=4556309;
 RT Liu W.-K., Nahn H.S., Sweeney C.M., Holcomb G.N., Ward D.N.;
 RT "The primary structure of ovine luteinizing hormone. II. The amino
 RT acid sequence of the reduced, S-carboxymethylated A-subunit (LH-
 RT beta).";
 RL J. Biol. Chem. 247:4365-4381(1972).
 RN [4]
 RP SEQUENCE OF 21-139.
 RX MEDLINE=73190035; PubMed=4575435;
 RA Sairam M.R., Samy T.S.A., Papkoff H., Li C.H.;
 RT "The primary structure of ovine interstitial cell-stimulating
 RT hormone. II. The beta-subunit.";
 RL Arch. Biochem. Biophys. 153:572-586(1972).
 RN [5]
 RP PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
 RX MEDLINE=76068152; PubMed=1201911;
 RA Chung D., Sairam M.R., Li C.H.;
 RT "The primary structure of ovine interstitial cell stimulating
 RT hormone. IV: Disulfide bridges of the beta subunit.";
 RL Int. J. Pept. Protein Res. 7:487-493(1975).
 RN [6]
 RP STRUCTURE OF CARBOHYDRATE.
 RX MEDLINE=91006170; PubMed=2209620;
 RA Weisshaar G., Hiyama J., Renwick A.G.C.;
 RT "Site-specific N-glycosylation of ovine lutropin. Structural analysis
 RT by one- and two-dimensional 1H-NMR spectroscopy.";
 RL Eur. J. Biochem. 192:741-751(1990).
 CC -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
 CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
 CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
 CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THROTROPIN,
 CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
 CC -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
 CC FAMILY.
 CC -----
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 CC -----
 DR EMBL; S64695; AAB27819.1; -;
 DR EMBL; X52488; CAA36729.1; -;
 DR PIR; A01500; UTSNB.
 DR PIR; S09232; S09232.
 DR HSP; P01233; LHRP.
 DR GlycoSuiteDB; P01231; -;
 DR InterPro; IPR000359; -;
 DR InterPro; IPR001545; -;
 DR InterPro; IPR002400; -;
 DR Pfam; PF00007; Cys_knot; 1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
 DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
 KW Hormone; Signal; Glycoprotein.
 FT SIGNAL 1 20
 FT CHAIN 21 141 LUTROPIN BETA CHAIN.
 FT DISULFID 29 77 BY SIMILARITY.
 FT DISULFID 43 92
 FT DISULFID 46 130
 FT DISULFID 54 108 BY SIMILARITY.
 FT DISULFID 58 110 BY SIMILARITY.
 FT DISULFID 113 120
 FT MOD_RES 21 21
 FT CARBOHYD 33 33
 FT VARIANT 138 141 N-LINKED (GLCNAC...).
 FT CONFLICT 30 30 MISSING (IN SOME MOLECULES).
 FT Q -> E (IN REF. 4).

```

QY      8  ILICQSIHLHTQLILRCYCACPCCRRSGSPG 37
      ::  | : | : : | | | | |
Db      84  LMTAASVLGLPAILLLLTLVPCIRMGQEPG 113

RESULT 15
P101_PIG
ID      P101_PIG      STANDARD;      PRT;      877 AA.
AC      002696;
DT      15-DEC-1998 (Rel. 37, Created)
DT      15-DEC-1998 (Rel. 37, Last sequence update)
DE      15-DEC-1998 (Rel. 37, Last annotation update)
DE      PHOSPHATIDYLINOSITOL 3-KINASE REGULATORY SUBUNIT (EC 2.7.1.137) (IB
DE      PI3-KINASE P101 SUBUNIT) (PTDINS-3-KINASE P101) (PI3K) (P101-PI3K).
DE      Sus scrofa (Pig).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX      NCBI_Taxid=9823;
RN      [1]
RP      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX      TISSUE=Neutrophils;
RX      MEDLINE=97248491; PubMed=9094719;
RA      Stephens L.R., Equino A., Erdjument-Bromage H., Lui M., Cooke F.,
RA      Coadwell J., Smrcka A.S., Thelen M., Cadwallader K., Tempst P.,
RA      Hawkins P.T.;
RT      "The G beta gamma sensitivity of a PI3K is dependent upon a tightly
RT      associated adaptor, p101."
RL      Cell 89:103-114(1997).
CC      -!- ENZYME REGULATION: WHEN BOUND TO P101 THE PI3K ACTIVITY OF P120
CC      COULD BE ACTIVATED GREATER THAN 100-FOLD BY THE BETA-GAMMA G
CC      PROTEINS.
CC      -!- PATHWAY: SIGNALING PATHWAYS REGULATING CELL GROWTH.
CC      -!- SUBUNIT: HETERODIMER OF A 101 KDA SUBUNIT AND A 120 KDA CATALYTIC
CC      SUBUNIT.
-----
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CC      or send an email to license@isb-sib.ch).
-----
DR      EMBL; Y10742; CAA71730.1; -.
KW      Transferase; Acetylation.
FT      MOD_RES      1      ACETYLATION.
FT      VARIANT      483      483      S -> G.
FT      SEQUENCE      877 AA; 96994 MW; 4903F957EFE64817 CRC64;
SQ
-----
Query Match      24.3%; Score 50; DB 1; Length 877;
Best Local Similarity 33.3%; Pred. No. 29;
Matches 11; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY      3  SPTVKIILCQSIHLHTQLILRCYCACPCCRRSGSS 35
      | : | | : | | : | | | | |
Db      809  SCPFAVCLDQDERKILQSVIRCEVSPCYKPEKS 841

Search completed: May 23, 2001, 15:36:17
Job time: 648 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:35:10 ; Search time 189.03 Seconds
(without alignments)
23.562 Million cell updates/sec

Title: US-08-887-977-10_COPY_1_38

Perfect score: 206

Sequence: 1 MFSTPVKIIILCSILHITQLILRCYCPCRRSGSPGY 38

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL15:*

1: sp.archaea:*

2: sp.bacteria:*

3: sp.fungi:*

4: sp.human:*

5: sp.invertebrate:*

6: sp.mammal:*

7: sp.mhc:*

8: sp.organelle:*

9: sp.phage:*

10: sp.plant:*

11: sp.rodent:*

12: sp.unclassified:*

13: sp.vertebrate:*

14: sp.virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	30.6	365	5 Q9W2E0	Q9W2E0 drosophila
2	56.5	27.4	120	1 Q9VAD0	Q9VAD0 aeropyrum p
3	56	27.2	227	4 Q9NV51	Q9NV51 homo sapien
4	54	26.2	279	2 P71734	P71734 mycobacteri
5	54	26.2	9376	2 O85168	O85168 pseudomonas
6	53.5	26.0	111	5 Q25104	Q25104 hirudo nipp
7	53	25.7	678	4 Q9NUT5	Q9NUT5 homo sapien
8	52.5	25.5	111	5 Q25102	Q25102 hirudo nipp
9	52.5	25.5	198	4 Q9P0S8	Q9P0S8 homo sapien
10	51.5	25.0	924	5 Q20016	Q20016 caenorhabdi
11	51	24.8	383	14 Q89609	Q89609 equine herp
12	50.5	24.5	816	5 Q9U274	Q9U274 caenorhabdi
13	50.5	24.5	1880	5 O18465	O18465 hirudo medi
14	50	24.3	578	11 Q9WU80	Q9WU80 mus musculus
15	50	24.3	1518	10 Q9SH34	Q9SH34 arabidopsis
16	49.5	24.0	249	6 Q9XSD3	Q9XSD3 macaca mula
17	49	23.8	38	6 Q46621	Q46621 tapirus ind
18	49	23.8	61	2 Q50154	Q50154 mycobacteri
19	49	23.8	80	11 Q63013	Q63013 rattus norv

20	49	23.8	82	6	O46622	ceratotheri
21	49	23.8	86	2	Q9WWL8	Q9WWL8 synchococc
22	49	23.8	129	5	O20552	O20552 caenorhabdi
23	49	23.8	135	6	O19102	O19102 ceratotheri
24	49	23.8	139	11	O62778	Q82778 rattus norv
25	49	23.8	141	6	O77835	O77835 ceratotheri
26	49	23.8	141	11	O60844	O60844 mus musculu
27	49	23.8	143	6	O77805	O77805 felis silve
28	49	23.8	157	6	O28306	O28306 canis famil
29	49	23.8	286	4	O9P2V3	O9P2V3 homo sapien
30	49	23.8	315	14	O55586	O55586 avian rotav
31	49	23.8	430	14	O9YTM9	O9YTM9 ateline her
32	49	23.8	687	3	O42955	O42955 schizosacch
33	49	23.8	880	4	O9V2Y2	O9V2Y2 homo sapien
34	48.5	23.5	123	1	O9VBC7	O9VBC7 aeropyrum p
35	48.5	23.5	413	13	O98860	O98860 cynops pyrr
36	48.5	23.5	446	11	O9QXV7	O9QXV7 mus musculu
37	48.5	23.5	683	3	O9P7Z1	O9P7Z1 schizosacch
38	48.5	23.5	1305	13	O91952	O91952 coturnix co
39	48	23.3	63	14	O64830	O64830 human adeno
40	48	23.3	198	5	O9ULD7	O9ULD7 leishmania
41	48	23.3	219	13	O99370	O99370 gallus gall
42	48	23.3	568	5	O23637	O23637 caenorhabdi
43	48	23.3	658	5	O18215	O18215 caenorhabdi
44	48	23.3	682	11	O9JH13	O9JH13 rattus norv
45	48	23.3	913	5	O9V7G6	O9V7G6 drosophila

ALIGNMENTS

RESULT	1
Q9W2E0	
ID	Q9W2E0 PRELIMINARY; PRT; 365 AA.
AC	Q9W2E0;
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE	CG15679 PROTEIN.
GN	CG15679.
OS	Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC	Ephydroidea; Drosophilidae; Drosophila.
OX	NCBI_TaxID=7227;
RP	[1]
RN	SEQUENCE FROM N.A.
RC	STRAIN=BERKELEY;
RX	MEDLINE=20196006; PubMed=10731132;
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Gale R.F.,
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA	Abriel J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA	Baliew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA	Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA	Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA	de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA	Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL; AF003454; AAF46752.1; -;
 DR FLYBASE; FBgn0034653; CG15679.
 SQ SEQUENCE 365 AA; 40978 MW; 1B51C4E809B0198 CRC64;

Query Match 30.6%; Score 63; DB 5; Length 365;
 Best Local Similarity 35.1%; Pred. No. 0.26;
 Matches 13; Conservative 7; Mismatches 9; Indels 8; Gaps 2;

QY 7 KILCOSILHI-----TQILRCYCAPCRSGSSP 36

Db 163 KVFCCSRVNRVDPPTGDETEMKQCFCICPCCR-GSRP 198

RESULT 2
 QYAD0 PRELIMINARY; PRT; 120 AA.
 ID QYAD0;
 AC QYAD0;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DE 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE HYPOTHETICAL 13.0 KDA PROTEIN APE2009.
 GN APE2009.
 OS Aeropyrum pernix.
 OC Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
 OC Aeropyrum.
 OX NCBI_TaxID=56636;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K1;
 RX MEDLINE=99310339; PubMed=10382966;
 RA Kavarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
 RA Jin-no K., Takahashi M., Sekine M., Baba S., Ankai A., Kosugi H.,
 RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
 RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
 RA Yamazaki J., Kushida N., Oguchi A., Aoki K., Kubota K., Nakamura Y.,
 RA Nomura N., Sako Y., Kikuchi H.;
 RT "Complete genome sequence of an aerobic hyper-thermophilic
 crenarchaeon, *Aeropyrum pernix* K1.";
 RL DNA Res. 6:83-101(1999).
 DR EMBL; AP000063; BAA81019.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 120 AA; 12969 MW; F796EE35809F4660 CRC64;

Query Match 27.4%; Score 56.5; DB 1; Length 120;
 Best Local Similarity 39.5%; Pred. No. 0.9;
 Matches 15; Conservative 5; Mismatches 11; Indels 7; Gaps 1;

QY 6 VKIILCQSLHITQILRC-----YCAPCRSGSSP 36

Db 19 VLLILSSLLILTSULLRCIRYWSAAYIPGRKPGYSP 56

RESULT 3
 Q9NV51 PRELIMINARY; PRT; 227 AA.
 ID Q9NV51
 AC Q9NV51;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE CDNA FLJ10920 FTS, CLONE OVARC1000384.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-OVARIAN CANCER;
 RA Isogai T., Oca T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K.,
 RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y.,
 RA Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K.,
 RA Masuho Y., Kanemori K.;
 RT "NEDO human cDNA sequencing project.";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK001782; BAA91907.1; -;
 SQ SEQUENCE 227 AA; 24072 MW; 03146D66E6FC4E30 CRC64;

Query Match 27.2%; Score 56; DB 4; Length 227;
 Best Local Similarity 31.2%; Pred. No. 1.8;
 Matches 15; Conservative 3; Mismatches 10; Indels 20; Gaps 2;

QY 4 TPVKIILCQSLHITQIL-----LRC-YCAPCCR 31

Db 129 TPAGVFLAESALHAGLAEPYMQGELASAISSGKKRRCGMCAPCCR 176

RESULT 4
 P71734 PRELIMINARY; PRT; 279 AA.
 ID P71734
 AC P71734;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DE 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE HYPOTHETICAL 31.0 KDA PROTEIN.
 GN RV2409C OR MTCY253.11.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skellern S., Squares S., Squires J.,
 RA Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of *Mycobacterium tuberculosis* from the
 complete genome sequence.";
 RL Nature 393:537-544(1998).
 DR EMBL; Z81368; CAB03718.1; -;
 DR TUBERCULIST; RV2409C; -;
 DR INTERPRO; IPR002931; -;
 DR PFAM; PF01841; Transglut_core; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 279 AA; 31029 MW; 0719C275EC8C9908 CRC64;

Query Match 26.2%; Score 54; DB 2; Length 279;
 Best Local Similarity 38.1%; Pred. No. 4.2;
 Matches 8; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 10 LCQSLHITQILRCYCAPCR 30

Db 174 VCQDFVHLSLMLVLRSMGIPCR 194

QY		8	IILCQSILHITQLILRCYCPCRRSGSPG	37
	:	:	: : : :	
D6		6	LVLCLSLHLVTRGVERRY	-----RLGSDEG 30

RESULT	9	
Q9P0S8		
ID	Q9P0S8	PRELIMINARY;
AC	Q9P0S8;	PRT;
DT	01-OCT-2000	15. Created

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DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
OS HSPC195.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=UMBILICAL CORD BLOOD;
RA Ye M., Zhang Q.H., Zhou J., Shen Y., Wu X.Y., Guan Z.Q., Wang L.,
RA Fan H.Y., Mao Y.F., Dai M., Huang Q.H., Chen S.J., Chen Z.;
RT "Human full length cDNA cloned from cd34+ stem cells.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF151029; AAF36115.1; -.
SQ SEQUENCE 198 AA; 21272 MW; EB6E198F2CE6AE58 CRC64;

Query Match 25.5%; Score 52.5; DB 4; Length 198;
Best Local Similarity 35.9%; Pred. No. 5.2;
Matches 14; Conservative 5; Mismatches 13; Indels 7; Gaps 1;

Qy 4 TPVKIILCSLHTLTQLI-----LRVCYCAPCRSGSS 35
Db 100 TPAGVFLAESALHAGLAIEYPMQGLPLPSAPARRSGNA 138

RESULT 10
Q20016 PRELIMINARY; PRT; 924 AA.
AC Q20016; Q22838;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE HYPOTHEICAL 104.3 KDA PROTEIN T27F2.2.
GN T27F2.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA White S.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Leonard N.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z74032; CAA98469.2; -.
DR EMBL; Z74045; CAA98469.2; JOINED.
DR EMBL; Z74045; CAA98554.2; -.
DR EMBL; Z74032; CAA98554.2; JOINED.
DR INTERPRO; IPR000331; -.
DR PFAM; PF02145; Rap_GAP; 1.
KW Hypothetical protein.
SQ SEQUENCE 924 AA; 104330 MW; 3F2EF474E885C1FB CRC64;

Query Match 25.0%; Score 51.5; DB 5; Length 924;
Best Local Similarity 34.1%; Pred. No. 26;
Matches 14; Conservative 4; Mismatches 14; Indels 9; Gaps 1;

Qy 1 MFSTPVVKIILCSL-----HITQILRLCYCAPCRRS 32
Db 590 LFSTPTHSITGWATSDGLKLYDHDGQDLLRCYSETCTDS 630
:||||| : : ||||| | |
:||||| : : ||||| | |

RESULT 11
Q89609 PRELIMINARY; PRT; 383 AA.
AC Q89609;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

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ID O18465 PRELIMINARY; PRT; 1880 AA.
AC O18465;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE TRACTIN.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OX NCBI_TaxID=6421;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92198663; PubMed=1550678;
RA Johansen K.M., Kopp D.M., Jellies J., Johansen J.;
RT "Tract formation and axon fasciculation of molecularly distinct
RT peripheral neuron subpopulations during leech embryogenesis.";
RN [2]
RN NEURON 8:559-572(1992).
RP SEQUENCE FROM N.A.
RX MEDLINE=97362067; PubMed=9214388;
RA Huang Y., Jellies J., Johansen K.M., Johansen J.;
RT "Differential glycosylation of tractin and LeechCAM, two novel Ig
RT superfamily members, regulates neurite extension and fascicle
RT formation.";
RN [3]
RN J. Cell Biol. 138:143-157(1997).
DR HSSP; P20241; 1CFB.
DR INTERPRO; IPR000087; -.
DR INTERPRO; IPR001777; -.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00041; fn3; 4.
DR PFAM; PF00047; ig; 6.
DR PRINTS; PR00014; ENTYPETII.
SQ SEQUENCE 1880 AA; 199867 MW; 174EC84DAC540DF0 CRC64;

Query Match 24.5%; Score 50.5; DB 5; Length 1880;
Best Local Similarity 37.9%; Pred. No. 66;
Matches 11; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

Oy 8 IILCOSILHITQILRCYCPCRRSGSP 36
Db 1755 LLICLLLLLLLLLLLLLILC-CIRCNRRGIYP 1782

RESULT 14
Q9WU80 PRELIMINARY; PRT; 578 AA.
AC Q9WU80;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CAMP INDUCIBLE 1 PROTEIN.
GN C11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Miyata M., Takahashi Y., Zheng P., Smith J.D.;
RT "Identification of three genes markedly induced by CAMP treatment of
RT RAW264 cells.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF121080; AAD24570.1; -.
DR INTERPRO; IPR000109; -.
DR PFAM; PF00854; PTR2; 2.
DR PROSITE; PS01023; PTR2_2; UNKNOWN_1.
SQ SEQUENCE 578 AA; 64022 MW; 9B56BEE7C3AB65A5 CRC64;

Query Match 24.3%; Score 50; DB 11; Length 578;
Best Local Similarity 30.6%; Pred. No. 29;

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Matches 11; Conservative 9; Mismatches 14; Indels 2; Gaps 1;

Oy 1 MFSTPVKIIILCOSILHITQILRCYC--CAPCRSGS 34
Db 245 LFATPVFTKPTGSGVSSMLKLAIFONCCPKRSSS 280

RESULT 15
Q9SH34 PRELIMINARY; PRT; 1518 AA.
AC Q9SH34;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE F2K11.14.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Shann P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
RA Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,
RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA Ecker J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC F2K11 from chromosome
RT I.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC008047; AAF19696.1; -.
DR INTERPRO; IPR000561; -.
DR INTERPRO; IPR001965; -.
DR INTERPRO; IPR002363; -.
DR PFAM; PF00628; PHD; 2.
DR PROSITE; PS01109; RIBOSOMAL_L10; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
SQ SEQUENCE 1518 AA; 173125 MW; 9750189E2A3DBDAD CRC64;

Query Match 24.3%; Score 50; DB 10; Length 1518;
Best Local Similarity 40.0%; Pred. No. 66;
Matches 8; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

Oy 9 ILCQSILHITQILRCYCPC 28
Db 623 IICQFLHLSAIV--CNCRP 640

Search completed: May 23, 2001, 15:35:12
Job time: 618 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:28:25 ; Search time 184.73 Seconds
(without alignments)
8.045 Million cell updates/sec

Title: US-08-887-977-10_COPY_39_64

Perfect score: 127

Sequence: 1 LVRIAYSLICVLGLNILWITFAF 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	127	100.0	365	19 W48086	Human dendritic ce
2	127	100.0	365	21 Y97077	Primate (human) ch
3	75	59.1	358	15 R53745	Partial sequence o
4	75	59.1	358	21 B21689	Human 7TM receptor
5	75	59.1	361	20 W97348	An Epstein-barr vi
6	75	59.1	378	15 R54079	Epstein Barr virus
7	75	59.1	378	15 R53744	Putative seven tra
8	75	59.1	378	19 W48724	Human V31 seven tr
9	75	59.1	378	19 W56164	G-protein coupled
10	75	59.1	378	19 W53622	Epstein Barr virus
11	75	59.1	378	21 B21688	Human 7TM receptor

12	75	59.1	378	21	Y90629	Human G protein-co
13	75	59.1	378	21	Y90663	Human mutant G pro
14	75	59.1	378	22	B50859	Human CCR7. Homo
15	75	59.1	410	15	R53743	Putative seven tra
16	75	59.1	410	19	W48723	Polypeptide sequen
17	75	59.1	410	21	B21687	Genomic clone of 7
18	71	55.9	359	15	R53747	Seven transmembran
19	71	55.9	359	19	W48728	Murine V31 seven t
20	71	55.9	359	21	B21691	Murine 7TM recepto
21	71	55.9	378	21	B21699	7TM receptor prote
22	69	54.3	372	20	W86323	Kidney injury asso
23	67	52.8	374	20	Y05643	Mouse Burkitt's ly
24	65	51.2	372	13	R27793	New platelet facto
25	65	51.2	372	16	R92239	Chemokine superfam
26	65	51.2	372	16	R68813	Human lymphocyte p
27	65	51.2	372	20	Y06644	Human Burkitt's ly
28	65	51.2	372	21	Y90627	Human G protein-co
29	65	51.2	372	21	Y90661	Human mutant G pro
30	63	49.6	355	15	R39995	Peptide effecting
31	63	49.6	355	15	R52749	C-C chemokine rece
32	63	49.6	355	18	W26588	Human MIP-1 alpha/
33	63	49.6	355	18	W25751	Human MIP-1alpha/R
34	63	49.6	355	21	R20571	Human CC-chemokine
35	62	48.8	428	14	R39264	Murine somatostati
36	61	48.0	30	18	W34015	Human mu opioid re
37	61	48.0	356	15	R65188	Murine mu-subtype
38	61	48.0	371	15	R65503	Murine delta opioi
39	61	48.0	372	15	R48629	Sequence of murine
40	61	48.0	372	16	R67682	Rat delta opiate r
41	61	48.0	372	16	R67670	Mouse delta opioi
42	61	48.0	372	19	W44938	Mouse delta opiate
43	61	48.0	372	21	Y80495	Mouse delta-opioi
44	61	48.0	380	21	Y68885	A murine mu-opioi
45	61	48.0	391	21	Y68886	A murine mu-opioi

ALIGNMENTS

RESULT 1
ID W48086 standard; Protein; 365 AA.
AC W48086;
XX
XX
DT 11-JUN-1998 (first entry)
XX
XX
DE Human dendritic cell chemokine receptor.
DE
DE
KW Human; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta;
KW receptor; dendritic cell; macrophage; inflammation; asthma.
XX
XX
OS Homo sapiens.

XX
XX
FH Key Location/Qualifiers
FH Misc-difference 193
FH /note= "encoded by CAN"
XX
XX
PN W09801557-A2.
XX
XX
PD 15-JAN-1998.
XX
XX
PF 02-JUL-1997; 97WO-US10819.
XX
XX
PR 04-JUN-1997; 97US-0048593.
PR 05-JUL-1996; 96US-0675814.
PR 11-OCT-1996; 96US-0028329.
XX
XX
PA (SCHE) SCHERING CORP.
XX
XX
PI Gish KC, Schall TJ, Vicari A, Wang W, Zlotnik A;
XX
XX
DR WPI; 1998-101054/09.

DR N-PSDB; V15418.
XX Novel chemokines, e.g. thymus expressed chemokine - used for
PT treating inflammatory conditions including asthma.
XX
PS Claim 3; Page 94-95; 202pp; English.
XX
CC The present sequence represents human dendritic cell chemokine receptor.
CC Antibodies which bind to the protein can be used in detecting or
CC diagnosing various immunological conditions related to expression
CC of the protein. The nucleic acid can be used for screening and
CC isolating DNA clones for the chemokines, especially from other
CC species. The chemokine can be used in the treatment of conditions
CC associated with abnormal physiology or development, including
CC inflammatory conditions such as asthma.
XX
SQ Sequence 365 AA;

Query Match 100.0%; Score 127; DB 19; Length 365;
Best Local Similarity 100.0%; Pred. No. 7.6e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LYRIAYSLICVLGLGNILVWITFAF 26
|||||
Db 39 lyriayslicvlgllgnilvwtfaf 64

RESULT 2
Y97077
ID Y97077 standard; Protein; 365 AA.
XX
XX Y97077;
AC
DT 04-DEC-2000 (first entry)
DE
DE Primate (human) chemokine receptor CCR6.
KW MIP-3-alpha; chemokine; CCR6 receptor; ligand; cytostatic; agonist;
KW antagonist; anti-psoriatic; dermatological; immunosuppressive;
KW anti-inflammatory.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
FH Misc-difference 193
FT /note= "Encoded by CAN#"
FT
XX WO200046248-A1.
XX
XX 10-AUG-2000.
XX
XX 02-FEB-2000; 2000WO-US00511.
XX
XX 03-FEB-1999; 99US-0244281.
XX
XX (SCHE) SCHERING CORP.
XX
XX Oldham ER, Homey B, Dieu-Nosjean M, Caux C, Zlotnik A;
XX
XX WPI; 2000-543477/49.
XX
XX N-PSDB; A51971.
XX
XX Novel methods for modulating the migration of cells within or to the
PT skin using MIP-3-alpha or CCR6 agonists or antagonists, useful for
PT treating skin disorders, e.g. cancer
XX
XX Disclosure; Page 53-54; 61pp; English.
XX
XX The MIP-3-alpha chemokine is expressed in inflamed skin cells. This
CC chemokine is the ligand for the CCR6 receptor. MIP-3-alpha or CCR6
CC agonists or antagonists can be used to modulate the migration of a cell
CC within or to the skin of a mammal. MIP-3-alpha can be used to purify a

CC population of cells expressing a MIP-3-alpha receptor. The methods are
CC useful for treating a mammalian subject with a skin disease or condition,
CC e.g. cancer, metastasis, psoriasis, atopic or contact dermatitis,
CC systemic lupus erythematosus and lichen ruber planus, or for treating
CC skin transplants or grafts.
XX
SQ Sequence 365 AA;

Query Match 100.0%; Score 127; DB 21; Length 365;
Best Local Similarity 100.0%; Pred. No. 7.6e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LYRIAYSLICVLGLGNILVWITFAF 26
|||||
Db 39 lyriayslicvlgllgnilvwtfaf 64

RESULT 3
R53745
ID R53745 standard; Protein; 358 AA.
XX
XX R53745;
AC
DT 02-FEB-1995 (first entry)
XX
DE Partial sequence of seven transmembrane receptor (V31).
XX
KW Primer; seven transmembrane receptor; receptor; amplification; PCR;
KW polymerase chain reaction.
XX
XX Homo sapiens.
XX
XX WO9412635-A.
XX
XX 09-JUN-1994.
XX
XX 17-NOV-1993; 93WO-US11153.
XX
XX 17-NOV-1992; 92US-0977452.
XX
XX (ICOS-) ICOS CORP.
XX
XX Godiska R, Gray PW, Schweickart VL;
XX
XX WPI; 1994-200264/24.
XX
XX N-PSDB; Q66162.
XX
XX DNA encoding seven transmembrane receptors - used to develop
PT prods. for use as therapeutic or diagnostic agents for conditions
PT involving the receptors.
XX
XX Example 3; Page 56-57; 100pp; English.
XX
XX Two primers (Q66148, Q66149) were used to amplify human genomic DNA
CC purified from leukocytes. Approximately 1000 clones were isolated
CC after the initial amplification reaction and probed with sequences
CC specific for seven transmembrane receptors IL8R1, AT2R and R20.
CC Clones which did not hybridise were then chosen for sequence
CC analysis. Three new clones were identified that appeared to encode
CC seven transmembrane receptor segments. Two more primers (Q66151,
CC Q66152) were used to isolate a full length version of one of these
CC clones designated V31 (See Q66153). This is the sequence encoded
CC by exon 3 of the V31 genomic clone
XX
XX Sequence 358 AA;

Query Match 59.1%; Score 75; DB 15; Length 358;
Best Local Similarity 60.9%; Pred. No. 0.0029;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 4 IAYSLICVLGLGNILVWITFAF 26


```

OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1..24
FT /label= Hydrophobic region.
FT /note= "Predicted to be a signal peptide for
FT membrane translocation."
FT
FT Modified-site 36
FT /note= "Potential N-linked glycosylation site."
FT Region 60..86
FT /label= Hydrophobic region.
FT Region 96..116
FT /label= Hydrophobic region.
FT Region 131..152
FT /label= Hydrophobic region.
FT Region 151..159
FT /note= "This sequences motif
FT (S-[I/V]-D-R-[Y/F]-X-X-X) is highly
FT conserved among a large number of G-protein
FT coupled receptors."
FT
FT Region 171..191
FT /label= Hydrophobic region.
FT Region 220..247
FT /label= Hydrophobic region.
FT Region 264..289
FT /label= Hydrophobic region.
FT Modified-site 292
FT /note= "Potential N-linked glycosylation site."
FT Region 314..331
FT /label= Hydrophobic region.
FT
XX W09412519-A.
XX
XX 09-JUN-1994.
XX
XX 08-OCT-1993; 93WO-US09636.
XX
XX 25-NOV-1992; 92US-0980518.
XX (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
XX Birkenbach M, Kieff E;
XX
XX WPI; 1994-200183/24.
XX N-PSDB; Q64125.
XX
XX DNA coding for Epstein Barr Virus induced (EBI) polypeptide(s)
XX and antibodies to EB1, 2 and 3 - useful for detecting EBV by
XX hybridisation or by immunoassay
XX
XX Claim 8; Page 54-56; 84pp; English.
XX
XX EBV infected B lymphocytes recapitulate features of antigen
XX stimulation in enlarging, increasing RNA synthesis, expressing
XX activation antigens and adhesion molecules, secreting Ig and
XX proliferating. Unlike antigen stimulated B lymphocytes, EBV
XX infected B lymphocytes continue to proliferate (in vitro) as
XX immortalised lymphoblastoid cell lines. Because of the similar
XX effects of EBV and antigen, EBV induced genes are likely to include
XX mediators of antigen induced B lymphocyte growth or differentiation.
XX
XX Sequence 378 AA;

Query Match 59.1%; Score 75; DB 15; Length 378;
Best Local Similarity 60.9%; Pred. No. 0.003;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 4 IAYSILICVLGLNLVITFAF 26
Db |||:|:||||| |||:|:|
63 imyslicfvlgllnglvltviy 85

OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1..24
FT /label= Hydrophobic region.
FT /note= "Predicted to be a signal peptide for
FT membrane translocation."
FT
FT Modified-site 36
FT /note= "Potential N-linked glycosylation site."
FT Region 60..86
FT /label= Hydrophobic region.
FT Region 96..116
FT /label= Hydrophobic region.
FT Region 131..152
FT /label= Hydrophobic region.
FT Region 151..159
FT /note= "This sequences motif
FT (S-[I/V]-D-R-[Y/F]-X-X-X) is highly
FT conserved among a large number of G-protein
FT coupled receptors."
FT
FT Region 171..191
FT /label= Hydrophobic region.
FT Region 220..247
FT /label= Hydrophobic region.
FT Region 264..289
FT /label= Hydrophobic region.
FT Modified-site 292
FT /note= "Potential N-linked glycosylation site."
FT Region 314..331
FT /label= Hydrophobic region.
FT
XX W09412519-A.
XX
XX 09-JUN-1994.
XX
XX 08-OCT-1993; 93WO-US09636.
XX
XX 25-NOV-1992; 92US-0980518.
XX (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
XX Birkenbach M, Kieff E;
XX
XX WPI; 1994-200183/24.
XX N-PSDB; Q64125.
XX
XX DNA coding for Epstein Barr Virus induced (EBI) polypeptide(s)
XX and antibodies to EB1, 2 and 3 - useful for detecting EBV by
XX hybridisation or by immunoassay
XX
XX Claim 8; Page 54-56; 84pp; English.
XX
XX EBV infected B lymphocytes recapitulate features of antigen
XX stimulation in enlarging, increasing RNA synthesis, expressing
XX activation antigens and adhesion molecules, secreting Ig and
XX proliferating. Unlike antigen stimulated B lymphocytes, EBV
XX infected B lymphocytes continue to proliferate (in vitro) as
XX immortalised lymphoblastoid cell lines. Because of the similar
XX effects of EBV and antigen, EBV induced genes are likely to include
XX mediators of antigen induced B lymphocyte growth or differentiation.
XX
XX Sequence 378 AA;

Query Match 59.1%; Score 75; DB 15; Length 378;
Best Local Similarity 60.9%; Pred. No. 0.003;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 4 IAYSILICVLGLNLVITFAF 26
Db |||:|:||||| |||:|:|
63 imyslicfvlgllnglvltviy 85

```

```

RESULT 7
R53744
ID R53744 standard; Protein; 378 AA.
XX
AC R53744;
XX
XX 02-FEB-1995 (first entry)
XX
XX Putative seven transmembrane receptor (V31).
XX
XX Primer; seven transmembrane receptor; receptor; amplification; PCR;
XX polymerase chain reaction.
XX
XX Homo sapiens.
XX
XX W09412635-A.
XX
XX 09-JUN-1994.
XX
XX 17-NOV-1993; 93WO-US11153.
XX
XX 17-NOV-1992; 92US-0977452.
XX
XX (ICOS-) ICOS CORP.
XX
XX Godiska R, Gray PW, Schweickart VL;
XX
XX WPI; 1994-200264/24.
XX N-PSDB; Q66160.
XX
XX DNA encoding seven transmembrane receptors - used to develop
XX prods. for use as therapeutic or diagnostic agents for conditions
XX involving the receptors.
XX
XX Claim 1; Page 52-53; 100pp; English.
XX
XX A human cDNA encoding the seven transmembrane receptor V31 was
XX isolated by first amplifying a partial cDNA clone from a human
XX tonsil cDNA library using two primers (Q66154, Q66155). The resulting
XX amplified products were probed using two radioactively labelled
XX sequences (Q66156, Q66157). A hybridising band was isolated from the
XX gel and cloned. The resulting clone was named pv31-5'end (Q66158). A
XX full length cDNA clone was isolated from a peripheral blood
XX mononuclear cell library using V31 specific primers (Q66159, Q66152).
XX Clone PBMC75 was isolated and the V31 cDNA insert in the clone was
XX designated cDNA V31-B (Q66160).
XX
XX Sequence 378 AA;

Query Match 59.1%; Score 75; DB 15; Length 378;
Best Local Similarity 60.9%; Pred. No. 0.003;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 4 IAYSILICVLGLNLVITFAF 26
Db |||:|:||||| |||:|:|
63 imyslicfvlgllnglvltviy 85

RESULT 8
W48724
ID W48724 standard; Protein; 378 AA.
XX
AC W48724;
XX
XX 25-SEP-1998 (first entry)
XX
XX Human V31 seven transmembrane receptor.
XX
XX V28; placenta; seven transmembrane receptor; 7TM; signal transduction;
XX immunology; inflammation; V31.
XX
XX Homo sapiens.
XX
OS

```

XX FH Key Location/Qualifiers
 FT Domain 58..86
 FT Domain /note= "Transmembrane domain 1"
 FT Domain 96..119
 FT Domain /note= "Transmembrane domain 2"
 FT Domain 131..152
 FT Domain /note= "Transmembrane domain 3"
 FT Domain 171..196
 FT Domain /note= "Transmembrane domain 4"
 FT Domain 219..247
 FT Domain /note= "Transmembrane domain 5"
 FT Domain 264..285
 FT Domain /note= "Transmembrane domain 6"
 FT Domain 306..331
 FT Domain /note= "Transmembrane domain 7"
 XX US5759804-A.
 XX 02-JUN-1998.
 XX 17-NOV-1993; 93US-0153848.
 XX 17-NOV-1992; 92US-0977452.
 XX (ICOS-) ICOS CORP.
 XX Godiska R, Gray PW, Schweickart VL;
 XX WPI; 1998-332132/29.
 XX N-PSDB; V18347.
 XX DNA encoding V28 seven transmembrane receptor polypeptide - useful
 PT in producing recombinant polypeptide and anti-V28 antibodies, and
 PT in screening assays for V28 agonists and antagonists
 XX
 XX Example 3; Columns 39-42; 56pp; English.
 XX
 XX The present sequence represents the V31 seven transmembrane (7TM)
 CC receptor encoded by the V31 cDNA (V18347). The invention claims for
 CC a full length V28 genomic DNA (V18343) and the V28 protein it
 CC encodes (W48722). V28 and V31 proteins are 7TM receptors which
 CC are probably involved in signal transduction. The invention also
 CC claims that cells transformed with V28 DNA can be used to produce the
 CC recombinant polypeptide, to produce anti-V28 antibodies or in screening
 CC assays for V28 agonists or antagonists. The antibodies, agonists and
 CC antagonists could then be used to modulate V28 receptor-ligand binding,
 CC for e.g. in immunological and/or inflammatory events in vivo.
 XX
 XX SQ Sequence 378 AA;
 Query Match 59.1%; Score 75; DB 19; Length 378;
 Best Local Similarity 60.9%; Pred. No. 0.003;
 Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 Qy 4 TAYSLICVLGLGNILVITFAF 26
 Db 63 imyslicfvglnglvltviy 85
 RESULT 9
 W56164
 ID W56164 standard; Protein; 378 AA.
 XX
 XX AC W56164;
 XX
 XX DT 20-JUL-1998 (first entry)
 XX G-protein coupled receptor (R7G) designated EB11.
 XX Lymphocyte R7G; EB11; G-protein coupled receptor;
 KW opiate/opioid recognition site; opiate; opioid; opiod binding protein;

KW screening; lymphocyte receptor; compound; agonist; antagonist;
 KW lymphocyte receptor protein; immune-cell specific lymphocyte receptor;
 KW neuronal type opiod receptor.
 XX Homo sapiens.
 XX US5753516-A.
 XX 19-MAY-1998.
 XX 03-FEB-1995; 95US-0383751.
 XX 03-FEB-1995; 95US-0383751.
 XX (FINB/) FINBERG R W.
 XX (HEAG/) HEAGY W E.
 XX Finberg RW, Heagy WE;
 XX WPI; 1998-311410/27.
 XX N-PSDB; V22684.
 XX Screening assay for lymphocyte opiod receptor ligands - using
 PT recombinant receptor protein
 XX
 XX Claim 1; Columns 87-88; 70pp; English.
 XX
 XX The present sequence represents a novel lymphocyte R7G, termed EB11. R7G
 CC proteins are part of the G-protein coupled receptor superfamily. EB11 is
 CC a functional opiate/opioid recognition site that probably plays a major
 CC role in mediating the effects that opiate/opioids have on lymphocytes.
 CC The EB11 protein is an opiod binding protein that is displayed on the
 CC surface of lymphocytes. A process for screening a candidate substance for
 CC ability to interact with a lymphocyte receptor comprises selecting a
 CC candidate substance having a chemical structure or biological activity
 CC suggestive of an ability to mimic the biological activity of an
 CC opiate, opiod drug or opiod peptide having known binding affinity for
 CC EB11. The ability of the candidate substance is tested to interact with
 CC the lymphocyte receptor protein. This method can be used to screen for
 CC agonists or antagonists to the lymphocyte receptor protein. The method
 CC can be modified and used to screen for agonists or antagonists to the
 CC immune-cell specific lymphocyte receptor polypeptide or the neuronal type
 CC opiod receptor polypeptide.
 XX
 XX SQ Sequence 378 AA;
 Query Match 59.1%; Score 75; DB 19; Length 378;
 Best Local Similarity 60.9%; Pred. No. 0.003;
 Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 Qy 4 TAYSLICVLGLGNILVITFAF 26
 Db 63 imyslicfvglnglvltviy 85
 RESULT 10
 W53622
 ID W53622 standard; Protein; 378 AA.
 XX
 XX AC W53622;
 XX
 XX DT 09-JUL-1998 (first entry)
 XX Epstein Barr virus induced protein 1 (EBI-1).
 XX Assessing; monitoring; foetal development; placental development;
 KW Epstein Barr virus; EBV; induced gene 1; EBI-1.
 XX Homo sapiens.
 XX US5744301-A.

PD 28-APR-1998.
 XX
 PF 02-FEB-1995; 95US-0383750.
 XX
 PR 02-FEB-1995; 95US-0383750.
 PR 25-NOV-1992; 92US-0980518.
 PR 30-NOV-1994; 94US-0352678.
 XX
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
 XX
 PI Birkenbach M, Kieff E;
 XX
 DR WPI; 1998-271060/24.
 DR N-PSDB; V25490.
 XX
 XX Assessing or monitoring foetal or placental development - comprises
 PT detecting the level or size of Epstein Barr virus induced nucleic
 PT acid or protein in maternal serum samples
 XX
 PS Example 2; Columns 37-40; 45pp; English.
 XX
 CC The present sequence was used in the development of a novel method
 CC for assessing or monitoring foetal or placental development. The
 CC method comprises taking a maternal serum sample, and detecting the
 CC level or size of Epstein Barr virus (EBV) induced gene or protein 3
 CC (EBI-3) to obtain a result, which can be compared to a control to
 CC assess or monitor foetal or placental development.
 XX
 SQ Sequence 378 AA;

Query Match 59.1%; Score 75; DB 19; Length 378;
 Best Local Similarity 60.9%; Pred. NO. 0.003;
 Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 4 IAYSLICVGLGNILVWITFAF 26
 | |||| :|||| |||: :
 Db 63 imyslicfvllnglvltviy 85

RESULT 11
 B21688
 ID B21688 standard; Protein; 378 AA.
 XX
 AC B21688;
 XX
 DT 26-JAN-2001 (first entry)
 XX
 DE Human 7TM receptor V31-B cDNA clone protein.
 XX
 KW Seven transmembrane receptor; 7TM; heptahelical; serpentine;
 KW G-protein-coupled; V28; V31; V112; R20; R2; R12; RM3; gene therapy;
 KW cancer.
 XX
 OS Homo sapiens.
 XX
 PN US6107475-A.
 XX
 PD 22-AUG-2000.
 XX
 PF 26-APR-1999; 99US-0299843.
 XX
 PR 17-MAY-1994; 94US-0245242.
 PR 01-JUN-1998; 98US-0083337.
 PR 17-NOV-1992; 92US-0977452.
 PR 17-NOV-1993; 93US-0153848.
 XX
 PA (ICOS-) ICOS CORP.
 XX
 PI Schweickart VL, Gray PW, Godiska R;
 XX
 DR WPI; 2000-571335/53.
 DR N-PSDB; A91707.

XX
 PT Polynucleotide encoding seven transmembrane receptors, antibody
 PT specific to the receptor, agonist and antagonist of the receptor useful
 PT for treating inflammation in a mammal
 XX
 PS Example 3; Columns 41-44; 61pp; English.
 XX
 CC The present sequence is a novel seven transmembrane (7TM) receptors
 CC (also known as heptahelical, serpentine or G-protein-coupled receptors).
 CC The coding sequence for the present sequence may be used for gene
 CC therapy for diseases such as cancer.
 XX
 SQ Sequence 378 AA;

Query Match 59.1%; Score 75; DB 21; Length 378;
 Best Local Similarity 60.9%; Pred. NO. 0.003;
 Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 4 IAYSLICVGLGNILVWITFAF 26
 | |||| :|||| |||: :
 Db 63 imyslicfvllnglvltviy 85

RESULT 12
 Y90629
 ID Y90629 standard; Protein; 378 AA.
 XX
 AC Y90629;
 XX
 DT 21-AUG-2000 (first entry)
 XX
 DE Human G protein-coupled receptor EB11.
 XX
 KW G protein-coupled receptor; GPCR; constitutively active;
 KW intracellular loop 3; transmembrane domain 6; drug screening;
 KW agonist; antagonist.
 XX
 OS Homo sapiens.
 XX
 PN WO200022129-A1.
 XX
 PD 20-APR-2000.
 XX
 PF 12-OCT-1999; 99WO-US23938.
 XX
 PR 13-OCT-1998; 98US-0170496.
 XX
 PA (AREN-) ARENA PHARM INC.
 XX
 PI Behan DP, Chalmers DT, Liaw CW;
 XX
 DR WPI; 2000-329165/28.
 DR N-PSDB; A30632.
 XX
 PT Non-endogenous constitutively activated human G protein-coupled
 PT receptors, useful for identifying agonists for use as pharmaceutical
 PT agents
 XX
 PS Example 1; Page 158-159; 341pp; English.
 XX
 CC The invention relates to constitutively active, non-endogenous versions
 CC of endogenous human orphan G protein-coupled receptors (GPCRs, Y90643-
 CC Y90677 and Y90683-Y90687), and to DNA encoding them (A30709-A30743 and
 CC A30775-A30779). The mutant proteins of the invention contain a
 CC mutation in a portion of the protein comprising intracellular loop 3
 CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
 CC is substituted for an endogenous residue in IC3 at a position 16 amino
 CC acids N-terminal of an endogenous proline in TM6 to form a sequence
 CC X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or
 CC Ala, and is preferably Lys. When the endogenous residue at this position
 CC is Lys, this residue is replaced by His, Arg or preferably Ala. The 15
 CC amino acid stretch between the substituted amino acid and the Pro may be

CC endogenous, non-endogenous, or a mixture of endogenous and non-endogenous
 CC residues. The constitutively active GPCRs are useful for identifying
 CC antagonists, agonists and partial agonists for use as pharmaceutical
 CC agents. The mutant proteins are also useful in research settings for
 CC elucidating the roles of the receptors in normal and diseased conditions.
 CC Antagonists for a particular GPCR are useful for treating diseases and
 CC disorders associated with that receptor. Because the novel mutant GPCRs
 CC are constitutively active, they can be used directly for screening of
 CC compounds without the need for endogenous ligands. The present
 CC sequence represents a human wild-type GPCR referred to in an
 CC exemplification of the invention.

XX
 SQ Sequence 378 AA;

Query Match 59.1%; Score 75; DB 21; Length 378;
 Best Local Similarity 60.9%; Pred. No. 0.003;
 Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 4 IAYSLICVLGLNGLVITFAF 26
 | | | | | : | | | | | | | | : :
 Db 63 imysiicfvllgnglvltviy 85

RESULT 13

ID Y90663 standard; Protein; 378 AA.

XX AC Y90663;

XX DT 21-AUG-2000 (first entry)

XX DE Human mutant G protein-coupled receptor EB11 (I262K).

XX KW G protein-coupled receptor; GPCR; constitutively active;
 KW intracellular loop 3; transmembrane domain 6; drug screening;
 KW agonist; antagonist; mutant; mutain.

XX OS Homo sapiens.
 OS Synthetic.

XX PN W0200022129-A1.

XX PD 20-APR-2000.

XX PF 12-OCT-1999; 99WO-US23938.

XX PR 13-OCT-1998; 98US-0170496.

XX PA (AREN-) ARENA PHARM INC.

XX PI Behan DP, Chalmers DT, Liaw CW;

XX DR WPI; 2000-329165/28.

XX DR N-PSDB; A30729.

XX PT Non-endogenous constitutively activated human G protein-coupled
 PT receptors, useful for identifying agonists for use as pharmaceutical
 PT agents

XX PS Example 2; Page 259-260; 341pp; English.

XX CC The invention relates to constitutively active, non-endogenous versions
 CC of endogenous human orphan G protein-coupled receptors (GPCRs, Y90643-
 CC Y90677 and Y90683-Y90687), and to DNA encoding them (A30709-A30743 and
 CC A30775-A30779). The mutant proteins of the invention contain a
 CC mutation in a portion of the protein comprising intracellular loop 3
 CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
 CC is substituted for an endogenous residue in IC3 at a position 16 amino
 CC acids N-terminal of an endogenous proline in TM6 to form a sequence
 CC X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or
 CC Ala, and is preferably Lys. When the endogenous residue at this position
 CC is Lys, this residue is replaced by His, Arg or preferably Ala. The 15

CC amino acid stretch between the substituted amino acid and the Pro may be
 CC endogenous, non-endogenous, or a mixture of endogenous and non-endogenous
 CC residues. The constitutively active GPCRs are useful for identifying
 CC antagonists, agonists and partial agonists for use as pharmaceutical
 CC agents. The mutant proteins are also useful in research settings for
 CC elucidating the roles of the receptors in normal and diseased conditions.
 CC Antagonists for a particular GPCR are useful for treating diseases and
 CC disorders associated with that receptor. Because the novel mutant GPCRs
 CC are constitutively active, they can be used directly for screening of
 CC compounds without the need for endogenous ligands. Sequences Y90643-
 CC Y90677 and Y90683-Y90687 the mutant human GPCRs of the invention.

XX
 SQ Sequence 378 AA;

Query Match 59.1%; Score 75; DB 21; Length 378;
 Best Local Similarity 60.9%; Pred. No. 0.003;
 Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 4 IAYSLICVLGLNGLVITFAF 26
 | | | | | : | | | | | | | | : :
 Db 63 imysiicfvllgnglvltviy 85

RESULT 14

B50859

ID B50859 standard; protein; 378 AA.

XX AC B50859;

XX DT 16-MAR-2001 (first entry)

XX DE Human CCR7.

XX KW Human; chemokine receptor 7; CCR7; chemokine beta-9; Ckbeta-9;
 KW allergy; autoimmune disease; ischaemia; atherosclerosis; cancer;
 KW chronic inflammatory disorder; organ transplant; tissue graft;
 KW chronic myelogenous leukaemia; infection.

XX OS Homo sapiens.

XX PN US6153441-A.

XX PD 28-NOV-2000.

XX PF 17-FEB-1999; 99US-0251545.

XX PR 17-FEB-1998; 98US-0074883.

XX PA (SMIK) SMITHKLINE BEECHAM CORP.

XX PI Appelbaum ER, White JR, Sarau HM;

XX DR WPI; 2001-049151/06.

XX PT Identifying agonists or antagonists of interaction between human
 PT protein, chemokine beta-9 and human CC chemokine receptor 7, by
 PT contacting cell expressing receptor with test compound

XX PS Claim 1; Fig 1; 20pp; English.

XX CC The present sequence is human chemokine receptor 7 (CCR7), a cellular
 CC receptor for chemokine beta-9 (Ckbeta-9). The sequence may be
 CC used in a method for discovering agonists and antagonists of the
 CC interaction between Ckbeta-9 and CCR7. A cell expressing CCR7
 CC polypeptide on its surface, associated with a component capable of
 CC providing a detectable signal in response to binding of Ckbeta-9, is
 CC contacted with a compound in the presence of labelled or unlabelled
 CC Ckbeta-9. The compound is identified as an agonist/antagonist by
 CC determining whether it activates or inhibits the detectable signal.
 CC The method is useful for identifying agonists and antagonists of the
 CC interaction between Ckbeta-9 and CCR7 which are useful for treating
 CC diseases including allergic disorders, autoimmune diseases,

Search completed: May 23, 2001, 15:28:26
Job time: 403 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:30:04 ; Search time 95.91 Seconds
(without alignments)
5.208 Million cell updates/sec

Title: US-08-887-977-10_COPY_39_64

Perfect score: 127

Sequence: 1 LRYIAVSLICVLGLLGNILVITFAF 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents_AA.*
- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pap.*
 - 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pap.*
 - 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pap.*
 - 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pap.*
 - 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pap.*
 - 6: /cgn2_6/ptodata/2/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	59.1	358	1 US-08-153-848-19	Sequence 19, Appl
2	75	59.1	358	5 US-09-299-843A-19	Sequence 19, Appl
3	75	59.1	358	3 PCT-US93-11153-19	Sequence 19, Appl
4	75	59.1	361	2 US-08-902-294-2	Sequence 2, Appl
5	75	59.1	361	3 US-09-178-637-2	Sequence 2, Appl
6	75	59.1	378	1 US-08-383-750-2	Sequence 2, Appl
7	75	59.1	378	1 US-08-383-751A-2	Sequence 2, Appl
8	75	59.1	378	1 US-08-153-848-15	Sequence 15, Appl
9	75	59.1	378	3 US-08-352-678-2	Sequence 2, Appl
10	75	59.1	378	3 US-09-299-843A-15	Sequence 15, Appl
11	75	59.1	378	4 US-09-251-545-1	Sequence 1, Appl
12	75	59.1	378	5 PCT-US93-09636-2	Sequence 2, Appl
13	75	59.1	378	5 PCT-US93-11153-15	Sequence 15, Appl
14	75	59.1	410	1 US-08-153-848-7	Sequence 7, Appl
15	75	59.1	410	3 US-09-299-843A-7	Sequence 7, Appl
16	75	59.1	410	5 PCT-US93-11153-7	Sequence 7, Appl
17	71	55.9	359	1 US-08-153-848-24	Sequence 24, Appl
18	71	55.9	359	3 US-09-299-843A-24	Sequence 24, Appl
19	71	55.9	359	5 PCT-US93-11153-24	Sequence 24, Appl
20	71	55.9	378	3 US-09-299-843A-66	Sequence 66, Appl
21	67	52.8	374	4 US-08-982-493-6	Sequence 6, Appl
22	65	51.2	372	1 US-08-202-056-5	Sequence 5, Appl
23	65	51.2	372	1 US-08-076-093A-6	Sequence 6, Appl
24	65	51.2	372	1 US-08-701-265-6	Sequence 6, Appl
25	65	51.2	372	1 US-08-284-586-6	Sequence 6, Appl
26	65	51.2	372	2 US-08-805-478-6	Sequence 6, Appl
27	65	51.2	372	2 US-08-802-627A-6	Sequence 6, Appl

28	65	51.2	372	2	US-08-801-238-6	Sequence 6, Appl
29	65	51.2	372	2	US-08-801-228-6	Sequence 6, Appl
30	65	51.2	372	3	US-09-104-296-6	Sequence 6, Appl
31	65	51.2	372	4	US-08-982-493-8	Sequence 8, Appl
32	63	49.6	355	1	US-08-012-988A-2	Sequence 2, Appl
33	63	49.6	355	1	US-08-450-393A-5	Sequence 5, Appl
34	63	49.6	355	4	US-08-446-669-5	Sequence 5, Appl
35	63	49.6	355	5	PCT-US95-00476-5	Sequence 5, Appl
36	62	48.8	428	1	US-07-816-283-12	Sequence 12, Appl
37	62	48.8	428	1	US-08-417-103-12	Sequence 12, Appl
38	61	48.0	367	2	US-08-454-549-4	Sequence 4, Appl
39	61	48.0	367	3	US-08-454-552-4	Sequence 4, Appl
40	61	48.0	367	3	US-08-676-351-3	Sequence 3, Appl
41	61	48.0	372	1	US-08-149-093A-6	Sequence 6, Appl
42	61	48.0	372	2	US-08-911-245-6	Sequence 6, Appl
43	61	48.0	372	2	US-08-411-859-10	Sequence 10, Appl
44	61	48.0	372	3	US-09-170-331-6	Sequence 6, Appl
45	61	48.0	372	3	US-08-147-592A-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-153-848-19
; Sequence 19, Application US/08153848
; Patent No. 5759804
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/153,848
; APPLICATION NUMBER: 514
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5759804and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-153-848-19

Query Match 59.1%; Score 75; DB 1; Length 358;
Best Local Similarity 60.9%; Pred. No. 0.0031;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

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Qy 4 IAYSILCVLGLGNLIVITFAF 26
    | |||| :|||| |::| :
Db 43 IMYSIICFVGLLGNLVLVTIY 65

RESULT 2
US-09-299-843A-19
; Sequence 19, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,843A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/088,337
; FILING DATE: 01-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jill E. Uhl
; REGISTRATION NUMBER: 43,213
; REFERENCE/DOCKET NUMBER: 27866/32059B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-299-843A-19

Query Match 59.1%; Score 75; DB 3; Length 358;
Best Local Similarity 60.9%; Pred. No. 0.0031;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 4 IAYSILCVLGLGNLIVITFAF 26
    | |||| :|||| |::| :
Db 43 IMYSIICFVGLLGNLVLVTIY 65

RESULT 3
PCT-US93-11153-19
; Sequence 19, Application PC/TUS9311153
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: Novel Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11153
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-11153-19

Query Match 59.1%; Score 75; DB 5; Length 358;
Best Local Similarity 60.9%; Pred. No. 0.0031;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 4 IAYSILCVLGLGNLIVITFAF 26
    | |||| :|||| |::| :
Db 43 IMYSIICFVGLLGNLVLVTIY 65

RESULT 4
US-08-902-294-2
; Sequence 2, Application US/08902294
; Patent No. 5874252
; GENERAL INFORMATION:
; APPLICANT: ZHU, YUAN
; TITLE OF INVENTION: A NOVEL SPLICING VARIANT OF
; THE EPSTEIN-BARR VIRUS-INDUCED G-PROTEIN COUPLED
; RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/902,294
FILING DATE: 29-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-70177
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-902-294-2

Query Match 59.1%; Score 75; DB 2; Length 361;
Best Local Similarity 60.9%; Pred. No. 0.0031;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 4 IAYSLLICVLGLLGNILVITFAF 26
| ||| : |||| ||| : :
Db 63 IMYSIIICFVGLLGNLWLTYY 85

RESULT 5
US-09-178-637-2
Sequence 2, Application US/09178637
Patent No. 6001972
GENERAL INFORMATION:
APPLICANT: ZHU, YUAN
TITLE OF INVENTION: A No. 6001972el Splicing Variant of
TITLE OF INVENTION: the Epstein-Barr Virus-Induced G-Protein Coupled Receptor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/178,637
FILING DATE: 26-OCT-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/902,294
FILING DATE: 29-JUL-1998
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-70177-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-178-637-2

Query Match 59.1%; Score 75; DB 3; Length 361;
Best Local Similarity 60.9%; Pred. No. 0.0031;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 4 IAYSLLICVLGLLGNILVITFAF 26
| ||| : |||| ||| : :
Db 63 IMYSIIICFVGLLGNLWLTYY 85

RESULT 6
US-08-383-750-2
Sequence 2, Application US/08383750
Patent No. 5744301
GENERAL INFORMATION:
APPLICANT: Birkenbach, Mark
APPLICANT: Kieff, Elliot
TITLE OF INVENTION: Epstein Barr Virus Induced Genes
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W.,
STREET: Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/383,750
FILING DATE: Herewith
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Fox, Samuel, L.
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 0627.3300001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-383-750-2

Query Match 59.1%; Score 75; DB 1; Length 378;
Best Local Similarity 60.9%; Pred. No. 0.0032;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 4 IAYSLLICVLGLLGNILVITFAF 26
| ||| : |||| ||| : :
Db 63 IMYSIIICFVGLLGNLWLTYY 85

RESULT 7
US-08-383-751A-2
Sequence 2, Application US/08383751A
Patent No. 5753516
GENERAL INFORMATION:
APPLICANT: Heavy, Wyrta E.
APPLICANT: Finberg, Robert W.
TITLE OF INVENTION: Identification and Uses of Opioid

;; TITLE OF INVENTION: Receptors
;; NUMBER OF SEQUENCES: 8
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Arnold, White & Durkee
;; STREET: P.O. Box 4433
;; CITY: Houston
;; STATE: Texas
;; COUNTRY: US
;; ZIP: 77210
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/383,751A
;; FILING DATE: 03-FEB-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Wilson, Mark B.
;; REGISTRATION NUMBER: 37,259
;; REFERENCE/DOCKET NUMBER: DFCI:001/WIM
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (512) 418-3000
;; TELEFAX: (512) 474-7577
;; TELEX: 79-0924
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 378 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-383-751A-2

Query Match 59.1%; Score 75; DB 1; Length 378;
Best Local Similarity 60.9%; Pred. No. 0.0032;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 4 IAYSLLCVLGLGNILVITFAF 26
| | | | | : | | | | | : | | | | | :
Db 63 IMYSIIICFVGLLGNLVLTYIY 85

RESULT 8
US-08-153-848-15
; Sequence 15, Application US/08153848
; Patent No. 5759804
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153,848
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992

;; ATTORNEY/AGENT INFORMATION:
;; NAME: No. 5759804and, Greta E.
;; REGISTRATION NUMBER: 35,302
;; REFERENCE/DOCKET NUMBER: 31794
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312) 474-6300
;; TELEFAX: (312) 474-0448
;; TELEX: 25-3856
;; INFORMATION FOR SEQ ID NO: 15:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 378 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-153-848-15

Query Match 59.1%; Score 75; DB 1; Length 378;
Best Local Similarity 60.9%; Pred. No. 0.0032;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 4 IAYSLLCVLGLGNILVITFAF 26
| | | | | : | | | | | : | | | | | :
Db 63 IMYSIIICFVGLLGNLVLTYIY 85

RESULT 9
US-08-352-678-2
; Sequence 2, Application US/08352678
; Patent No. 6043351
; GENERAL INFORMATION:
; APPLICANT: Birkenbach, Mark
; APPLICANT: Kieff, Elliott
; TITLE OF INVENTION: EPSTEIN BARR VIRUS. INDUCED GENES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/352,678
; FILING DATE: 30-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/980,518
; FILING DATE: 25-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gates, Edward R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: B0801/7044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-352-678-2

Query Match 59.1%; Score 75; DB 3; Length 378;
Best Local Similarity 60.9%; Pred. No. 0.0032;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 4 IAYSLICVLGLGNLIVITFAF 26
| | | | | : | | | | | : | | | | | :
Db 63 IMYSIICFVGLLGNLGLVLTYY 85

RESULT 10

US-09-299-843A-15
; Sequence 15, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS: 66
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,843A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/088,337
; FILING DATE: 01-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jill E. Uhl
; REGISTRATION NUMBER: 43,213
; REFERENCE/DOCKET NUMBER: 27866/32059B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-299-843A-15

Query Match 59.1%; Score 75; DB 3; Length 378;
Best Local Similarity 60.9%; Pred. No. 0.0032;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 4 IAYSLICVLGLGNLIVITFAF 26
| | | | | : | | | | | : | | | | | :
Db 63 IMYSIICFVGLLGNLGLVLTYY 85

RESULT 11

US-09-251-545-1
; Sequence 1, Application US/09251545
; Patent No. 6153441
; GENERAL INFORMATION:

; APPLICANT: Edward R. Appelbaum
; APPLICANT: Henry M. Sarau
; APPLICANT: John R. White
; TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND
; TITLE OF INVENTION: ANTAGONISTS OF THE INTERACTION BETWEEN HUMAN CCR7 RECEPTOR
; TITLE OF INVENTION: AND CK(-9) LIGAND AND INTERACTION THEREOF
; FILE REFERENCE: P50753
; CURRENT APPLICATION NUMBER: US/09/251,545
; CURRENT FILING DATE: 1999-02-17
; EARLIER APPLICATION NUMBER: 60/074,883
; EARLIER FILING DATE: 1998-02-17
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Human
US-09-251-545-1

Query Match 59.1%; Score 75; DB 4; Length 378;
Best Local Similarity 60.9%; Pred. No. 0.0032;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 4 IAYSLICVLGLGNLIVITFAF 26
| | | | | : | | | | | : | | | | | :
Db 63 IMYSIICFVGLLGNLGLVLTYY 85

- RESULT 12

PCT-US93-09636-2
; Sequence 2, Application PC/TUS9309636
; GENERAL INFORMATION:
; APPLICANT: Birkenbach, Mark
; APPLICANT: Kieff, Elliot
; TITLE OF INVENTION: Epstein Barr Virus Induced Genes
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/09636
; FILING DATE: herewith
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
PCT-US93-09636-2

Query Match 59.1%; Score 75; DB 5; Length 378;
Best Local Similarity 60.9%; Pred. No. 0.0032;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 4 IAYSLICVLGLGNLIVITFAF 26
| | | | | : | | | | | : | | | | | :
Db 63 IMYSIICFVGLLGNLGLVLTYY 85

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153.848
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: NO. 5759804and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 410 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-153-848-7

Query Match 59.1%; Score 75; DB 1; Length 410;
Best Local Similarity 60.9%; Pred. No. 0.0035;
Matches 14; Conservative 5; Mismatches 4; Indels 0;

QY 4 IAYSLICVLGLGNILVWTFAP 26
| |||| :|||| |||:| :
Db 95 IMYSIIICVGLLGNLWLTYY 117

RESULT 15
US-09-299-843A-7
; Sequence 7, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska Ronald

```

```

;
; APPLICANT: Schwelkart, Vicki L.
; TITLE OF INVENTION: NO. 6107475el Seven Transmembrane Receptors
;
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
;

```

ADDRESSEE: Borun
ADDRESS: Marshall, O'Toole, Gerstein, Murray
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/299,843A
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/088,337
 FILING DATE: 01-JUN-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/153,848
 FILING DATE: 17-NOV-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/977,452

FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Jill E. Uhl
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-299-843A-7

Query Match 59.1%; Score 75; DB 3; Length 410;
Best Local Similarity 60.9%; Pred. NO. 0.0035;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 4 IAYSLICVLGLNGLVLTAF 26
Db 95 IMYSIICFVGLGLVLTAF 117

Search completed: May 23, 2001, 15:30:05
Job time: 412 sec

Search completed: May 23, 2001, 15:30:05
Job time: 412 sec

A:Residues: 1-378 <BIR>
 A:Cross-references: GB:L08176; NID:g183484; PID:g183485
 A:Experimental source: B-lymphocytes
 A:Note: sequence extracted from NCBI backbone (NCBIN:127094, NCBI:P.127095)
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 59.1%; Score 75; DB 2; Length 378;
 Best Local Similarity 60.9%; Pred. No. 0.005;
 Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 QY 4 IAYSLICVLGLGNILVITFAF 26
 | | | | | : | | | | | : | | | | | : | | | | | :
 Db 63 IMYSIICFVGLLGNGLVLTIIY 85

RESULT 3
 B55735
 Lymphocyte-specific G protein-coupled receptor EB11 - human
 N:Alternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1
 C:Species: Homo sapiens (man)
 C>Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 19-May-2000
 C:Accession: B55735; S52443
 R:Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.
 Genomics 23, 643-650, 1994
 A:Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor
 A:Reference number: A55735; MUID:95154835
 A:Accession: B55735
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-378 <SCH>
 A:Cross-references: GB:L31581; NID:g468319; PID:AAA74231.1; PID:g468320
 R:Burgstahler, R.; Kempkes, B.; Staube, K.; Lipp, M.
 submitted to the EMBL Data Library, February 1995
 A:Description: The expression of the chemokine receptor BLR2/EB11 is specifically transcribed in the brain.
 A:Reference number: S52443
 A:Accession: S52443
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 21-378 <BUR>
 A:Cross-references: EMBL:X84702
 C:Genetics:
 A:Gene: GDB:CMKBR7; EB11; BLR2; CCR7
 A:Cross-references: GDB:342065; OMIM:600242
 A:Map position: 17q12-17q21.2
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor

Query Match 59.1%; Score 75; DB 2; Length 378;
 Best Local Similarity 60.9%; Pred. No. 0.005;
 Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 QY 4 IAYSLICVLGLGNILVITFAF 26
 | | | | | : | | | | | : | | | | | : | | | | | :
 Db 63 IMYSIICFVGLLGNGLVLTIIY 85

RESULT 4
 JC5498
 G protein-coupled receptor DEZ - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 19-May-2000
 C:Accession: JC5498
 R:Metner, A.; Herney, G.; Schinke, B.; Hermans-Borgmeyer, I.
 Biochem. Biophys. Res. Commun. 233, 336-342, 1997
 A:Title: A novel G protein-coupled receptor with homology to neuropeptide and chemoattractant receptors
 A:Reference number: JC5498; MUID:97289630
 A:Contents: Brain
 A:Accession: JC5498
 A:Molecule type: mRNA
 A:Residues: 1-371 <MET>

A:Cross-references: GB:U79525; NID:g1732346; PID:AA53789.1; PID:g1732347
 C:Comment: This protein is involved in the bone metabolism.
 C:Superfamily: vertebrate rhodopsin
 F:110-187/Disulfide bonds: #status predicted

Query Match 55.9%; Score 71; DB 2; Length 371;
 Best Local Similarity 56.5%; Pred. No. 0.017;
 Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 QY 4 IAYSLICVLGLGNILVITFAF 26
 : | | | | | : | | | | | : | | | | | : | | | | | :
 Db 43 VIYSLVCFVGLLGNGLVIVITAF 65

RESULT 5
 A55735
 G protein-coupled receptor EB11 - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 24-Nov-1999
 C:Accession: A55735
 R:Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.
 Genomics 23, 643-650, 1994
 A:Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor
 A:Reference number: A55735; MUID:95154835
 A:Accession: A55735
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-378 <SCH>
 A:Cross-references: GB:L31580; NID:g468340; PID:AAA74232.1; PID:g468341
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor

Query Match 55.9%; Score 71; DB 2; Length 378;
 Best Local Similarity 52.2%; Pred. No. 0.018;
 Matches 12; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
 QY 4 IAYSLICVLGLGNILVITFAF 26
 : | | | | | : | | | | | : | | | | | : | | | | | :
 Db 63 LMYSVICFVGLLGNGLVLTIIY 85

RESULT 6
 JC5796
 Probable chemoattractant receptor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 24-Jan-1998 #sequence_revision 13-Mar-1998 #text_change 20-Jun-2000
 C:Accession: JC5796
 R:Owman, C.; Lolait, S.J.; Santen, S.; Olde, B.
 Biochem. Biophys. Res. Commun. 241, 390-394, 1997
 A:Title: Molecular cloning and tissue distribution of cDNA encoding a novel chemoattractant receptor
 A:Reference number: JC5796; MUID:98086361
 A:Accession: JC5796
 A:Molecule type: mRNA
 A:Residues: 1-371 <OWM>
 A:Cross-references: DDBJ:AJ002745; NID:g2624397; PIDN:CAA05715.1; PID:g2624398
 A:Experimental source: liver
 C:Comment: This protein regulates the trafficking of immune cells during a microbial infection.

Query Match 54.3%; Score 69; DB 2; Length 371;
 Best Local Similarity 52.2%; Pred. No. 0.033;
 QY 4 IAYSLICVLGLGNILVITFAF 26
 : | | | | | : | | | | | : | | | | | : | | | | | :
 Db 63 LMYSVICFVGLLGNGLVLTIIY 85

RESULT 7
 JC5796
 Probable chemoattractant receptor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 24-Jan-1998 #sequence_revision 13-Mar-1998 #text_change 20-Jun-2000
 C:Accession: JC5796
 R:Owman, C.; Lolait, S.J.; Santen, S.; Olde, B.
 Biochem. Biophys. Res. Commun. 241, 390-394, 1997
 A:Title: Molecular cloning and tissue distribution of cDNA encoding a novel chemoattractant receptor
 A:Reference number: JC5796; MUID:98086361
 A:Accession: JC5796
 A:Molecule type: mRNA
 A:Residues: 1-371 <OWM>
 A:Cross-references: DDBJ:AJ002745; NID:g2624397; PIDN:CAA05715.1; PID:g2624398
 A:Experimental source: liver
 C:Comment: This protein regulates the trafficking of immune cells during a microbial infection.

Qy 4 IAYS LICVLGLGNILVVI 22
:|||||:|||||:|:
Db 58 VAYS LI FLGLMMGNILVLV 76

C;GENETICS:
A:Gene: GDB:RI.R1

Qy 4 IAYS LICVLGLGNILVVI 22
:|||||:|||||:|:
Db 58 VAYS LI FLGLMMGNILVLV 76

A:Map position: 15q26.1-15q26.1
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 51.2%; Score 65; DB 2; Length 372;
 Best Local Similarity 57.9%; Pred. No. 0.12;
 Matches 11; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 4 IAYSLICVLGLGNILVVI 22
 :|||||:|:|:|:|:|:|:
 Db 56 VAYSLIFLGVIGNVILV 74

RESULT 12

A45177
 chemokine (C-C) receptor 1 - human
 N:Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
 C:Accession: A45177; 155671
 R:Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.
 Cell 72, 415-425, 1993
 A:Title: Molecular cloning, functional expression, and signaling characteristics of a C-
 A:Reference number: A45177; MUID:93161416
 A:Accession: A45177
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-355 <NEO>
 A:Cross-references: GB:L10918; NID:9292416; PIDN:AAA36543.1; PID:g292417
 A:Experimental source: HL60 cells
 A:Note: sequence extracted from NCBI backbone (NCBIP:124876)
 R:Gao, J.
 J. Exp. Med. 177, 1421-1427, 1993
 A:Title: Structure and functional expression of the human macrophage inflammatory 1 alpha
 A:Reference number: 155671; MUID:93240122
 A:Accession: 155671
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-355 <RES>
 A:Cross-references: GB:L10918; NID:9292416; PIDN:AAA36543.1; PID:g292417
 C:Genetics:
 A:Gene: GDB:CMKBR1; CMKR-1
 A:Cross-references: GDB:138446; OMIM:601159
 A:Map position: 3p21-3p21
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; tr
 F:36-60/Domain: transmembrane #status predicted <TM1>
 F:71-91/Domain: transmembrane #status predicted <TM2>
 F:108-129/Domain: transmembrane #status predicted <TM3>
 F:147-171/Domain: transmembrane #status predicted <TM4>
 F:205-223/Domain: transmembrane #status predicted <TM5>
 F:240-264/Domain: transmembrane #status predicted <TM6>
 F:288-305/Domain: transmembrane #status predicted <TM7>
 F:5/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:24-273,106-183/disulfide bonds: #status predicted
 F:345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 49.6%; Score 63; DB 2; Length 355;
 Best Local Similarity 70.6%; Pred. No. 0.21;
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 6 YSLICVLGLGNILVVI 22
 ||||:|:|:|:|:|:
 Db 41 YSLVFVIGLVGNILV 57

RESULT 13

A44021
 somatostatin receptor SSTR3 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 11-Jan-2000

C:Accession: A44021
 R:Yasuda, K.; Rens-Domiano, S.; Breder, C.D.; Law, S.F.; Saper, C.B.; Reisine, T.; Be
 J. Biol. Chem. 267, 20422-20428, 1992
 A:Title: Cloning of a novel somatostatin receptor, SSTR3, coupled to adenylylcyclase.
 A:Reference number: A44021; MUID:93015924
 A:Accession: A44021
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-428 <YAS>
 A:Cross-references: GB:M91000; NID:g201065; PIDN:AAA40144.1; PID:g201066
 A:Note: sequence extracted from NCBI backbone (NCBIP:115746)
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 48.8%; Score 62; DB 2; Length 428;
 Best Local Similarity 52.4%; Pred. No. 0.34;
 Matches 11; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 LYRIAYSLICVLGLGNILV 21
 :|:|:|:|:|:|:|:
 Db 47 LISLVLVVCVVGILGNLSVI 67

RESULT 14

S30508
 probable G protein-coupled receptor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 11-Jan-2000
 C:Accession: S30508
 R:Meyerhof, W.; Wulfsen, I.; Schoenrock, C.; Fehr, S.; Richter, D.
 Proc. Natl. Acad. Sci. U.S.A. 89, 10267-10271, 1992
 A:Title: Molecular cloning of a somatostatin-28 receptor and comparison of its expres
 A:Reference number: S30508; MUID:93066220
 A:Accession: S30508
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-428 <MEY>
 A:Cross-references: EMBL:X63574; NID:g56315; PIDN:CAA45130.1; PID:g56316
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 48.8%; Score 62; DB 2; Length 428;
 Best Local Similarity 52.4%; Pred. No. 0.34;
 Matches 11; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 LYRIAYSLICVLGLGNILV 21
 :|:|:|:|:|:|:|:
 Db 47 LISLVLVVCVVGILGNLSVI 67

RESULT 15

B48227
 delta opioid receptor 1 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 24-Nov-1999
 C:Accession: B48227; S37807; A48685; S36745
 R:Yasuda, K.; Raynor, K.; Kong, H.; Breder, C.D.; Takeda, J.; Reisine, T.; Bell, G.I.
 Proc. Natl. Acad. Sci. U.S.A. 90, 6736-6740, 1993
 A:Title: Cloning and functional comparison of kappa and delta opioid receptors from m
 A:Reference number: A48227; MUID:93342064
 A:Accession: B48227
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-372 <YAS>
 A:Cross-references: GB:L11064; NID:g348246; PIDN:AAA37520.1; PID:g348247
 R:Kieffer, B.L.; Befort, K.; Gaveriaux-Ruff, C.; Hirth, C.G.
 submitted to the EMBL Data Library, February 1993
 A:Reference number: S37807
 A:Accession: S37807
 A:Status: preliminary
 A:Molecule type: mRNA

A:Residues: 1-372 <KIE>
 A:Cross-references: EMBL:L06322; NID:g192942; PIDN:AAA37522.1; PID:g192943
 R:Bzdega, T.; Chin, H.; Kim, H.; Jung, H.H.; Kozak, C.A.; Klee, W.A.
 Proc. Natl. Acad. Sci. U.S.A. 90, 9305-9309, 1993
 A:Title: Regional expression and chromosomal localization of the delta opiate receptor gene
 A:Reference number: A48685; MUID:94022364
 A:Accession: A48685
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 8-372 <B2D>
 A:Cross-references: GB:S66181; NID:g435781; PIDN:AAB28546.1; PID:g435782
 A:Experimental source: NCI08-15 hybrid cells
 A:Note: sequence extracted from NCBI backbone (NCBIN:138618, NCBIP:138619)
 R:Kieffer, B.L.; Befort, K.; Gaveriaux-Ruff, C.; Hirth, C.G.
 Proc. Natl. Acad. Sci. U.S.A. 89, 12048-12052, 1992
 A:Title: The delta-opioid receptor: isolation of a cDNA by expression cloning and pharmacological characterization
 A:Reference number: S36745; MUID:93101664
 A:Accession: S36745
 A:Molecule type: mRNA
 A:Residues: 1-189, 'N', 191, 'GMVQ', 207-208, 'ACSSSPVQLVL', 210-372 <KIW>
 A:Cross-references: EMBL:L06322
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: brain; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein

\ Query Match 48.0%; Score 61; DB 2; Length 372;
 Best Local Similarity 62.5%; Pred. No. 0.41;
 Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 6 YSLICVLGLLGNILVY 21
 |||:|||||:
 Db 56 YSAVCAVGLLGNILVM 71

Search completed: May 23, 2001, 15:31:58
 Job time: 505 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:36:17 ; Search time 62.39 Seconds
(without alignments)
14.275 Million cell updates/sec

Title: US-08-887-977-10_COPY_39_64

Perfect score: 127

Sequence: 1 LYRIAYSLICVLGLGNILVITPAF 26

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	107	84.3	374	1	CKR6_HUMAN
2	102	80.3	367	1	CKR6_MOUSE
3	75	59.1	378	1	CKR7_HUMAN
4	71	55.9	371	1	CML1_MOUSE
5	71	55.9	378	1	CKR7_MOUSE
6	69	54.3	371	1	CH23_HUMAN
7	69	54.3	371	1	CML1_RAT
8	69	54.3	373	1	CML1_HUMAN
9	69	54.3	399	1	OPS2_PATYE
10	67	52.8	374	1	CCR5_MOUSE
11	67	52.8	374	1	CCR5_RAT
12	65	51.2	372	1	CCR5_HUMAN
13	63	49.6	355	1	CKR1_HUMAN
14	62	48.8	428	1	SSR3_MOUSE
15	62	48.8	428	1	SSR3_RAT
16	61	48.0	372	1	OPRD_HUMAN
17	61	48.0	372	1	OPRD_MOUSE
18	61	48.0	372	1	OPRD_RAT
19	61	48.0	398	1	OPRM_MOUSE
20	61	48.0	398	1	OPRM_RAT
21	61	48.0	400	1	OPRM_HUMAN
22	61	48.0	401	1	OPRM_BOVIN
23	61	48.0	401	1	OPRM_PIG
24	61	48.0	418	1	SSR3_HUMAN
25	60	47.2	359	1	AG2R_SHEEP
26	60	47.2	359	1	CKR3_MOUSE
27	60	47.2	408	1	NK1R_RANCA
28	59	46.5	359	1	CKR3_RAT
29	59	46.5	384	1	SSR4_MOUSE
30	59	46.5	384	1	SSR4_RAT
31	59	46.5	388	1	SSR4_HUMAN
32	58	45.7	355	1	CKR1_MACMU
33	58	45.7	359	1	AG2R_BOVIN

34	58	45.7	359	1	AG2R_CANFA	P43240 canis famil
35	58	45.7	359	1	AG2R_CAVPO	Q9WV26 cavia porce
36	58	45.7	359	1	AG2R_HUMAN	P30556 homo sapien
37	58	45.7	359	1	AG2R_MERUN	O35210 meriones un
38	58	45.7	359	1	AG2R_MOUSE	P29754 mus musculu
39	58	45.7	359	1	AG2R_PIG	P30555 sus scrofa
40	58	45.7	359	1	AG2R_RAT	P25095 rattus norv
41	58	45.7	359	1	AG2S_HUMAN	Q13725 homo sapien
42	58	45.7	359	1	AG2S_MOUSE	P29755 mus musculu
43	58	45.7	359	1	AG2S_RAT	P29089 rattus norv
44	57	44.9	308	1	P2Y5_CHICK	P23250 gallus gall
45	57	44.9	350	1	IL8A_HUMAN	P25024 homo sapien

ALIGNMENTS

RESULT 1

ID	CKR6_HUMAN	STANDARD:	PRT:	374 AA.
AC	P51684; Q92846; P78553;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CCR-6) (IARC			
DE	RECEPTOR) (GPR-CY4) (GPCY4) (CHEMOKINE RECEPTOR-LIKE 3) (CKR-L3)			
DE	(DRY6).			
GN	CKR6 OR CMKBR6 OR STRL22 OR GPR29 OR CKRL3.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND FUNCTION.			
RX	MEDLINE-97313465; PubMed=9169459;			
RA	Baba M., Imal T., Nishimura M., Kakizaki M., Takagi S., Hieshima K.,			
RA	Nomiyama H., Yoshie O.;			
RT	"Identification of CKR6, the specific receptor for a novel			
RT	lymphocyte-directed CC chemokine LARC.;"			
RL	J. Biol. Chem. 272:14893-14898(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Lautens L.L., Modi W., Bonner T.I.;			
RL	Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-97040707; PubMed=8886020;			
RA	Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G.;			
RT	"Molecular cloning and RNA expression of two new human chemokine			
RT	receptor-like genes.;"			
RL	Biochem. Biophys. Res. Commun. 227:846-853(1996).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	McCoy R., Perlmutter D.H.;			
RL	Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-97224503; PubMed=9070937;			
RA	Liao F., Lee H.-H., Farber J.M.;			
RT	"Cloning of STRL22, a new human gene encoding a G-protein-coupled			
RT	receptor related to chemokine receptors and located on chromosome			
RT	6q27.;"			
RL	Genomics 40:175-180(1997).			
CC	-1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-			
CC	ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE			
CC	INTRACELLULAR CALCIUM IONS LEVEL.			
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	-1- TISSUE SPECIFICITY: SPLEEN, LYMPH NODES, APPENDIX, AND FETAL			
CC	LIVER. EXPRESSED IN LYMPHOCYTES, T CELLS AND B CELLS BUT NOT IN			
CC	NATURAL KILLER CELLS, MONOCYTES, OR GRANULOCYTES.			
CC	-1- INDUCTION: INTERLEUKIN-2.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-6 IS THE INITIATOR.			

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 CC -----
 DR EMBL; U45984; AAB62714.1; -;
 DR EMBL; 279784; CAB02144.1; ALT_INIT.
 DR EMBL; U60000; AAB06949.1; -;
 DR EMBL; U68030; AAC51124.1; -;
 DR EMBL; U68032; AAC51125.1; -;
 DR HSSP; P34996; 1DDO.
 DR GCRDB; GCR_1037; -;
 DR GCRDB; GCR_1075; -;
 DR GCRDB; GCR_1906; -;
 DR GCRDB; GCR_1919; -;
 DR GCRDB; GCR_1941; -;
 DR GCRDB; GCR_2110; -;
 DR MIM; 601835; -;
 DR InterPro; IPR000276; -;
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G-PROTEIN_RECP_FL_1; 1.
 DR PROSITE; PS0262; G-PROTEIN_RECP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 47
 FT TRANSMEM 48 74
 FT DOMAIN 75 83
 FT TRANSMEM 84 104
 FT DOMAIN 105 119
 FT TRANSMEM 120 141
 FT DOMAIN 142 159
 FT TRANSMEM 160 180
 FT DOMAIN 181 211
 FT TRANSMEM 212 238
 FT DOMAIN 239 254
 FT TRANSMEM 255 279
 FT DOMAIN 280 303
 FT TRANSMEM 304 321
 FT DOMAIN 322 374
 FT DISULFID 118 197
 FT CARBOHYD 23 23
 FT CONFLICT 60 60
 FT CONFLICT 74 74
 FT CONFLICT 86 86
 FT CONFLICT 164 164
 FT CONFLICT 182 182
 FT CONFLICT 192 192
 FT CONFLICT 206 206
 FT CONFLICT 225 225
 FT CONFLICT 370 374
 SQ SEQUENCE 374 AA; 42494 MW; D7F963534E990BC4 CRC64;

Query Match 84.3%; Score 107; DB 1; Length 374;
 Best Local Similarity 95.7%; Pred. No. 1.2e-07;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 IAYSILCVGLGNILVITFAF 26
 ||||| ||||| ||||| ||||| |||||
 Db 51 IAYSILCVGLGNILVITFAF 73

RESULT 2
 ID CKR6_MOUSE STANDARD; PRT; 367 AA.
 AC O54689;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CCR-6) (KY411).
 GN CKR6 OR CKMR6.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yanagihara S., Komura E., Yamaguchi Y.;
 RT "Mouse G protein-coupled receptor KY411.";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99077268; PubMed=9862452;
 RA Varona R., Zaballio A., Gutierrez J., Martin P., Roncal F.,
 RA Albar J.P., Ardavin C., Marquez G.;
 RT "Molecular cloning, functional characterization and mRNA expression
 RT analysis of the murine chemokine receptor CCR6 and its specific ligand
 RT MIP-3alpha.";
 RL FEBS Lett. 440:188-194(1998).
 CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-
 CC ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE
 CC INTRACELLULAR CALCIUM IONS LEVEL.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 DR EMBL; AB009369; BAA23776.1; -;
 DR EMBL; AJ222714; CAA10956.1; -;
 DR MGD; MGI:1333797; Cmkbr6.
 DR InterPro; IPR000276; -;
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G-PROTEIN_RECP_FL_1; 1.
 DR PROSITE; PS0262; G-PROTEIN_RECP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 39
 FT TRANSMEM 40 66
 FT DOMAIN 67 75
 FT TRANSMEM 76 96
 FT DOMAIN 97 111
 FT TRANSMEM 112 133
 FT DOMAIN 134 151
 FT TRANSMEM 152 172
 FT DOMAIN 173 203
 FT TRANSMEM 204 230
 FT DOMAIN 231 246
 FT TRANSMEM 247 271
 FT DOMAIN 272 295
 FT TRANSMEM 296 313
 FT DOMAIN 314 367
 FT DISULFID 110 189
 FT CARBOHYD 2 2
 FT CARBOHYD 35 35
 SQ SEQUENCE 367 AA; 42102 MW; 6A309AF833B117E CRC64;

Query Match 80.3%; Score 102; DB 1; Length 367;
 Best Local Similarity 87.0%; Pred. No. 5.7e-07;
 Matches 20; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 IAYSILCVGLGNILVITFAF 26
 ||||| ||||| ||||| ||||| |||||
 Db 43 IAYSILCVGLGNILVITFAF 65

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RESULT 3
CKR7_HUMAN
ID CKR7_HUMAN STANDARD; PRT; 378 AA.
AC P32248;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 7 PRECURSOR (C-C CKR-7) (CCR-7)
DE (MIP-3 BETA RECEPTOR) (EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 1)
DE (EBI1) (BLR2).
GN CKR7 OR CMKBR7 OR EBI1 OR EVI1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9318173; PubMed=8383238;
RA Birkenbach M.P., Josefsen K., Yalanchilli R.R., Lenoir G.M.,
RA Elliott K.;
RT "Epstein-Barr virus-induced genes: first lymphocyte-specific G
RT protein-coupled peptide receptors.";
RL J. Virol. 67:2209-2220(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=95154835; PubMed=7851893;
RA Schweickart V.L., Raport C.J., Godiska R., Byers M.G., Eddy R.L. Jr.,
RA Shows T.B., Gray P.W.;
RT "Cloning of human and mouse EBIL, a lymphoid-specific
RT G-protein-coupled receptor encoded on human chromosome 17q12-q21.2.";
RL Genomics 23:643-650(1994).
CC -!- FUNCTION: RECEPTOR FOR THE MIP-3-BETA CHEMOKINE. PROBABLE MEDIATOR
CC OF EBV EFFECTS ON B LYMPHOCYTES OR OF NORMAL LYMPHOCYTE FUNCTIONS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN VARIOUS LYMPHOID TISSUES AND
CC ACTIVATED B AND T LYMPHOCYTES, STRONGLY UPREGULATED IN B CELLS
CC INFECTED WITH EPSTEIN-BARR VIRUS AND T CELLS INFECTED WITH
CC HERPESVIRUS 6 OR 7.
CC -!- INDUCTION: BY EBV.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
-----
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-----
DR EMBL; L08176; AAA58615.1; -
DR EMBL; L31584; AAA74230.1; -
DR EMBL; L31582; AAA74230.1; JOINED.
DR EMBL; L31583; AAA74230.1; JOINED.
DR EMBL; L31581; AAA74231.1; -
DR PIR; A45680; A45680.
DR HSSP; P34996; IDDD.
DR GCRDb; GCR_0492; -
DR GCRDb; GCR_0958; -
DR MTM; 600242; -
DR InterPro; IPR000276; -
DR InterPro; IPR001718; -
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODSPN.
DR PRINTS; PR00641; CHEMOKINER7.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 378 C-C CHEMOKINE RECEPTOR TYPE 7.
FT DOMAIN 25 59 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 60 86 1 (POTENTIAL).
-----
FT DOMAIN 87 95 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 96 116 2 (POTENTIAL).
FT DOMAIN 117 130 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 131 152 3 (POTENTIAL).
FT DOMAIN 153 170 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 171 191 4 (POTENTIAL).
FT DOMAIN 192 219 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 220 247 5 (POTENTIAL).
FT DOMAIN 248 263 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 264 289 6 (POTENTIAL).
FT DOMAIN 290 313 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 314 331 7 (POTENTIAL).
FT DOMAIN 332 378 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 36 36 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 129 210 BY SIMILARITY.
FT CONFLICT 182 183 IW -> SA (IN REF. 1).
FT CONFLICT 337 337 L -> I (IN REF. 1).
SQ SEQUENCE 378 AA; 42874 MW; D4CB4213841AIBD4 CRC64;

Query Match 59.1%; Score 75; DB 1; Length 378;
Best Local Similarity 60.9%; Pred. No. 0.0028;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 4 IAYSLICVLGLGNILVITFAF 26
DB 63 IMYSIICFVGLGNGLVLTYY 85

RESULT 4
CM1L_MOUSE STANDARD; PRT; 371 AA.
AC P97468;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CHEMOKINE RECEPTOR-LIKE 1 (G-PROTEIN COUPLED RECEPTOR DEZ).
GN CMKLR1 OR DEZ OR GPCR27.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97289630; PubMed=9144535;
RA Methner A., Hermey G., Schinke B., Hermans-Borgmeyer I.;
RT "A novel G protein-coupled receptor with homology to neuropeptide and
RT chemottractant receptors expressed during bone development.";
RL Biochem. Biophys. Res. Commun. 233:336-342(1997)
CC -!- FUNCTION: ORPHAN RECEPTOR. COULD BE A CHEMOTACTIC PEPTIDE
CC RECEPTOR. MAY HAVE A FUNCTION IN BONE METABOLISM.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED DURING BONE DEVELOPMENT AND IN
CC ADULT PARATHYROID GLANDS. EXPRESSED AT DAY E11 IN THE CAUDAL PART
CC OF THE TONGUE AND THE UMBILICAL CORD AND THE EXPRESSION IN THE
CC TONGUE WAS MAINTAINED THROUGHOUT ADULTHOOD. EXPRESSION INCREASES
CC IN BONE AND CARTILAGINOUS FORMING ZONES OF EMBRYO UPTO STAGE E14.5
CC AND AT E16.5 EXPRESSION IS SEEN IN THE LUNG.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
-----
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-----
DR EMBL; U79525; AAB53789.1; -
DR GCRDb; GCR_1301; -
DR MGI; MGI:109603; Cmk1r1.
DR InterPro; IPR000276; -

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DR InterPro: IPR002258; -
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR InterPro: IPR000276; -
 DR PROSITE: PR01126; DEORPHAN.
 DR PROSITE: PS00237; G-PROTEIN_RECF_F1_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECF_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 40 62 1 (POTENTIAL).
 FT DOMAIN 63 73 2 (POTENTIAL).
 FT TRANSMEM 74 95 3 (POTENTIAL).
 FT DOMAIN 96 112 4 (POTENTIAL).
 FT TRANSMEM 113 133 5 (POTENTIAL).
 FT DOMAIN 134 152 6 (POTENTIAL).
 FT TRANSMEM 153 174 7 (POTENTIAL).
 FT DOMAIN 175 222 8 (POTENTIAL).
 FT TRANSMEM 223 243 9 (POTENTIAL).
 FT DOMAIN 244 259 10 (POTENTIAL).
 FT TRANSMEM 260 280 11 (POTENTIAL).
 FT DOMAIN 281 298 12 (POTENTIAL).
 FT TRANSMEM 299 318 13 (POTENTIAL).
 FT DOMAIN 319 371 14 (POTENTIAL).
 FT CARBOHYD 7 7 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 190 190 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 110 187 POTENTIAL.
 SQ SEQUENCE 371 AA; 41815 MW; CDBE19305244C0B3 CRC64;

Query Match 55.9%; Score 71; DB 1; Length 371;
 Best Local Similarity 56.5%; Pred. No. 0.0096; 6; Indels 0; Gaps 0;
 Matches 13; Conservative 4; Mismatches 6;

QY 4 IAYSLICVLGLGNLIVITFAF 26
 : |||: ||||| ||:: |
 DB 43 VYSLVCLGLGLGNLIVITFAF 65

RESULT 5
 CKR7_MOUSE
 ID CKR7_MOUSE STANDARD; PRT; 378 AA.
 AC P47774;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 7 PRECURSOR (C-C CKR-7) (CCR-7)
 DE (MIP-3 BETA RECEPTOR) (EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 1)
 DE (EB11).
 GN CKR7 OR CMKBR7 OR EB11 OR EB11H.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B6/CBA; TISSUE=Thymus;
 RX MEDLINE=95154835; PubMed=7851893;
 RA Schweickart V.L., Raport C.J., Godiska R., Byers M.G., Eddy R.L. Jr.,
 RA Shows T.B., Gray P.W.;
 RA "Cloning of human and mouse EB11, a lymphoid-specific
 RT G-protein-coupled receptor encoded on human chromosome 17q12-q21.2";
 RL Genomics 23:643-650(1994).
 CC -!- FUNCTION: RECEPTOR FOR THE MIP-3-BETA CHEMOKINE. PROBABLE MEDIATOR
 CC OF EBV EFFECTS ON B LYMPHOCYTES OR OF NORMAL LYMPHOCYTE FUNCTIONS.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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CC EMBL: L31580; AAA74232.1; -
 DR MGD; MGI:103011; Cmkbr7.
 DR InterPro: IPR000276; -
 DR InterPro: IPR001718; -
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR PRINTS: PR00641; CHEMOKINER7.
 DR PROSITE: PS00237; G-PROTEIN_RECF_F1_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECF_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 378 C-C CHEMOKINE RECEPTOR TYPE 7.
 FT DOMAIN 25 59 1 (POTENTIAL).
 FT TRANSMEM 60 86 2 (POTENTIAL).
 FT DOMAIN 87 95 3 (POTENTIAL).
 FT TRANSMEM 96 116 4 (POTENTIAL).
 FT DOMAIN 117 130 5 (POTENTIAL).
 FT TRANSMEM 131 152 6 (POTENTIAL).
 FT DOMAIN 153 170 7 (POTENTIAL).
 FT TRANSMEM 171 191 8 (POTENTIAL).
 FT DOMAIN 192 219 9 (POTENTIAL).
 FT TRANSMEM 220 247 10 (POTENTIAL).
 FT DOMAIN 248 263 11 (POTENTIAL).
 FT TRANSMEM 264 289 12 (POTENTIAL).
 FT DOMAIN 290 313 13 (POTENTIAL).
 FT TRANSMEM 314 331 14 (POTENTIAL).
 FT DOMAIN 332 378 15 (POTENTIAL).
 FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 129 210 BY SIMILARITY.
 SQ SEQUENCE 378 AA; 42941 MW; ACBIA422CF54AA54 CRC64;

Query Match 55.9%; Score 71; DB 1; Length 378;
 Best Local Similarity 52.2%; Pred. No. 0.0097; 7; Indels 0; Gaps 0;
 Matches 12; Conservative 7; Mismatches 4;

QY 4 IAYSLICVLGLGNLIVITFAF 26
 : |||: ||||| ||:: |
 DB 63 LMYSVICFVGLGNLIVITFAF 85

RESULT 6
 CH23_HUMAN
 ID CH23_HUMAN STANDARD; PRT; 371 AA.
 AC O75748;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE PROBABLE G PROTEIN-COUPLED RECEPTOR CHEMR23.
 DE CHEMR23.
 GN CHEMR23.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98264639; PubMed=9603476;
 RA Samson M., Edinger A.L., Stordeur P., Rucker J., Verhasselt V.,
 RA Sharron M., Govaerts C., Mollereau C., Vassart G., Doms R.W.,
 RA Parmentier M.;
 RA "ChemR23, a putative chemotactant receptor, is expressed in
 RT monocyte-derived dendritic cells and macrophages and is a coreceptor
 RT for HIV and some primary HIV-1 strains";
 RL Eur. J. Immunol. 28:1689-1700(1998).
 CC -!- FUNCTION: ORPHAN RECEPTOR. COULD BE A CHEMOATTRACTANT RECEPTOR.
 CC USED AS A CORECEPTOR FOR SEVERAL HIV STRAINS (SIVMAC316,
 CC SIVMAC239, SIVMAC17E-FR AND SIVMAC62A), AS WELL AS A PRIMARY HIV-1
 CC STRAIN (92UG024-2). STRAIN (92UG024-2).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE C-X-C CHEMOKINE RECEPTOR TYPE 5 (CXCR-5) (CXCR-5) (BURKITT'S LYMPHOMA
 DE RECEPTOR 1 HOMOLOG).
 GN BLR1 OR CXCR5 OR GPCR6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALE/C; TISSUE=Liver;
 RX MEDLINE=94009211; PubMed=8405054;
 RA Kaiser E., Foerster R., Wolf I., Epenberger C., Kuehl W.M., Lipp M.;
 RT "The G protein-coupled receptor BLR1 is involved in murine B cell
 RT differentiation and is also expressed in neuronal tissues.";
 RL Eur. J. Immunol. 23:2532-2539(1993).
 RN [2]
 RP SEQUENCE OF 151-269 FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=94116980; PubMed=8288218;
 RA Wilkie T.M., Chen Y., Gilbert D.J., Moore K.J., Yu L., Simon M.I.,
 RA Copeland N.G., Jenkins N.A.;
 RT "Identification, chromosomal location, and genome organization of
 RT mammalian G-protein-coupled receptors.";
 RL Genomics 18:175-184(1993).
 RN [3]
 RP CHARACTERIZATION.
 RX MEDLINE=97133211; PubMed=8978608;
 RA Foerster R., Mattis A.E., Kremmer E., Wolf E., Brem G., Lipp M.;
 RT "A putative chemokine receptor, BLR1, directs B cell migration to
 RT defined lymphoid organs and specific anatomic compartments of the
 RT spleen.";
 RL Cell 87:1037-1047(1996).
 RN [4]
 RP LIGAND BINDING.
 RX MEDLINE=98146056; PubMed=9486651;
 RA Gunn M.D., Ngo V.N., Ansel K.M., Ekland E.H., Cyster J.G.,
 RA Williams L.T.;
 RT "A B-cell-homing chemokine made in lymphoid follicles activates
 RT Burkitt's lymphoma receptor-1.";
 RL Nature 391:799-803(1998).
 CC -!- FUNCTION: CYTOKINE RECEPTOR THAT BINDS TO B LYMPHOCYTE
 CC CHEMOATTRACTANT (BLC). INVOLVED IN B-CELL MIGRATION INTO B-CELL
 CC FOLLICLES OF SPLEEN AND PEYER'S PATCHES, BUT NOT IN THOSE OF
 CC MESENTERIC OR PERIPHERAL LYMPH NODES.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: MAINLY IN SPLEEN, IN RESTING B-CELLS.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X71788; CAA50673.1; -;
 DR EMBL; L20332; AAA16852.1; -;
 DR PIR; S42628; S42628.
 DR GCRDB; GCR_0809; -;
 DR MGD; MGI:103567; Brl1.
 DR InterPro; IPR000276; -;
 DR InterPro; IPR001053; -;
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00564; BURKITTSLYMR.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_FL1; 1.
 DR PROSITE; PS0262; G-PROTEIN_RECEP_FL2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; B-cell.

FT DOMAIN 1 57 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 58 78 1 (POTENTIAL).
 FT DOMAIN 79 90 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 91 111 2 (POTENTIAL).
 FT DOMAIN 112 126 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 127 147 3 (POTENTIAL).
 FT DOMAIN 148 169 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 170 190 4 (POTENTIAL).
 FT DOMAIN 191 221 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 222 242 5 (POTENTIAL).
 FT DOMAIN 243 261 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 262 282 6 (POTENTIAL).
 FT DOMAIN 283 306 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 307 327 7 (POTENTIAL).
 FT DOMAIN 328 374 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 28 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 198 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT DISULFID 124 204 POTENTIAL.
 SQ SEQUENCE 374 AA; 42100 MW; 385258420C1EDE30 CRC64;

 Query Match 52.8%; Score 67; DB 1; Length 374;
 Best Local Similarity 63.2%; Pred. NO. 0.034;
 Matches 12; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

 QY 4 IAYSLICVGLGLGNILVVI 22
 Db 58 VAYSLIFLLGMGMNILLV 76

 RESULT 11
 CCR5_RAT
 ID CCR5_RAT STANDARD; PRT; 374 AA.
 AC P34997;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE C-X-C CHEMOKINE RECEPTOR TYPE 5 (CXCR-5) (CXCR-5) (BURKITT'S LYMPHOMA
 DE RECEPTOR 1 HOMOLOG) (NEUROLIMPHATIC RECEPTOR) (NLR).
 GN BLR1 OR CXCR5.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=93238948; PubMed=8386678;
 RA Kouba M., Vanetti M., Wang X., Schaefer M., Hoellt V.;
 RT "Cloning of a novel putative G-protein-coupled receptor (NLR) which
 RT is expressed in neuronal and lymphatic tissue.";
 RL FEBS Lett. 321:173-178(1993).
 CC -!- FUNCTION: CYTOKINE RECEPTOR THAT BINDS TO B LYMPHOCYTE
 CC CHEMOATTRACTANT (BLC) (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN NEURONAL AND LYMPHATIC TISSUE.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 DR EMBL; X71463; CAA50582.1; -;
 DR PIR; S32785; S32785.
 DR GCRDB; GCR_0648; -;
 DR InterPro; IPR000276; -;
 DR InterPro; IPR001053; -;
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.

CC PRINTS: PR00564; BURKITTSLYMR.
CC PROSITE; PS00237; G_PROTEIN_RECEPT_FL1; 1.
CC PROSITE; PS00262; G_PROTEIN_RECEPT_FL2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; B-cell.
CC DOMAIN 1 57 EXTRACELLULAR (POTENTIAL).
CC TRANSSEM 58 78 1 (POTENTIAL).
CC DOMAIN 79 90 CYTOPLASMIC (POTENTIAL).
CC TRANSSEM 91 111 2 (POTENTIAL).
CC DOMAIN 112 126 EXTRACELLULAR (POTENTIAL).
CC TRANSSEM 127 147 3 (POTENTIAL).
CC DOMAIN 148 169 CYTOPLASMIC (POTENTIAL).
CC TRANSSEM 170 190 4 (POTENTIAL).
CC DOMAIN 191 221 EXTRACELLULAR (POTENTIAL).
CC TRANSSEM 222 242 5 (POTENTIAL).
CC DOMAIN 243 261 CYTOPLASMIC (POTENTIAL).
CC TRANSSEM 262 282 6 (POTENTIAL).
CC DOMAIN 283 306 EXTRACELLULAR (POTENTIAL).
CC TRANSSEM 307 327 7 (POTENTIAL).
CC DOMAIN 328 374 CYTOPLASMIC (POTENTIAL).
CC CARBOHYD 28 28 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC DISULFID 124 204 POTENTIAL.
CC SEQUENCE 374 AA; 42012 MW; D87A3AC816207319 CRC64;

CC Query Match 52.8%; Score 67; DB 1; Length 374;
CC Best Local Similarity 63.2%; Pred. No. 0.034;
CC Matches 12; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

CC QY 4 IAYSLICVLGLGNILVVI 22
CC :||||:||||:||||:
CC DB 58 VAYSLIFLLGMGMNVLV 76

CC RESULT 12
CC CCR5_HUMAN STANDARD; PRT; 372 AA.
CC ID CCR5_HUMAN Q14811;
CC AC P32302; Q14811;
CC DT 01-OCT-1993 (Rel. 27, Created)
CC DT 01-OCT-1993 (Rel. 27, Last sequence update)
CC DT 01-OCT-2000 (Rel. 40, Last annotation update)
CC DE C-X-C CHEMOKINE RECEPTOR TYPE 5 (CXCR-5) (CXCR-5) (BURKITT'S LYMPHOMA
CC DE RECEPTOR 1) (MONOCYTE-DERIVED RECEPTOR 15) (MDR15).
CC BLR1 OR CXCR5.
CC OS Homo sapiens (Human).
CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CC ON NCBI_Taxid=9606;
CC RX [1]
CC RC SEQUENCE FROM N.A. (LONG FORM).
CC RC TISSUE=Lymphocytes;
CC RX MEDLINE=93049615; PubMed=1425907;
CC RA Dobner T., Wolf I., Enrich T., Lipp M.;
CC RT "Differential expression of a novel G protein-coupled
CC RT receptor from Burkitt's lymphoma."
CC RL Eur. J. Immunol. 22:2795-2799(1992).
CC RN [2]
CC RP SEQUENCE FROM N.A. (SHORT FORM).
CC RP TISSUE=Blood;
CC RC MEDLINE=95366951; PubMed=7639692;
CC RA Barella L., Loetscher M., Tobler A., Baggiolini M., Moser B.;
CC RT "Sequence variation of a novel heptahelical leucocyte receptor
CC RT through alternative transcript formation."
CC RL Biochem. J. 309:773-779(1995).
CC RN [3]
CC RP LIGAND BINDING.
CC RP MEDLINE=98130629; PubMed=9463416;
CC RA Legler D.F., Loetscher M., Stuber Roos R., Clark-Lewis I.,
CC RA Baggiolini M., Moser B.;
CC RT "B cell-attracting chemokine 1, a human CXCL12 chemokine expressed in
CC RT lymphoid tissues, selectively attracts B lymphocytes via
CC RT BLR1/CXCR5."
CC RL J. Exp. Med. 187:655-660(1998).
CC LN

DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 1 (C-C CKR-1) (CC-CKR-1) (CCR-1) (CCR1)
DE (MACROPHAGE INFLAMMATORY PROTEIN-1 ALPHA RECEPTOR) (MIP-1ALPHA-R)
DE (RANTES-R) (HM145) (LD78 RECEPTOR).
GN CCR1 OR CCR2 OR CCR3
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93161416; PubMed=7679328;
RT Neote K., Digregorio D., Mak J.Y., Horuk R., Schall T.J.;
RT "Molecular cloning, functional expression, and signaling
RT characteristics of a C-C chemokine receptor.";
RL Cell 72:415-425(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93240122; PubMed=7683036;
RT Gao J.-L., Kuhns D., Tiffany H.L., McDermott D., Li X., Francke U.,
RA Murphy P.M.;
RT "Structure and functional expression of the human macrophage
RT inflammatory protein 1 alpha/RANTES receptor.";
RL J. Exp. Med. 177:1421-1427(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Monocytes;
RX MEDLINE=94092629; PubMed=7505609;
RA Nomura H., Nielsen B.W., Matsushima K.;
RT "Molecular cloning of cDNAs encoding a LD78 receptor and putative
RT leukocyte chemotactic peptide receptors.";
RL Int. Immunol. 5:1239-1249(1993).
CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1 DELTA, RANTES, AND MCP-3 AND, LESS EFFICIENTLY, TO MIP-1-
CC BETA OR MCP-1 AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING
CC THE INTRACELLULAR CALCIUM IONS LEVEL. RESPONSIBLE FOR AFFECTING
CC STEM CELL PROLIFERATION.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN DIFFERENT HEMATOPOIETIC
CC CELLS.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L09230; AAA58408.1; -
CC EMBL; L10918; AAA36543.1; -
CC EMBL; D10925; BAA01723.1; -
CC PIR; A45177; A45177.
CC GCRdb; GCR_0498; -
CC GCRdb; GCR_0557; -
CC GCRdb; GCR_0573; -
CC MIM; 601159; -
CC InterPro; IPR000276; -
CC InterPro; IPR000355; -
CC InterPro; IPR002236; -
CC Pfam; PF00001; 7tm1.1; -
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PRINTS; PR00657; CCHEMOKINER.
CC PRINTS; PR01106; CHEMOKINER1.
CC PROSITE; PS00237; G-PROTEIN RECEPTOR_F1_1; 1.
CC PROSITE; PS00262; G-PROTEIN RECEPTOR_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 34
FT TRANSMEM 35 60
FT DOMAIN 61 64
FT DOMAIN 65 91
FT TRANSMEM 65 91

FT DOMAIN 92 107
FT TRANSMEM 108 129
FT DOMAIN 130 146
FT TRANSMEM 147 171
FT DOMAIN 172 197
FT TRANSMEM 198 223
FT DOMAIN 224 239
FT TRANSMEM 240 264
FT DOMAIN 265 281
FT TRANSMEM 282 305
FT DOMAIN 306 355
FT CARBOHYD 5 5
FT DISULFID 106 183
FT CONFLICT 337 337
SQ SEQUENCE 355 AA; 41172 MW; B2C100FFED275985 CRC64;
Query Match 49.6%; Score 63; DB 1; Length 355;
Best Local Similarity 70.6%; Pred. No. 0.11;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 6 YSLICVLGLGNILWVI 22
DB 41 YSLVFVIGLVGNILWVL 57
|||||:|||||:
|:::|:|||||:
RESULT 14
SSR3_MOUSE STANDARD; PRT; 428 AA.
ID SSR3_MOUSE
AC P30935;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE SOMATOSTATIN RECEPTOR TYPE 3 (SSR) (SSR-28).
GN SSR3 OR SMSTR3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93015924; PubMed=1328199;
RA Yasuda K., Rens-Domiano S., Breder C.D., Law S.F., Saper C.B.,
RA Reisine T., Bell G.I.;
RT "Cloning of a novel somatostatin receptor, SSR3, coupled to
RT adenylyl cyclase.";
RL J. Biol. Chem. 267:20422-20428(1992).
CC -1- FUNCTION: RECEPTOR FOR SOMATOSTATINS-14 AND -28. THIS RECEPTOR IS
CC COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF
CC ADENYLYL CYCLASE.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
CC EMBL; M91000; AAA40144.1; -
CC PIR; A44021; A44021.
CC HSPSP; P34996; 1DDO.
CC GCRdb; GCR_0470; -
CC MGD; MGI:98329; Smstr3.
CC InterPro; IPR000276; -
CC InterPro; IPR000586; -
CC InterPro; IPR001856; -
CC Pfam; PF00001; 7tm1.1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PRINTS; PR00246; SOMATOSTATINR.
CC PRINTS; PR00589; SOMATOSTATINR3.

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	102	80.3	367	11	Q9R1V0	Q9riv0 mus musculus
2	69	54.3	373	13	O57585	O57585 brachydanio
3	65	51.2	383	13	O42324	O42324 catostomus
4	64	50.4	355	6	Q9MYJ8	Q9myj8 callithrix
5	64	50.4	393	5	Q9VVQ0	Q9vvq0 drosophila
6	62	48.8	339	6	Q9RTU4	Q9rtu4 lemur varie
7	62	48.8	339	6	Q9RTU3	Q9rtu3 lemur catia
8	62	48.8	339	6	Q9RTU2	Q9rtu2 lemur catia
9	62	48.8	339	6	Q9RTU1	Q9rtu1 lemur varie
10	62	48.8	339	6	Q9RTU0	Q9rtu0 lemur varie
11	62	48.8	339	6	Q9RTU3	Q9rtu3 lemur catia
12	62	48.8	351	6	Q9MTJ9	Q9mtj9 oryctolagus
13	61	48.0	393	11	Q9R1M0	Q9rlm0 mus musculus
14	61	48.0	400	6	Q9MTW9	Q9myw9 macaca mula
15	61	48.0	401	11	Q9R1L9	Q9rl19 mus musculus
16	61	48.0	438	11	Q9R0D1	Q9rod1 mus musculus
17	61	48.0	444	11	Q9JIY1	Q9jiy1 mus musculus
18	60	47.2	353	13	Q93247	Q93247 cyprinus ca
19	60	47.2	358	6	Q9N0M0	Q9n0m0 ovnis arles

RESULT 2

```

057585
ID O57585 PRELIMINARY; PRT; 373 AA.
AC O57585;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE OPIOID RECEPTOR HOMOLOG.
GN OPRD1.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99141513; PubMed=9987040;
RA Barralio A., Gonzalez-Sarmiento R., Porteros A., Garcia-Isidoro F.,
RA Rodriguez R.E.;
RT Cloning, molecular characterization, and distribution of a gene
RT homologous to delta opioid receptor from zebrafish (Danio rerio).;
RL Biochem. Biophys. Res. Commun. 245:544-548(1998).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AJ001596; CAA04862.1; -
DR ZFIN; ZDB-GENE-990415-199; oprd1.
DR INTERPRO; IPR000276; -
DR PFAM; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
SQ SEQUENCE 373 AA; 42520 MW; FF15794192DAB934 CRC64;

Query Match 54.3%; Score 69; DB 13; Length 373;
Best Local Similarity 81.2%; Pred. No. 0.077; Mismatches 0; Indels 0; Gaps 0;
Matches 13; Conservative 3;

Oy 6 YSLICVGLLGNILVV 21
Db 59 YSVICVGLLGNILVM 74

RESULT 3
ID O42324 PRELIMINARY; PRT; 383 AA.
AC O42324;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE MU-OPIOID RECEPTOR.
OS Catostomus commersoni (White sucker).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Catostomidae; Catostomus.
OX NCBI_TaxID=7971;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=CNS.
RA Darlison M.G., Harvey R.J., Greten F.R., Kreienkamp H.J., Zwieters H.,
RA Stthmer T., Lederis K., Richter D.;
RA Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; Y10904; CAA71843.1; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR001418; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR00384; OPIOIDR.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
SQ SEQUENCE 383 AA; 43232 MW; F58838B57A107305 CRC64;

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Query Match 51.2%; Score 65; DB 13; Length 383;
Best Local Similarity 62.5%; Pred. No. 0.28;
Matches 10; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Oy 6 YSLICVGLLGNILVV 21
Db 64 YSIVCVGLVGNILVM 79

RESULT 4
ID O9MYJ8 PRELIMINARY; PRT; 355 AA.
AC O9MYJ8;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CHEMOKINE RECEPTOR.
GN CCRI.
OS Callithrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
OX NCBI_TaxID=9483;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20153429; PubMed=10686294;
RA Liang M., Rosser M.P., Ng H.P., May K., Bauman J.G., Islam I.,
RA Ghannam A., Kretschmer P.J., Pu H., Dunning L., Snider R.M.,
RA Morrissey M.M., Hesselgesser J., Perez H.D., Horuk R.;
RT "Species selectivity of a small molecule antagonist for the CCRI
RT chemokine receptor.";
RL Eur. J. Pharmacol. 389:41-49(2000).
DR EMBL; AF127528; AAF36453.1; -
KW Receptor.
SQ SEQUENCE 355 AA; 40928 MW; 2B01C47E9874A2C1 CRC64;

Query Match 50.4%; Score 64; DB 6; Length 355;
Best Local Similarity 70.6%; Pred. No. 0.35;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Oy 6 YSLICVGLLGNILVV 22
Db 41 YSLVEVIGLVGNILVV 57

RESULT 5
ID O9VVQ0 PRELIMINARY; PRT; 393 AA.
AC O9VVQ0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE CGI3702 PROTEIN.
GN CGI3702.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballev R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

```


DR PFAM; PF00001; 7tm.1; 1.
 DR PRINTS; GPCRHHODOPSN.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PRINTS; PR00241; ANGIOTENSINR.
 DR PRINTS; PR00645; LCRIORPHANR.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01106; CHEMOKINER1.
 DR PRINTS; PR01107; CHEMOKINER2.
 DR PRINTS; PR01108; CHEMOKINER3.
 DR PRINTS; PR01110; CHEMOKINER5.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN1.
 KW Receptor.
 FT NON_TER 1 1
 FT NON_TER 339 339
 SQ SEQUENCE 339 AA; 38713 MW; 77DCE451AA3A4CB6 CRC64;

Query Match 48.8%; Score 62; DB 6; Length 339;
 Best Local Similarity 61.1%; Pred. No. 0.64;
 Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 6 YSLICVLGLGNILVWIT 23
 |||: : ||: ||: ||: ||:
 Db 30 YSLVFIPLGNMLVLT 47

RESULT 11

ID Q9TQ03 PRELIMINARY; PRT; 339 AA.
 AC Q9TQ03;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
 GN CCR5.
 OS Lemur catta (Ring-tailed lemur).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Strepsirhini; Lemuridae; Lemur.
 OX NCBI_TaxID=9447;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
 RA Shibata K., Yoder A., Pillai S., Kuiken C., Marx P., Wollinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 species.";
 RT Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF162011; AAD47766.1; -;
 DR EMBL; AF162008; AAD47763.1; -;
 DR INTERPRO; IPR000248; -;
 DR INTERPRO; IPR000276; -;
 DR INTERPRO; IPR000355; -;
 DR INTERPRO; IPR001277; -;
 DR INTERPRO; IPR002236; -;
 DR INTERPRO; IPR002237; -;
 DR INTERPRO; IPR002238; -;
 DR INTERPRO; IPR002240; -;
 DR PFAM; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PRINTS; PR00241; ANGIOTENSINR.
 DR PRINTS; PR00645; LCRIORPHANR.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01106; CHEMOKINER1.
 DR PRINTS; PR01107; CHEMOKINER2.
 DR PRINTS; PR01108; CHEMOKINER3.
 DR PRINTS; PR01110; CHEMOKINER5.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN1.
 KW Receptor.
 FT NON_TER 1 1
 FT NON_TER 339 339
 SQ SEQUENCE 339 AA; 38712 MW; 8A2D0D74093A56AE CRC64;

Query Match 48.8%; Score 62; DB 6; Length 339;
 Best Local Similarity 61.1%; Pred. No. 0.64;

Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 6 YSLICVLGLGNILVWIT 23
 |||: : ||: ||: ||: ||:
 Db 30 YSLVFIPLGNMLVLT 47

RESULT 12

ID Q9MYJ9 PRELIMINARY; PRT; 351 AA.
 AC Q9MYJ9;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE CHEMOKINE RECEPTOR.
 GN CCR1.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20153429; PubMed=10686294;
 RA Liang M., Rosser M.P., Ng H.P., May K., Bauman J.G., Islam I.,
 RA Ghanam A., Kretschmer P.J., Pu H., Dunning L., Snider R.M.,
 RA Morrissey M.M., Hesselgeser J., Perez H.D., Horuk R.;
 RT "Species selectivity of a small molecule antagonist for the CCR1
 chemokine receptor.";
 RT Eur. J. Pharmacol. 389:41-49(2000).
 RL EMBL; AF127527; AAF36452.1; -;
 KW Receptor.
 SQ SEQUENCE 351 AA; 40534 MW; B3FED6117A141552 CRC64;

Query Match 48.8%; Score 62; DB 6; Length 351;
 Best Local Similarity 64.7%; Pred. No. 0.66;
 Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 6 YSLICVLGLGNILVWI 22
 |||: : ||: ||: ||: ||:
 Db 41 YSLVFIPLGNMLVLT 57

RESULT 13

ID Q9R1M0 PRELIMINARY; PRT; 393 AA.
 AC Q9R1M0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE MU OPIOID RECEPTOR MORID.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=99348417; PubMed=10419560;
 RA Pan Y.X., Xu J., Bolan E., Abbadi C., Chang A., Zuckerman A.,
 RA Rossi G., Pasternak G.W.;
 RT "Identification and characterization of three new alternatively
 spliced mu-opioid receptor isoforms.";
 RL Mol. Pharmacol. 56:396-403(1999).
 DR EMBL; AF074973; AAD51861.1; -;
 DR INTERPRO; IPR000105; -;
 DR INTERPRO; IPR000276; -;
 DR INTERPRO; IPR000586; -;
 DR INTERPRO; IPR000611; -;
 DR INTERPRO; IPR000826; -;
 DR INTERPRO; IPR001418; -;
 DR PFAM; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.

DR PRINTS; PR00246; SOMATOSTATNPR.
DR PRINTS; PR00384; OPIOIDR.
DR PRINTS; PR00526; FMETLEUPHER.
DR PRINTS; PR00537; MUOPIOIDR.
DR PRINTS; PR01012; NRPEPTIDEYR.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
KW Receptor.
SQ SEQUENCE 393 AA; 43942 MW; 44A102A98DA09EAC CRC64;

Query Match 48.0%; Score 61; DB 11; Length 393;
Best Local Similarity 62.5%; Pred. No. 1;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 6 YSLICVGLGLGNILVV 21
II::II::II II II:
DB 75 YSIVCVVGLFGNFLVM 90

RESULT 14
Q9MYW9 PRELIMINARY; PRT; 400 AA.
AC Q9MYW9:
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE MU OPIOID RECEPTOR.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-STRIATUM;
RA Miller G.M., Madras B.K.;
RT "Cloning of the Macaca mulatta mu opioid receptor.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF286024; AAF97249.1; -
KW Receptor.
SQ SEQUENCE 400 AA; 44922 MW; C6EAE7847179DD3 CRC64;

Query Match 48.0%; Score 61; DB 6; Length 400;
Best Local Similarity 62.5%; Pred. No. 1;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 6 YSLICVGLGLGNILVV 21
II::II::II II II:
DB 77 YSIVCVVGLFGNFLVM 92

RESULT 15
Q9RIL9 PRELIMINARY; PRT; 401 AA.
AC Q9RIL9:
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE MU OPIOID RECEPTOR MORIE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=99348417; PubMed=10419560;
RA Pan Y.X., Xu J., Bolan E., Abbadie C., Chang A., Zuckerman A.,
RA Rossi G., Pasternak G.W.;
RT "Identification and characterization of three new alternatively
RT spliced mu-opioid receptor isoforms.";
RL Mol. Pharmacol. 56:396-403(1999).

DR EMBL; AF074974; AAD51862.1; -
DR INTERPRO; IPR000105; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR000586; -
DR INTERPRO; IPR000611; -
DR INTERPRO; IPR000826; -
DR INTERPRO; IPR001418; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR00246; SOMATOSTATNPR.
DR PRINTS; PR00384; OPIOIDR.
DR PRINTS; PR00526; FMETLEUPHER.
DR PRINTS; PR00537; MUOPIOIDR.
DR PRINTS; PR01012; NRPEPTIDEYR.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
KW Receptor.
SQ SEQUENCE 401 AA; 44847 MW; 2C72C33B40623D9C CRC64;

Query Match 48.0%; Score 61; DB 11; Length 401;
Best Local Similarity 62.5%; Pred. No. 1;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 6 YSLICVGLGLGNILVV 21
II::II::II II II:
DB 75 YSIVCVVGLFGNFLVM 90

Search completed: May 23, 2001, 15:35:12
Job time: 618 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:28:26 ; Search time 184.73 Seconds
(without alignments)
3.404 Million cell updates/sec

Title: US-08-887-977-10_COPY_65_75

Perfect score: 57

Sequence: 1 YKKARSMTDVY 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A_Geneseq_0401.*
- 1: /SID56/gcgdata/geneseq/geneseq/AA1980.DAT.*
 - 2: /SID56/gcgdata/geneseq/geneseq/AA1981.DAT.*
 - 3: /SID56/gcgdata/geneseq/geneseq/AA1982.DAT.*
 - 4: /SID56/gcgdata/geneseq/geneseq/AA1983.DAT.*
 - 5: /SID56/gcgdata/geneseq/geneseq/AA1984.DAT.*
 - 6: /SID56/gcgdata/geneseq/geneseq/AA1985.DAT.*
 - 7: /SID56/gcgdata/geneseq/geneseq/AA1986.DAT.*
 - 8: /SID56/gcgdata/geneseq/geneseq/AA1987.DAT.*
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 - 12: /SID56/gcgdata/geneseq/geneseq/AA1991.DAT.*
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 - 22: /SID56/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	365	19	Human dendritic ce
2	57	100.0	365	21	Primate (human) ch
3	49	86.0	360	17	Chemokine receptor
4	49	86.0	360	21	A human CCR4 chemo
5	43	75.4	159	21	Human OREF ORF1550
6	43	75.4	246	20	Human BGCKr protei
7	43	75.4	333	20	Human BGCKr partia
8	43	75.4	349	20	Human HFAO41 prot
9	43	75.4	350	20	Human BGCKr protei
10	43	75.4	350	20	Mouse BGCKr protei
11	43	75.4	350	20	A human seven-pass

12	43	75.4	350	20	Y17435	Human signal pepti
13	43	75.4	350	20	W93169	Human HFAO41 prot
14	43	75.4	350	21	B37788	Human TSC7. Homo
15	43	75.4	350	21	Y71301	Human orphan G pro
16	43	75.4	350	21	B02835	Human G protein co
17	43	75.4	350	21	Y94325	Human seven transm
18	41	71.9	355	18	W07618	Human G-protein re
19	41	71.9	355	19	W49807	Human G-protein ch
20	41	71.9	355	19	W56689	Human MCP-4 recept
21	41	71.9	355	20	W97868	Human CC chemokine
22	39	68.4	92	20	W97363	A partial CXCR4B p
23	39	68.4	116	21	G01911	Human secreted pro
24	39	68.4	337	15	R53753	Seven transmembran
25	39	68.4	337	19	W48734	Human RM3 seven tr
26	39	68.4	337	21	B21698	Human 7TM receptor
27	39	68.4	352	13	R27792	New platelet facto
28	39	68.4	352	16	R68812	Human monocyte pf4
29	39	68.4	352	16	R80757	Chemokine superfam
30	39	68.4	352	20	Y39993	Human CXCR4 protei
31	39	68.4	352	21	Y52507	Human CXC-chemokin
32	39	68.4	356	20	W97362	G-protein coupled
33	39	68.4	359	19	W64778	A murine CXC chemo
34	39	68.4	359	20	Y39994	Mouse CXCR4 protei
35	38	66.7	100	20	W88231	HIV-1 co-receptor
36	38	66.7	184	18	W27406	Inactive human CCR
37	38	66.7	193	19	W70000	Rodent chemokine r
38	38	66.7	215	18	W27408	Inactive human CCR
39	38	66.7	215	20	W82338	HIV-1 co-receptor
40	38	66.7	302	19	W70001	Rodent chemokine r
41	38	66.7	332	18	W26766	Human chemokine re
42	38	66.7	351	20	Y23825	A7 times membrane
43	38	66.7	352	18	W27407	Human CCR5. Homo
44	38	66.7	352	18	W27123	Human chemokine re
45	38	66.7	352	18	W27125	Macaque chemokine

ALIGNMENTS

RESULT	1
W48086	
ID	W48086 standard; Protein; 365 AA.
XX	
AC	W48086;
XX	
DT	11-JUN-1998 (first entry)
XX	
DE	Human dendritic cell chemokine receptor.
XX	
KW	Human: thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta;
KW	receptor; dendritic cell; macrophage; inflammation; asthma.
XX	
OS	Homo sapiens.
XX	
EH	Key Location/Qualifiers
FT	Misc-difference 193
FT	/note= "encoded by CAN"
XX	
PN	W09801557-A2.
XX	
PD	15-JAN-1998.
XX	
PF	02-JUL-1997; 97WO-US10819.
XX	
PR	04-JUN-1997; 97US-0048593.
PR	05-JUL-1996; 96US-0675814.
PR	11-OCT-1996; 96US-0028329.
XX	
PA	(SCHE) SCHERING CORP.
XX	
PI	Gish KC, Schall TJ, Vicari A, Wang W, Zlotnik A;
XX	
DR	WPI; 1998-101054/09.

DR N-PSDB; V15418.
XX Novel chemokines, e.g. thymus expressed chemokine - used for
PT treating inflammatory conditions including asthma.
XX
XX
PS Claim 3; Page 94-95; 202pp; English.
XX
CC The present sequence represents human dendritic cell chemokine receptor.
CC Antibodies which bind to the protein can be used in detecting or
CC diagnosing various immunological conditions related to expression
CC of the protein. The nucleic acid can be used for screening and
CC isolating DNA clones for the chemokines, especially from other
CC species. The chemokine can be used in the treatment of conditions
CC associated with abnormal physiology or development, including
CC inflammatory conditions such as asthma.
XX
XX
SQ Sequence 365 AA;

Query Match 100.0%; Score 57; DB 19; Length 365;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YKKARSMTDYY 11
Db 65 ykkarsmtdiv 75
|||||

RESULT 2
Y97077
ID Y97077 standard; Protein; 365 AA.
XX Y97077;
XX
XX
XX 04-DEC-2000 (first entry)
XX
XX Primate (human) chemokine receptor CCR6.
XX
XX MIP-3-alpha; chemokine; CCR6 receptor; ligand; cytostatic; agonist;
KW antagonist; anti-psoriatic; dermatological; immunosuppressive;
KW anti-inflammatory.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT Misc-difference 193
FT /note= "Encoded by CAN#"
XX
XX WO2000046248-A1.
XX
XX 10-AUG-2000.
XX
XX 02-FEB-2000; 2000WO-US00511.
XX
XX 03-FEB-1999; 99US-0244281.
XX
XX (SCHE) SCHERING CORP.
XX
XX Oldham ER, Homey B, Dieu-Nosjean M, Caux C, Zlotnik A;
XX
XX WPI; 2000-543477/49.
XX N-PSDB; A51971.
XX
XX Novel methods for modulating the migration of cells within or to the
PT skin using MIP-3-alpha or CCR6 agonists or antagonists, useful for
PT treating skin disorders, e.g. cancer
XX
XX Disclosure; Page 53-54; 61pp; English.
XX
XX The MIP-3-alpha chemokine is expressed in inflamed skin cells. This
CC chemokine is the ligand for the CCR6 receptor. MIP-3-alpha or CCR6
CC agonists or antagonists can be used to modulate the migration of a cell
CC within or to the skin of a mammal. MIP-3-alpha can be used to purify a

CC population of cells expressing a MIP-3-alpha receptor. The methods are
CC useful for treating a mammalian subject with a skin disease or condition,
CC e.g. cancer, metastasis, psoriasis, atopic or contact dermatitis,
CC systemic lupus erythematosus and lichen ruber planus, or for treating
CC skin transplants or grafts.
XX
XX
SQ Sequence 365 AA;

Query Match 100.0%; Score 57; DB 21; Length 365;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YKKARSMTDYY 11
Db 65 ykkarsmtdiv 75
|||||

RESULT 3
R99274
ID R99274 standard; Protein; 360 AA.
XX
XX R99274;
XX
XX 09-DEC-1996 (first entry)
XX
XX Chemokine receptor K5.5.
XX
XX Chemokine receptor K5.5; MIP-1-alpha; RANTES; MCP-1; allergy;
KW atheroma; HIV; AIDS; graft rejection; stem cell.
XX
XX Homo sapiens.
XX
XX WO9623068-A1.
XX
XX 01-AUG-1996.
XX
XX 24-JAN-1996; 96WO-GB00143.
XX
XX 27-JAN-1995; 95GB-0001683.
XX
XX (GLAX) GLAXO GROUP LTD.
XX
XX Power CA, Wells TNC;
XX
XX WPI; 1996-362692/36.
XX N-PSDB; T35277.
XX
XX Chemokine receptor which binds MIP-1-alpha, RANTES and/or MCP-1 -
PT useful in screening for agents to treat asthma, hay fever, eczema,
PT allergies, atopic dermatitis, rhinitis or conjunctivits.
XX
XX Claim 1; Fig 3; 47pp; English.
XX
XX Human chemokine receptor K5.5 (R99274) binds MIP-1-alpha, RANTES
CC and/or MCP-1. Its amino acid sequence was deduced from a cDNA
CC clone (r35277) obtd. from a human spleen lambda gt11 cDNA
CC library. Recombinant chemokine receptor K5.5 can be expressed
CC in transformed host cells. It can be used to screen for agents
CC which act as antagonists to MCP-1, MIP-1-alpha and/or RANTES.
CC Such agents may be useful in treating allergies, atheromas and
CC diseases mediated by viruses, such as AIDS. They can also be
CC used to prevent graft rejection or to protect stem cells from
CC the effects of chemotherapy.
XX
XX
SQ Sequence 360 AA;

Query Match 86.08; Score 49; DB 17; Length 360;
Best Local Similarity 81.88; Pred. No. 0.047;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 YKKARSMTDYY 11

Db 67 ykrlrsmtdiv 77
 ||: |||||

RESULT 4
 B07498
 ID B07498 standard; Protein; 360 AA.

XX AC B07498;
 XX DT 20-OCT-2000 (first entry)

DE A human CCR4 chemokine receptor polypeptide.

XX KW Systemic memory T cell; CCR4; TARC; integrin dependent arrest;
 KW thymus and activation-regulated chemokine; vascular receptor;
 KW MDC; monokine derived chemokine; adhesion trigger; inflammation.

XX OS Homo sapiens.

XX PN WO200041724-A1.

XX PD 20-JUL-2000.

XX PF 14-JAN-2000; 2000WO-US00953.

XX PR 15-JAN-1999; 99US-0232878.

XX PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PA (LEUK-) LEUKOSITE INC.

XX PI Butcher EC, Campbell JJ, Wu L, Rottman JB;

XX DR WPI; 2000-475957/41.
 DR N-PSDB; A58872.

XX PT Modulating the trafficking of systemic memory T cells in mammals by
 PT administering a CCR4 modulating agent, useful for the treatment of
 PT inflammation -

XX PS Disclosure; Page 35-36; 39pp; English.

XX CC The specification describes a method of modulating the trafficking of
 CC systemic memory T cells in a mammalian host. The method comprises
 CC administering a CCR4 modulating agent. It has been found that systemic
 CC T cells such as express high levels of CCR4. Ligands of CCR4 such as
 CC TARC (thymus and activation-regulated chemokine) and MDC (monokine
 CC derived chemokine) act as an adhesion trigger and, upon CCR4 binding,
 CC these cells undergo integrin dependent arrest to the appropriate
 CC vascular receptors. This arrest acts to localize the cells at the
 CC target site. The method modulates this triggering and CCR4 mediated
 CC chemotaxis to affect the localization of T cells in targeted tissues.
 CC The active agent may be a CCR4 agonist that acts to enhance T cell
 CC localization. Alternatively, it may be an antagonist that blocks CCR4
 CC biological activity. A CCR4 antagonist may be administered for the
 CC treatment of inflammation. The present sequence represents a human CCR4.

XX SQ Sequence 360 AA;

Query Match 86.0%; Score 49; DB 21; Length 360;
 Best Local Similarity 81.8%; Pred. No. 0.047; Indels 0; Gaps 0;
 Matches 9; Conservative 1; Mismatches 1

QY 1 YKARSMTDIV 11
 ||: |||||

Db 67 ykrlrsmtdiv 77

RESULT 5
 B41786
 ID B41786 standard; Protein; 159 AA.

AC B41786;

XX DT 08-FEB-2001 (first entry)

XX DE Human ORFX ORF1550 polypeptide sequence SEQ ID NO:3100.

XX KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
 KW vulnery; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 KW hypotensive; dermatological; immunosuppressive; antinflammatory;
 KW antiviral; antibacterial; antifungal; cancer; proliferative disorder; hypertension;
 KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antinflammatory disease; coagulation;
 KW thrombosis; contraceptive.

XX OS Homo sapiens.

XX PN WO200058473-A2.

XX PD 05-OCT-2000.

XX PF 31-MAR-2000; 2000WO-US08621.

XX PR 31-MAR-1999; 99US-0127607.

XX PR 02-APR-1999; 99US-0127636.

XX PR 05-APR-1999; 99US-0127728.

XX PR 30-MAR-2000; 2000US-0540763.

XX PA (CURA-) CURAGEN CORP.

XX PI Shimkets RA, Leach M;

XX DR WPI; 2000-602362/57.

XX DR N-PSDB; C75995.

XX PT Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease -

XX PS Claim 11; Page 2318-2319; 5507pp; English.

XX CC C74446 to C77606 encode the proteins given in B40237 to B43397, which
 CC represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnery;
 CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic;
 CC anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;
 CC cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
 CC dermatological; immunosuppressive; antinflammatory; antibacterial;
 CC antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The
 CC sequences can be used for determining the presence of or predisposition
 CC to, or preventing or treating pathological conditions associated with an
 CC ORFX-associated disorder. The nucleic acids can be used to express ORFX
 CC proteins in gene therapy vectors. The proteins and nucleic acids may be
 CC used to treat cancers, proliferative disorders, neurodegenerative
 CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
 CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
 CC storage, systemic lupus erythematosus, severe combined immunodeficiency
 CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
 CC disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
 CC cartilage damage, nocturnal haemoglobinuria, antinflammatory disease; to
 CC enhance coagulation; to inhibit thrombosis; and as a contraceptive.

XX SQ Sequence 159 AA;

Query Match 75.4%; Score 43; DB 21; Length 159;
 Best Local Similarity 72.7%; Pred. No. 0.31;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YKARSMTDVI 11
 III I: IIII
 Db 10 ykkqrktdiv 20

RESULT 6

ID Y57292 standard; Protein; 246 AA.

AC Y57292;

XX 05-JUN-2000 (first entry)

XX Human BGCKr protein fragment (residues 58-303).

KW BGCKr protein; G-protein coupled receptor; human; chemokine; exocytosis;
 KW cell proliferation; anti-inflammatory; anti-angiogenic; antitumor; HIV;
 KW anti-allergic; antiviral.

XX Homo sapiens.

XX WO9952945-A2.

XX 21-OCT-1999.

XX 16-APR-1999; 99WO-US08395.

XX 16-APR-1998; 98US-0061753.

XX 16-APR-1999; 99US-0061753.

XX (MILL-) MILLENIUM PHARM INC.

PI Gonzalo JA, Gutierrez-Ramos JC;

XX WPI; 1999-620375/53.

XX New nucleic acid encoding human BGCKr receptor, used e.g. for
 PT modulating inflammation and tumor growth

PS Disclosure; Fig 10; 123pp; English.

XX The invention relates to a human BGCKr protein, a G-protein coupled
 CC receptor. The BGCKr protein can be expressed by standard recombinant
 CC methodology. BGCKr are receptor proteins possibly involved in modulation
 CC of proinflammatory or stimulatory functions of chemokines; cell
 CC proliferation, migration, adhesion and targeting, and exocytosis. The
 CC BGCKr nucleic acids and derived proteins (or their variants), antibodies
 CC and modulators are potentially useful for modulating inflammation;
 CC chemoattractant activity of leucocytes; angiogenesis; cell proliferation;
 CC tumour growth; allergic reactions and entry of human immune deficiency
 CC virus into cells, for therapeutic or prophylactic purposes. They are also
 CC used for diagnosis and in drug-screening assays. The present sequence
 CC represents a human BGCKr protein fragment.

XX Sequence 246 AA;

Query Match 75.4%; Score 43; DB 20; Length 246;

Best Local Similarity 72.7%; Pred. No. 0.51;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YKARSMTDVI 11
 III I: IIII
 Db 12 ykkqrktdiv 22

RESULT 7

Y57289

ID Y57289 standard; Protein; 333 AA.

XX Y57289;

AC Y57289;

XX

DT 05-JUN-2000 (first entry)

XX Human BGCKr partial amino acid sequence.

XX BGCKr protein; G-protein coupled receptor; human; chemokine; exocytosis;
 KW cell proliferation; anti-inflammatory; anti-angiogenic; antitumor; HIV;
 KW anti-allergic; antiviral.

XX Homo sapiens.

XX WO9952945-A2.

XX 21-OCT-1999.

XX 16-APR-1999; 99WO-US08395.

XX 16-APR-1998; 98US-0061753.

XX 16-APR-1999; 99US-0061753.

XX (MILL-) MILLENIUM PHARM INC.

XX Gonzalo JA, Gutierrez-Ramos JC;

XX WPI; 1999-620375/53.

XX N-PSDB; 290527.

XX New nucleic acid encoding human BGCKr receptor, used e.g. for
 PT modulating inflammation and tumor growth

PS Claim 1; Fig 1A-B; 123pp; English.

XX The invention relates to a human BGCKr protein, a G-protein coupled
 CC receptor. The BGCKr protein can be expressed by standard recombinant
 CC methodology. BGCKr are receptor proteins possibly involved in modulation
 CC of proinflammatory or stimulatory functions of chemokines; cell
 CC proliferation, migration, adhesion and targeting, and exocytosis. The
 CC BGCKr nucleic acids and derived proteins (or their variants), antibodies
 CC and modulators are potentially useful for modulating inflammation;
 CC chemoattractant activity of leucocytes; angiogenesis; cell proliferation;
 CC tumour growth; allergic reactions and entry of human immune deficiency
 CC virus into cells, for therapeutic or prophylactic purposes. They are also
 CC used for diagnosis and in drug-screening assays. The present sequence
 CC represents the sequence of a partial human BGCKr protein.

XX Sequence 333 AA;

Query Match 75.4%; Score 43; DB 20; Length 333;

Best Local Similarity 72.7%; Pred. No. 0.73;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YKARSMTDVI 11

III I: IIII

Db 52 ykkqrktdiv 62

RESULT 8

W93170

ID W93170 standard; Protein; 349 AA.

XX W93170;

XX 24-MAY-1999 (first entry)

XX Human HFIAO41 protein.

XX HFIAO41; G-coupled receptor; disease susceptibility; diagnosis; immunise;
 KW treatment; FIAO41 protein; gene therapy; immune response; vaccine; HIV-2;
 KW inoculate; bacterial; fungal; protozoan; viral; infection; HIV-1; cancer;
 KW diabetes; anorexia; bulimia; Parkinson's disease; acute heart failure;
 KW hypotension; hypertension; urinary retention; osteoporosis; allergy;
 KW angina pectoris; myocardial infarction; ulcer; asthma; schizophrenia;

benign prostatic hypertrophy; psychotic disorder; neurological disorder;
anxiety; manic depression; delirium; dementia; severe mental retardation;
dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome;
linkage analysis; gene mapping; human; ss.

Human BGCKr protein.
BGCKr protein; G-protein coupled receptor; human; chemokine; exocytosis;
cell proliferation; anti-inflammatory; anti-angiogenic; antitumor; HIV;
anti-allergic; antiviral.
Homo sapiens.
WO9952945-A2.
21-OCT-1999.
16-APR-1999; 99WO-US08395.
16-APR-1998; 98US-0061753.
16-APR-1999; 99US-0061753.
(MILL-) MILLENIUM PHARM INC.
Gonzalo JA, Gutierrez-Ramos JC;
WPI; 1999-620375/53.
N-PSDB; Z90528.
New nucleic acid encoding human BGCKr receptor, used e.g. for
modulating inflammation and tumor growth
Claim 8; Fig 2A-B; 123pp; English.
The invention relates to a human BGCKr protein, a G-protein coupled
receptor. The BGCKr protein can be expressed by standard recombinant
methodology. BGCKr are receptor proteins possibly involved in modulation
of proinflammatory or stimulatory functions of chemokines; cell
proliferation, migration, adhesion and targeting, and exocytosis. The
BGCKr nucleic acids and derived proteins (or their variants), antibodies
and modulators are potentially useful for modulating inflammation;
chemoattractant activity of leucocytes; angiogenesis; cell proliferation;
tumor growth; allergic reactions and entry of human immune deficiency
virus into cells, for therapeutic or prophylactic purposes. They are also
used for diagnosis and in drug-screening assays. The present sequence
represents the full-length human BGCKr protein.
Sequence 350 AA;
Query Match 75.4%; Score 43; DB 20; Length 350;
Best Local Similarity 72.7%; Pred. No. 0.77;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 YKKARSMTDVY 11
||| | : ||||
Db 69 ykkqrkttdvy 79
RESULT 10
Y57291
ID Y57291 standard; Protein; 350 AA.
XX
AC Y57291;
XX
DT 05-JUN-2000 (first entry)
XX
DE Mouse BGCKr protein.
XX
KW BGCKr protein; G-protein coupled receptor; human; chemokine; exocytosis;
KW cell proliferation; anti-inflammatory; anti-angiogenic; antitumor; HIV;
KW anti-allergic; antiviral.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Misc-difference 170

benign prostatic hypertrophy; psychotic disorder; neurological disorder;
anxiety; manic depression; delirium; dementia; severe mental retardation;
dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome;
linkage analysis; gene mapping; human; ss.
Homo sapiens.
EP899332-A2.
03-MAR-1999.
17-FEB-1998; 98EP-0301170.
27-OCT-1997; 97US-0962922.
15-AUG-1997; 97US-0055895.
(SMK) SMITHKLINE BEECHAM CORP.
Ellis CE;
WPI; 1999-144803/13.
N-PSDB; X22558.
New G-coupled receptor (HFIA041) polypeptide and polynucleotide -
useful as diagnostic reagents and for prevention and treatment of
cancer, HIV infections and Parkinson's disease
Disclosure; Page 25-26; 27pp; English.
This sequence encodes a G-coupled receptor, HFIA041 which is useful for
diagnosing susceptibility to diseases by detecting mutations in the
HFIA041 gene, and can diagnose diseases associated with HFIA041 protein
imbalance by determining HFIA041 polypeptide expression levels. Agonists
and antagonists of the protein can be used in treatment to activate
(agonist) or inhibit (antagonist) HFIA041 activity, in addition to direct
administration of antisense sequences to prevent expression, or HFIA041
polynucleotides to treat conditions associated with a lack of HFIA041
protein. Gene therapy may also be used to affect endogenous HFIA041
polypeptide expression. HFIA041 antibodies are useful for inducing an
immune response to immunize and prevent disease, and for isolating
HFIA041 clones or purifying the polypeptides by affinity chromatography.
HFIA041 polypeptides can be administered directly or as a vaccine to
inoculate against disease. Diseases diagnosed, prevented and treated
include bacterial, fungal, protozoan and viral infections, particularly
HIV-1 or -2 infections; cancer; diabetes; anorexia; bulimia; Parkinson's
disease; acute heart failure; hypotension; hypertension; urinary
retention; osteoporosis; angina pectoris; myocardial infarction; ulcers;
asthma; allergies; benign prostatic hypertrophy; and psychotic and
neurological disorders, including anxiety, schizophrenia, manic
depression, delirium, dementia, severe mental retardation and dyskinesias
such as Huntington's disease or Gilles de la Tourette's syndrome. The
HFIA041 polypeptide is also useful for mapping the gene to a chromosome,
allowing gene inheritance to be studied through linkage analysis.
Sequence 349 AA;
Query Match 75.4%; Score 43; DB 20; Length 349;
Best Local Similarity 72.7%; Pred. No. 0.77;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 YKKARSMTDVY 11
||| | : ||||
Db 68 ykkqrkttdvy 78
RESULT 9
Y57290
ID Y57290 standard; Protein; 350 AA.
XX
AC Y57290;
XX
DT 05-JUN-2000 (first entry)

/note= "encoded by ATN"

FT
XX
PN WO9952945-A2.
XX
PD 21-OCT-1999.
XX
XX 16-APR-1999; 99WO-US08395.
PF
XX 16-APR-1998; 98US-0061753.
PR
XX 16-APR-1999; 99US-0061753.
XX
XX (MILL-) MILLENIUM PHARM INC.
PA
XX
XX Gonzalo JA, Gutierrez-Ramos JC;
PI
XX
XX WPI: 1999-620375/53.
DR
XX N-PSDB: 290529.
XX

PT New nucleic acid encoding human BGCR receptor, used e.g. for
XX modulating inflammation and tumor growth
XX
XX Disclosure; Fig 3; 123pp; English.

XX The invention relates to a human BGCR protein, a G-protein coupled
CC receptor. The BGCR protein can be expressed by standard recombinant
CC methodology. BGCR are receptor proteins possibly involved in modulation
CC of proinflammatory or stimulatory functions of chemokines; cell
CC proliferation, migration, adhesion and targeting, and exocytosis. The
CC BGCR nucleic acids and derived proteins (or their variants), antibodies
CC and modulators are potentially useful for modulating inflammation;
CC chemoattractant activity of leucocytes; angiogenesis; cell proliferation;
CC tumour growth; allergic reactions and entry of human immune deficiency
CC virus into cells, for therapeutic or prophylactic purposes. They are also
CC used for diagnosis and in drug-screening assays. The present sequence
CC represents the mouse BGCR protein.

XX Sequence 350 AA;

Query Match 75.4%; Score 43; DB 20; Length 350;

Best Local Similarity 72.7%; Pred. No. 0.77; Mismatches 1; Indels 0; Gaps 0;

OY 1 YKARSMTDYY 11
Db 69 ykkqrkttdy 79

RESULT 11

ID Y30125 standard; Protein; 350 AA.

AC AC Y30125;

XX 14-OCT-1999 (first entry)

XX A human seven-pass transmembrane receptor protein.

XX Seven-pass transmembrane receptor; autoimmune disease;
KW white blood cell dysfunction.

XX Homo sapiens.

OS WO9933876-A1.

XX 08-JUL-1999.

XX 24-DEC-1998; 98WO-JP05886.

XX 24-DEC-1997; 97JP-0354537.

XX (ASAH) ASAH KASEI KOGYO KK.

XX

PI Ishimaru H, Koshio T, Ohno T;

XX WPI: 1999-493806/41.

XX N-PSDB: X86674.

XX New seven-pass transmembrane receptor protein useful for treating,
PT preventing or diagnosing autoimmune diseases
XX
XX Claim 1; Page 101-103; 118pp; Japanese.

XX The present sequence represents a seven-pass transmembrane receptor
CC protein. The protein and its DNA can be used to screen substances
CC for the diagnosis, prevention and treatment of autoimmune diseases,
XX particularly those due to white blood cell dysfunction.

XX Sequence 350 AA;

Query Match 75.4%; Score 43; DB 20; Length 350;

Best Local Similarity 72.7%; Pred. No. 0.77; Mismatches 1; Indels 0; Gaps 0;

OY 1 YKARSMTDYY 11
Db 69 ykkqrkttdy 79

RESULT 12

ID Y17435 standard; Protein; 350 AA.

XX AC Y17435;

XX 29-JUL-1999 (first entry)

XX Human signal peptide-containing protein SP-16.

XX Human; signal peptide-containing protein; SP; cell proliferation;
KW cancer; neuronal disorder; immune response; detection.

XX Homo sapiens.

OS WO9924463-A2.

XX 20-MAY-1999.

XX 04-NOV-1998; 98WO-US23578.

XX 07-NOV-1997; 97US-0966316.

XX (INCY-) INCYTE PHARM INC.

XX Au-Young J, Lal P, Mathur P, Murry LE, Reddy R;

XX WPI: 1999-337694/28.

XX N-PSDB: X61288.

XX cDNA clones encoding signal peptide-containing proteins

XX Claim 1; Fig 1; 83pp; English.

XX The present sequence represents a human signal peptide-containing
CC protein (SP), designated SP-16. SP proteins can be used to stimulate
CC cell proliferation or to treat or prevent cancer. SP antagonists are
CC also used to treat or prevent cancer, and also for treating or
CC preventing neuronal disorders or immune responses. Polynucleotide
CC sequences complementary to the SP-encoding polynucleotides are useful
CC for the detection of SP-encoding nucleic acid molecules in biological
CC samples.

XX Sequence 350 AA;

XX

Query Match 75.4%; Score 43; DB 20; Length 350;

Best Local Similarity 72.7%; Pred. NO. 0.77; Mismatches 1; Indels 2; Gaps 0;

Matches 8; Conservative 1; Mismatches 1; Indels 2; Gaps 0;

QY 1 YKARSMTDVI 11

III I: IIII

Db 69 ykkqrkttdv 79

RESULT 13

W93169

ID W93169 standard; Protein; 350 AA.

XX AC W93169;

XX AC W93169;

XX AC W93169;

DT 24-MAY-1999 (first entry)

XX Human HFIAO41 protein.

DE Human HFIAO41 protein.

XX HFIAO41; G-coupled receptor; disease susceptibility; diagnosis; immunise;

XX treatment; FIAO41 protein; gene therapy; immune response; vaccine; HIV-2;

KW inoculates; bacterial; fungal; protozoan; viral; infection; HIV-1; cancer;

KW diabetes; anorexia; bulimia; Parkinson's disease; acute heart failure;

KW hypotension; hypertension; urinary retention; osteoporosis; allergy;

KW angina pectoris; myocardial infarction; ulcer; asthma; schizophrenia;

KW benign prostatic hypertrophy; psychotic disorder; neurological disorder;

KW anxiety; manic depression; delirium; dementia; severe mental retardation;

KW dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome;

KW linkage analysis; gene mapping; human.

XX Homo sapiens.

OS Homo sapiens.

XX EP899332-A2.

PN EP899332-A2.

XX 03-MAR-1999.

PD 03-MAR-1999.

XX 17-FEB-1998; 98EP-0301170.

XX 27-OCT-1997; 97US-0962922.

PR 15-AUG-1997; 97US-0055895.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX Ellis CE;

XX WPI; 1999-144803/13.

DR N-PSDB; X22557.

XX New G-coupled receptor (HFIAO41) polypeptide and polynucleotide -

XX useful as diagnostic reagents and for prevention and treatment of

XX cancer, HIV infections and Parkinson's disease

XX Claim 1; Page 22-23; 27pp; English.

XX This sequence represents a G-coupled receptor, HFIAO41 which is useful

XX for diagnosing susceptibility to diseases by detecting mutations in the

XX HFIAO41 gene, and can diagnose diseases associated with HFIAO41 protein

XX imbalance by determining HFIAO41 polypeptide expression levels. Agonists

XX and antagonists of the protein can be used in treatment to activate

XX (agonist) or inhibit (antagonist) HFIAO41 activity. In addition to direct

XX administration of antisense sequences to prevent expression, or HFIAO41

XX polynucleotides to treat conditions associated with a lack of HFIAO41

XX protein. Gene therapy may also be used to affect endogenous HFIAO41

XX polypeptide expression. HFIAO41 antibodies are useful for inducing an

XX immune response to immunise and prevent disease, and for isolating

XX HFIAO41 clones or purifying the polypeptides by affinity chromatography.

XX HFIAO41 polypeptides can be administered directly or as a vaccine to

XX inoculate against disease. Diseases diagnosed, prevented and treated

XX include bacterial, fungal, protozoan and viral infections, particularly

XX HIV-1 or -2 infections; cancer; diabetes; anorexia; bulimia; Parkinson's

XX disease; acute heart failure; hypotension; hypertension; urinary

XX retention; osteoporosis; angina pectoris; myocardial infarction; ulcers;

XX asthma; allergies; benign prostatic hypertrophy; and psychotic and

CC neurological disorders, including anxiety, schizophrenia, manic

CC depression, delirium, dementia, severe mental retardation and dyskinesias

CC such as Huntington's disease or Gilles de la Tourette's syndrome. The

CC HFIAO41 polypeptide is also useful for mapping the gene to a chromosome,

CC allowing gene inheritance to be studied through linkage analysis.

XX

SQ Sequence 350 AA;

Query Match 75.4%; Score 43; DB 20; Length 350;

Best Local Similarity 72.7%; Pred. NO. 0.77;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YKARSMTDVI 11

III I: IIII

Db 69 ykkqrkttdv 79

RESULT 14

B37788

ID B37788 standard; Protein; 350 AA.

XX AC B37788;

XX AC B37788;

XX DT 23-FEB-2001 (first entry)

XX Human TSC7.

XX Human TSC7.

XX Human; TSC; tuberous sclerosis complex; cytostatic; antimicrobial;

KW osteopathic; antiulcer; antiallergic; antineoplastic; neuroprotective;

KW analgesic; tranquiliser; immunosuppressive; antiinflammatory;

KW gene therapy; TSC7; infection; cancer; autoimmune disorder;

KW Parkinson's disease; osteoporosis; neurological disorder.

XX Homo sapiens.

OS WO2000064941-A2.

PN WO2000064941-A2.

XX 02-NOV-2000.

PD 02-NOV-2000.

XX 21-APR-2000; 2000WO-US10979.

XX 23-APR-1999; 99US-0130817.

PR 20-APR-2000; 2000US-0556002.

XX (CURA-) CURAGEN CORP.

XX Gould-Rothberg BE;

PI WPI; 2000-679670/66.

XX N-PSDB; C68722.

XX Novel nucleic acid encoding G-protein coupled receptor for diagnosis

XX and treatment of conditions associated with disorder in a G-protein

XX mediated pathway such as cancer, neurological disorders and infections

XX Claim 12; Page 8; 132pp; English.

XX The present sequence is human tuberous sclerosis complex 7 (TSC7).

XX TSC7 polynucleotides and polypeptides are useful for determining the

XX presence or predisposition to a disease associated with altered levels of

XX TSC7. TSC7 polynucleotides, polypeptides and antibodies specific for the

XX polypeptide are useful for treating or preventing pathological conditions

XX associated with the disorder in a G-protein mediated pathway. They are

XX useful for diagnosing a hyperproliferative condition such as a neoplasm

XX or dermatological condition. TSC7 nucleic acids and polypeptides are

XX useful in the treatment of microbial infections, pain, cancer, anorexia,

XX asthma, autoimmune disorders, Parkinson's disease, acute heart failure,

XX hypo/hypertension, osteoporosis, multiple sclerosis, angina pectoris,

XX myocardial infarction, ulcers, allergies, benign prostatic hypertrophy

XX and psychotic and neurological disorders, including schizophrenia,

CC dementia, severe mental retardation and dyskinesias, such as
 CC Huntington's disease and/or other pathologies and disorders. TSC7
 CC polypeptides are also useful as immunogens to produce antibodies and as
 CC vaccines.

XX Sequence 350 AA;

Query Match 75.4%; Score 43; DB 21; Length 350;

Best Local Similarity 72.7%; Pred. No. 0.77; Mismatches 2; Indels 0; Gaps 0;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YKARSMTDVI 11

Db 69 ykkqrktkdv 79

RESULT 15

Y71301

ID Y71301 standard; Protein; 350 AA.

XX AC Y71301;

XX AC Y71301;

XX DT 02-NOV-2000 (first entry)

XX Human orphan G protein-coupled receptor hpprl.

XX Human; orphan G protein-coupled receptor; GPCR; hpprl; drug screening;

XX transmembrane receptor; expressed sequence tag; EST; signal cascade.

XX Homo sapiens.

XX WO200031258-A2.

XX 02-JUN-2000.

XX 13-OCT-1999; 99WO-US23687.

XX 20-NOV-1998; 98US-0109213.

XX 16-FEB-1999; 99US-0120416.

XX 26-FEB-1999; 99US-0121852.

XX 12-MAR-1999; 99US-0123946.

XX 12-MAR-1999; 99US-0123949.

XX 28-MAY-1999; 99US-0136437.

XX 28-MAY-1999; 99US-0136439.

XX 28-MAY-1999; 99US-0136567.

XX 28-MAY-1999; 99US-0137127.

XX 29-JUN-1999; 99US-0141448.

XX 29-SEP-1999; 99US-0156555.

XX 29-SEP-1999; 99US-0156633.

XX 29-SEP-1999; 99US-0156634.

XX 29-SEP-1999; 99US-0156653.

XX 01-OCT-1999; 99US-0157280.

XX 01-OCT-1999; 99US-0157281.

XX 01-OCT-1999; 99US-0157282.

XX 01-OCT-1999; 99US-0157293.

XX 01-OCT-1999; 99US-0157294.

XX 12-OCT-1999; 99US-0416760.

XX 12-OCT-1999; 99US-0417044.

XX (AREN-) ARENA PHARM INC.

XX Chen R, Dang HT, Liaw CW, Lin I;

XX WPI; 2000-400068/34.

XX N-PSDB; D01128.

XX Novel human orphan G protein-coupled receptors and the encoding cDNAs

XX for use in the identification of G protein-coupled receptor agonists -

XX Claim 42; Page 69-70; 102pp; English.

XX

XX

CC The present amino acid sequence is the hpprl, an endogenous human
 CC orphan G protein-coupled receptor (GPCR), expressed in the pituitary
 CC gland, heart, salivary gland, small intestine and testis. The hpprl cDNA
 CC was identified using EST (expressed sequence tag) AA359504 and 238667 as
 CC a probe. The orphan GPCR of the invention, like all GPCRs has seven
 CC transmembrane alpha helices with an extracellular N-terminus and an
 CC intracellular C-terminus. However, no endogenous ligands has yet been
 CC identified for the proteins of the invention. The orphan GPCRs may be
 CC used in the identification of their endogenous ligands, and to screen
 CC potential GPCR agonists and antagonists for use as pharmaceutical agents.
 CC The proteins may also be used in the study of GPCR-mediated signalling
 CC cascades, and to elucidate their precise role in normal and diseased
 CC human conditions. Nucleic acid encoding human orphan GPCRs may be used
 CC for tissue localisation expression analysis to provide information about
 CC their function in healthy and pathological states.

XX Sequence 350 AA;

Query Match 75.4%; Score 43; DB 21; Length 350;

Best Local Similarity 72.7%; Pred. No. 0.77; Mismatches 2; Indels 0; Gaps 0;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YKARSMTDVI 11

Db 69 ykkqrktkdv 79

Search completed: May 23, 2001, 15:28:27

Job time: 404 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 23, 2001, 15:30:05 ; Search time 95.91 Seconds
(without alignments)
2.203 Million cell updates/sec

Title: US-08-887-977-10_COPY_65_75

Perfect score: 57

Sequence: 1 YKARSMWDVY 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued_Patents_AA.*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCT05_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	86.0	360	4	US-08-875-573-20
2	43	75.4	350	2	US-08-966-316-16
3	43	75.4	350	2	US-08-966-316-18
4	41	71.9	355	1	US-08-461-244-2
5	39	68.4	337	1	US-08-153-848-46
6	39	68.4	337	3	US-09-299-843A-46
7	39	68.4	337	5	PCT-US93-11153-46
8	39	68.4	352	1	US-08-202-056-3
9	39	68.4	352	1	US-08-076-093A-4
10	39	68.4	352	1	US-08-450-393A-6
11	39	68.4	352	1	US-08-701-265-4
12	39	68.4	352	2	US-08-284-586-4
13	39	68.4	352	2	US-08-805-478-4
14	39	68.4	352	2	US-08-802-627A-4
15	39	68.4	352	2	US-08-801-238-4
16	39	68.4	352	2	US-08-801-228-4
17	39	68.4	352	3	US-09-104-296-4
18	39	68.4	352	4	US-08-446-669-6
19	39	68.4	352	5	PCT-US95-00476-6
20	38	66.7	87	4	US-09-087-232A-18
21	38	66.7	100	4	US-09-087-232A-15
22	38	66.7	215	4	US-09-087-232A-17
23	38	66.7	352	4	US-09-087-232A-13
24	38	66.7	727	1	US-08-424-424B-2
25	38	66.7	727	5	PCT-US94-05363A-2
26	37	64.9	355	1	US-08-153-848-28
27	37	64.9	355	1	US-08-153-848-32

28	37	64.9	355	3	US-09-299-843A-28	Sequence 28, Appl
29	37	64.9	355	3	US-09-299-843A-32	Sequence 32, Appl
30	37	64.9	355	5	PCT-US93-11153-28	Sequence 28, Appl
31	37	64.9	355	5	PCT-US93-11153-32	Sequence 32, Appl
32	36	63.2	355	1	US-08-012-988A-2	Sequence 2, Appl
33	36	63.2	355	4	US-08-450-393A-5	Sequence 5, Appl
34	36	63.2	355	4	US-08-446-669-5	Sequence 5, Appl
35	36	63.2	355	5	PCT-US95-00476-5	Sequence 5, Appl
36	35	61.4	40	1	US-08-383-751A-3	Sequence 3, Appl
37	35	61.4	342	2	US-08-742-011-2	Sequence 2, Appl
38	35	61.4	358	1	US-08-153-848-19	Sequence 19, Appl
39	35	61.4	358	3	US-09-299-843A-19	Sequence 19, Appl
40	35	61.4	358	5	PCT-US93-11153-19	Sequence 19, Appl
41	35	61.4	359	1	US-08-153-848-24	Sequence 24, Appl
42	35	61.4	359	3	US-09-299-843A-24	Sequence 24, Appl
43	35	61.4	359	5	PCT-US93-11153-24	Sequence 24, Appl
44	35	61.4	361	2	US-08-902-294-4	Sequence 2, Appl
45	35	61.4	361	3	US-09-178-637-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-875-573-20
; Sequence 20, Application US/08875573
; Patent No. 6150132
; GENERAL INFORMATION:
; APPLICANT: Wells, Timothy N.C.
; APPLICANT: Power, Christine A.
; TITLE OF INVENTION: A CHEMOKINE RECEPTOR ABLE TO BIND TO
; TITLE OF INVENTION: MCP-1, MIP-1 ALPHA AND/OR RANTES. ITS USES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 No. 6150132th Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,573
; FILING DATE: 31-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/00143
; FILING DATE: 24-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9501683.8
; FILING DATE: 27-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mary J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1430-172
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-573-20

Query Match 86.0%; Score 49; DB 4; Length 360;
Best Local Similarity 81.8%; Pred. No. 0.056;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YKARSMTDXY 11
||: |||||
Db 67 YKRLRMTDXY 77

RESULT 2

US-08-966-316-16
; Sequence 16, Application US/08966316
; Patent No. 5932445

GENERAL INFORMATION:

; APPLICANT: Lal, Preeti
; APPLICANT: Au-Young, Janice
; APPLICANT: Reddy, Roopa
; APPLICANT: Murty, Lynn E.
; APPLICANT: Mathur, Preete
; TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/966,316
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0424 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:

INFORMATION FOR SEQ ID NO: 16:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: UTRSN011
; CLONE: 2547002
US-08-966-316-16

Query Match 75.4%; Score 43; DB 2; Length 350;
Best Local Similarity 72.7%; Pred. No. 0.75;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YKARSMTDXY 11
||: |||||
Db 69 YKQRTKTDVY 79

RESULT 3

US-08-966-316-18
; Sequence 18, Application US/08966316
; Patent No. 5932445

GENERAL INFORMATION:

; APPLICANT: Lal, Preeti

; APPLICANT: Au-Young, Janice
; APPLICANT: Reddy, Roopa
; APPLICANT: Murty, Lynn E.
; APPLICANT: Mathur, Preete
; TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/966,316
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0424 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:

INFORMATION FOR SEQ ID NO: 18:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 399711
US-08-966-316-18

Query Match 75.4%; Score 43; DB 2; Length 350;
Best Local Similarity 72.7%; Pred. No. 0.75;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YKARSMTDXY 11
||: |||||
Db 69 YKRTKTDVY 79

RESULT 4

US-08-461-244-2
; Sequence 2, Application US/08461244
; Patent No. 5776729

GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel R.
; APPLICANT: Yi, Li
; APPLICANT: Ruben, Steven M.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBR32
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,244
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-445
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-461-244-2

Query Match 71.9%; Score 41; DB 1; Length 355;
Best Local Similarity 80.0%; Pred. No. 1.8;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KKRSMTDXY 11
||| ||| |||
Db 64 KKLRSITDXY 73

RESULT 5
US-08-153-848-46
; Sequence 46, Application US/08153848
; Patent No. 5759804
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153,848
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5759804and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 46:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 337 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-153-848-46

Query Match 68.4%; Score 39; DB 1; Length 337;
Best Local Similarity 80.0%; Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KKRSMTDXY 11
||| ||| |||
Db 52 KKLRSMTDXY 61

RESULT 6
US-09-299-843A-46
; Sequence 46, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,843A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/088,337
; FILING DATE: 01-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jill E. Uhl
; REGISTRATION NUMBER: 43,213
; REFERENCE/DOCKET NUMBER: 27866/32059B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX:
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 337 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-299-843A-46

Query Match 68.4%; Score 39; DB 3; Length 337;
Best Local Similarity 80.0%; Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY      2 KKARSMTDVY 11
      11 1111111
Db      52 KKLRSMTDKY 61

RESULT 7
PCT-US93-11153-46
; Sequence 46, Application PC/TUS9311153
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: Novel Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: PCT/US93/11153
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 337 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-11153-46

Query Match      68.4%; Score 39; DB 5; Length 337;
Best Local Similarity 80.0%; Pred. No. 4.2;
Matches      8; Conservative      0; Mismatches      2; Indels      0; Gaps      0;

QY      2 KKARSMTDVY 11
      11 1111111
Db      52 KKLRSMTDKY 61

RESULT 8
US-08-202-056-3
; Sequence 3, Application US/08202056
; Patent No. 5440021
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Hebert, Caroline
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Lee, James
; TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,056
; FILING DATE: 25-FEB-1994
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/677211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 706P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-202-056-3

Query Match      68.4%; Score 39; DB 1; Length 352;
Best Local Similarity 80.0%; Pred. No. 4.4;
Matches      8; Conservative      0; Mismatches      2; Indels      0; Gaps      0;

QY      2 KKARSMTDVY 11
      11 1111111
Db      67 KKLRSMTDKY 76

RESULT 9
US-08-076-093A-4
; Sequence 4, Application US/08076093A
; Patent No. 5543503
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: Jin Kim, K.
; TITLE OF INVENTION: Antibodies to Human PF4A Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/076,093A
; FILING DATE: 11-Jun-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991

```

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/677211
;; FILING DATE: 29-MAR-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Love, Richard B
;; REGISTRATION NUMBER: 34,659
;; REFERENCE/DOCKET NUMBER: 706P2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415/225-5530
;; TELEFAX: 415/952-9881
;; TELEX: 910/371-7168
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 352 amino acids
;; TYPE: Amino Acid
;; TOPOLOGY: Linear
US-08-076-093A-4

Query Match 68.4%; Score 39; DB 1; Length 352;
Best Local Similarity 80.0%; Pred. No. 4.4;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KKARSMTDVY 11
|| ||||| |
Db 67 KKLRSMTDKY 76

RESULT 10
US-08-450-393A-6
;; Sequence 6, Application US/08450393A
;; Patent No. 5707815
;; GENERAL INFORMATION:
;; APPLICANT: Charo, Israel
;; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
;; TITLE OF INVENTION: PROTEIN RECEPTORS
;; NUMBER OF SEQUENCES: 14
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
;; STREET: 5 Palo Alto Square
;; CITY: Palo Alto
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94306-2155
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/450,393A
;; FILING DATE: May 25, 1995
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Cseir, Luann
;; REGISTRATION NUMBER: 31,822
;; REFERENCE/DOCKET NUMBER: UCAL-237/0205
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-843-5165
;; TELEFAX: 415-8857-0663
;; TELEX: 380816CooleyPA
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 352 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
US-08-450-393A-6

Query Match 68.4%; Score 39; DB 1; Length 352;

Best Local Similarity 80.0%; Pred. No. 4.4;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 KKARSMTDVY 11
|| ||||| |
Db 67 KKLRSMTDKY 76

RESULT 11
US-08-701-265-4
;; Sequence 4, Application US/08701265
;; Patent No. 5776457
;; GENERAL INFORMATION:
;; APPLICANT: Chuntharapai, Anan
;; APPLICANT: Lee, James
;; APPLICANT: Hebert, Caroline
;; APPLICANT: Jin Kim, K.
;; TITLE OF INVENTION: Antibodies to Human PF4A Receptors
;; NUMBER OF SEQUENCES: 6
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Genentech, Inc.
;; STREET: 460 Point San Bruno Blvd
;; CITY: South San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94080
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WinPatIn (Genentech)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/701,265
;; FILING DATE: 22-AUG-1996
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/076093
;; FILING DATE: 11-Jun-1993
;; APPLICATION NUMBER: 07/810782
;; FILING DATE: 19-DEC-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/677211
;; FILING DATE: 29-MAR-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Love, Richard B
;; REGISTRATION NUMBER: 34,659
;; REFERENCE/DOCKET NUMBER: 706P2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415/225-5530
;; TELEFAX: 415/952-9881
;; TELEX: 910/371-7168
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 352 amino acids
;; TYPE: Amino Acid
;; TOPOLOGY: Linear
US-08-701-265-4

Query Match 68.4%; Score 39; DB 1; Length 352;
Best Local Similarity 80.0%; Pred. No. 4.4;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KKARSMTDVY 11
|| ||||| |
Db 67 KKLRSMTDKY 76

RESULT 12
US-08-284-586-4
;; Sequence 4, Application US/08284586
;; Patent No. 5840856
;; GENERAL INFORMATION:

APPLICANT: Chuntharapai, Anan
APPLICANT: Lee, James
APPLICANT: Hebert, Caroline
APPLICANT: Jin Kim, K.
TITLE OF INVENTION: Antibodies to Human PF4A Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,586
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/076,093A
FILING DATE: 11-Jun-1993
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-284-586-4

Query Match 68.4%; Score 39; DB 2; Length 352;
Best Local Similarity 80.0%; Pred. No. 4.4;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KKARSMTDXY 11
|| ||||| |
Db 67 KKLRSMTDXY 76

RESULT 13
US-08-805-478-4
; Sequence 4, Application US/08805478
; Patent No. 5874543
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: Jin Kim, K.
; TITLE OF INVENTION: ANTIBODIES TO PF4A RECEPTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/805,478
FILING DATE: 25-Feb-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/284586
FILING DATE: 10-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076093
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0706P2PIC1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-805-478-4

Query Match 68.4%; Score 39; DB 2; Length 352;
Best Local Similarity 80.0%; Pred. No. 4.4;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KKARSMTDXY 11
|| ||||| |
Db 67 KKLRSMTDXY 76

RESULT 14
US-08-802-627A-4
; Sequence 4, Application US/08802627A
; Patent No. 5892017
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING PF4A RECEPTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,627A
FILING DATE: 19-Feb-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/284586
FILING DATE: 10-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076093

;
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2PID2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-802-627A-4

Query Match 68.4%; Score 39; DB 2; Length 352;
Best Local Similarity 80.0%; Pred. No. 4.4;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KKARSMTDVY 11
|| ||||| |
Db 67 KKLRSMTDKY 76

RESULT 15
US-08-801-238-4
; Sequence 4, Application US/08801238
; Patent No. 5919896
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: PF4A RECEPTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,238
; FILING DATE: 19-Feb-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/284586
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2PID1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:

;
; LENGTH: 352 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-801-238-4

Query Match 68.4%; Score 39; DB 2; Length 352;
Best Local Similarity 80.0%; Pred. No. 4.4;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KKARSMTDVY 11
|| ||||| |
Db 67 KKLRSMTDKY 76

Search completed: May 23, 2001, 15:30:05
Job time: 412 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:31:58 ; Search time 110.15 Seconds
(without alignments)
6.863 Million cell updates/sec

Title: US-08-887-977-10_COPY_65_75
Perfect score: 57
Sequence: 1 YKKARSMTDVY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_67: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	369	JC5068	G protein-coupled
2	49	86.0	360	A57160	chemokine (C-C) re
3	46	80.7	360	JC4587	chemokine (C-C) re
4	43	75.4	350	JN0621	G protein-coupled
5	41	71.9	355	JC5067	G protein-coupled
6	39	68.4	352	G00048	fusin (LESTRA) - c
7	39	68.4	352	A45747	neuropeptide Y/pep
8	39	68.4	353	S28787	neuropeptide Y/pep
9	38	66.7	352	A43113	chemokine (C-C) re
10	37	64.9	273	F71605	hypothetical prote
11	37	64.9	355	JC4304	orphan G protein-c
12	36	63.2	292	B70385	hypothetical prote
13	36	63.2	354	A58186	probable G protein
14	36	63.2	355	A45177	chemokine (C-C) re
15	36	63.2	719	T47727	hypothetical prote
16	36	63.2	916	S22864	DNA topoisomerase
17	35	61.4	186	H75106	hypothetical prote
18	35	61.4	378	A45680	G protein-coupled
19	35	61.4	378	B55735	lymphocyte-specifi
20	35	61.4	378	A55735	G protein-coupled
21	35	61.4	502	T48560	hypothetical prote
22	35	61.4	510	D70009	probable ABC trans
23	35	61.4	544	S42723	matricin - mouse
24	35	61.4	545	S43082	CCF (chaperonin co
25	35	61.4	953	T46227	hypothetical prote
26	35	61.4	1208	T23222	hypothetical prote
27	35	61.4	2810	T22298	hypothetical prote
28	34	59.6	198	S60923	hypothetical prote
29	34	59.6	306	T05605	hypothetical prote

chemokine (C-C) re
MIP-1 alpha recept
cellular tumor ant
cellular tumor ant
cellular tumor ant
tumor suppressor p
DNA primase (EC 2
neurotransmitter t
Na+/Cl(-)-depend
hypothetical prote
hypothetical prote
hypothetical prote
lysophospholipase
tungsten formylmet
MIP-1 alpha recept
chemokine (C-C) re

30 34 59.6 355 2 G02436
31 34 59.6 356 2 I49340
32 34 59.6 381 2 S38824
33 34 59.6 390 1 DNMS53
34 34 59.6 391 1 S02192
35 34 59.6 391 2 JC6193
36 34 59.6 409 2 S48352
37 34 59.6 727 2 S27043
38 34 59.6 727 2 I56506
39 34 59.6 1047 2 T21306
40 34 59.6 1805 1 A64224
41 33 57.9 223 2 D75040
42 33 57.9 259 2 D69998
43 33 57.9 306 2 F69129
44 33 57.9 359 2 I49341
45 33 57.9 360 2 JC2443

ALIGNMENTS

RESULT 1
JC5068
G protein-coupled receptor CKR-L3 - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
C:Accession: JC5068
R:Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
Biochem. Biophys. Res. Commun. 227, 846-853, 1996
A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-lik
A:Reference number: JC5067; MUID:97040707
A:Accession: JC5068
A:Molecule type: DNA
A:Residues: 1-369 <ZAB>
A:Cross-references: EMBL:Z79784; NID:gl668737; PIDN:CAB02144.1; PID:gl668738
C:Comment: This protein belongs to the family of alpha chemokine receptors.
C:Genetics:
A:Gene: GDB:CMKBP6; STRL22; GPR29; CCR6; CKR-L3; GPR-CY4
A:Cross-references: GDB:5370639; OMIM:601835
A:Map position: 6q27-6q27
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein
F:42-68/Domain: transmembrane #status predicted <TM1>
F:79-99/Domain: transmembrane #status predicted <TM2>
F:115-136/Domain: transmembrane #status predicted <TM3>
F:160-180/Domain: transmembrane #status predicted <TM4>
F:212-233/Domain: transmembrane #status predicted <TM5>
F:250-271/Domain: transmembrane #status predicted <TM6>
F:292-315/Domain: transmembrane #status predicted <TM7>

Query Match 100.0%; Score 57; DB 2; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.00074;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YKKARSMTDVY 11
| | | | | | | | | | |
DB 69 YKKARSMTDVY 79

RESULT 2
A57160
chemokine (C-C) receptor 4 - human
N:Alternate names: C-C CKR-4
C:Species: Homo sapiens (man)
C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C:Accession: A57160
R:Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.
J. Biol. Chem. 270, 19495-19500, 1995
A:Title: Molecular cloning and functional expression of a novel CC chemokine receptor
A:Reference number: A57160; MUID:95370289
A:Accession: A57160
A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA
 A:Residues: 1-360 <POM>
 A:Cross-references: GB:X85740; NID:gl370103; PIDN:CAA59743.1; PID:9971452
 A:Note: source clone K5-5
 C:Genetics:
 A:Gene: GDB:CMKBR4
 A:Cross-references: GDB:677463
 A:Map position: 3p21-3p21
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
 F:40-65/Domain: transmembrane #status predicted <TM1>
 F:76-97/Domain: transmembrane #status predicted <TM2>
 F:112-133/Domain: transmembrane #status predicted <TM3>
 F:151-175/Domain: transmembrane #status predicted <TM4>
 F:208-226/Domain: transmembrane #status predicted <TM5>
 F:243-264/Domain: transmembrane #status predicted <TM6>
 F:291-308/Domain: transmembrane #status predicted <TM7>
 F:29-276.110-187/Disulfide bonds: #status predicted
 F:72.350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
 F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
 F:183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 86.0%; Score 49; DB 2; Length 360;
 Best Local Similarity 81.8%; Pred. No. 0.031;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YKARSMTDYY 11
 ||: |||||
 Db 67 YKRLRSMTDYY 77

RESULT 3

JC4587
 Chemokine (C-C) receptor 4 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
 C:Accession: JC4587
 R:Hoogwerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
 Biochem. Biophys. Res. Commun. 218, 337-343, 1996
 A:Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to
 A:Reference number: JC4587; MUID:96136324
 A:Accession: JC4587
 A:Molecule type: mRNA
 A:Residues: 1-360 <HO>
 A:Cross-references: EMBL:X90862; NID:gl167851; PIDN:CAA62372.1; PID:gl167852
 A:Experimental source: thymus
 C:Genetics:
 A:Gene: cc ckr-4
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: glycoprotein; phosphoprotein; receptor; thymus
 F:2183.194/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:72.202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status pred
 F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
 F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 80.7%; Score 46; DB 2; Length 360;
 Best Local Similarity 72.7%; Pred. No. 0.13;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YKARSMTDYY 11
 ||: |||||
 Db 67 YKRLKSMTDYY 77

RESULT 4

JN0621
 G protein-coupled receptor type B - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 19-May-2000
 C:Accession: JN0621

R:Matsuoka, I.; Mori, T.; Aoki, J.; Sato, T.; Kurihara, K.
 Biochem. Biophys. Res. Commun. 194, 504-511, 1993
 A:Title: Identification of novel members of G-protein coupled receptor superfamily ex
 A:Reference number: JN0621; MUID:93326166
 A:Accession: JN0621
 A:Molecule type: mRNA
 A:Residues: 1-350 <MAT>
 A:Cross-references: GB:S63848; NID:g399710; PIDN:AAB27547.1; PID:g399711
 A:Experimental source: Tongue taste papillae
 C:Comment: This protein is involved in modulating taste sensitivity or regeneration o
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein
 F:42-66/Domain: transmembrane #status predicted <TM1>
 F:80-99/Domain: transmembrane #status predicted <TM2>
 F:114-135/Domain: transmembrane #status predicted <TM3>
 F:154-175/Domain: transmembrane #status predicted <TM4>
 F:200-222/Domain: transmembrane #status predicted <TM5>
 F:242-265/Domain: transmembrane #status predicted <TM6>
 F:284-306/Domain: transmembrane #status predicted <TM7>
 F:6.19/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 75.4%; Score 43; DB 2; Length 350;
 Best Local Similarity 72.7%; Pred. No. 0.51;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YKARSMTDYY 11
 ||: |||||
 Db 69 YKRRRTKTDYY 79

RESULT 5

JC5067
 G protein-coupled receptor CKR-L1 - human
 N:Alternate names: chemokine receptor-like protein TER1; GPR-CY6
 C:Species: Homo sapiens (man)
 C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
 C:Accession: JC5067; G02776; G02387
 R:Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
 Biochem. Biophys. Res. Commun. 227, 846-853, 1996
 A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-lik
 A:Reference number: JC5067; MUID:97040707
 A:Accession: JC5067
 A:Molecule type: DNA
 A:Residues: 1-355 <ZAB>
 A:Cross-references: EMBL:Z79782; NID:gl668735; PIDN:CAB02142.1; PID:gl668736
 R:Napolitano, M.; Zingoni, A.; Bernardini, G.; Spinetti, G.; Rocchi, M.; Santoni, A.
 submitted to the EMBL Data Library, June 1996
 A:Reference number: H01714
 A:Accession: G02776
 A:Status: translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-355 <NAP>
 A:Cross-references: EMBL:U62556; NID:gl1468978; PID:gl1468979
 R:Bonner, T.I.
 submitted to the EMBL Data Library, January 1996
 A:Reference number: H01154
 A:Accession: G02387
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-355 <BON>
 A:Cross-references: EMBL:U45983; NID:gl245056; PID:gl245057
 C:Comment: This protein belongs to the family of beta chemokine receptors.

A:Gene: GDB:CMKBR8; CMKBRL2; TER1; CKR-L1
 A:Cross-references: GDB:6053733; OMIM:601834
 A:Map position: 3p21-3p21
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein
 F:36-63/Domain: transmembrane #status predicted <TM1>
 F:73-94/Domain: transmembrane #status predicted <TM2>
 F:108-129/Domain: transmembrane #status predicted <TM3>
 F:147-171/Domain: transmembrane #status predicted <TM4>

Accession	Protein	Domain	Transmembrane	Status	Predicted
F200-222	Domain	transmembrane	#status	predicted	<TM5>
F239-260	Domain	transmembrane	#status	predicted	<TM6>
F281-304	Domain	transmembrane	#status	predicted	<TM7>

Query Match 71.9%; Score 41; DB 2; Length 355;
Best Local Similarity 80.0%; Pred. No. 1.3;
Matches 8; Conservative 1; Mismatches 1; Indels

Qy 2 KKARSM TDVY . 11
11 11:1111
Db 64 KKLRSITDVY 73

RESULTS

RESOL 0
 G00048
 C: Species: Macaca fascicularis (Crab-eating macaque)
 C: Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_
 C: Accession: G00048
 R: Tatsumi, M.
 submitted to GenBank, July 1996
 A: Reference number: H00048
 A: Accession: G00048
 A: Status: preliminary; translated from GB/EMBL/DDBJ
 A: Molecule type: mRNA
 A: Residues: 1-352 <TAT>
 A: Cross-references: GB:D86579; NID:g1468948; PID:g1468949
 C: Superfamily: vertebrate rhodopsin

Query Match 68.4%; Score 39; DB 2; Length 352;
Best Local Similarity 80.0%; Pred. No. 3.3;
Matches 8; Conservative 0; Mismatches 2; Indels

Qy 2 KKARSMTDVY 11
111111111
Db 67 KKLRSMTDKY 76

RESULT

neuropeptide Y/peptide YY receptor Y3 - human
N/Alternate names: fusin; HM89; leukocyte-derived seven-transmembrane receptor LESTR; re
C/Species: Homo sapiens (man)
C/Date: 03-May-1994 #sequence revision 03-May-1994 #text change 05-Nov-1999
C/Accession: A45747; A53103; I53006; I59444; I69203; S32761
R/Federspiel, B.; Melhado, I.G.; Duncan, A.M.V.; Delaney, A.; Schappert, K.; Clark-Lewis
Genomics 16, 707-712, 1993
A/Title: Molecular cloning of the cDNA and chromosomal localization of the gene for a pu
A/Reference number: A45747; MUID:93315164
A/Accession: A45747
A/Molecule type: mRNA
A/Residues: 1-352 <FE>
A/Cross-references: GB:M99293; NID:Q292516; PIDN:AAAL6617.1; PID:g292517
R/Loetscher, M.; Geisler, T.; O'Reilly, T.; Zwaalen, R.; Baggiolini, M.; Moser, B.
J. Biol. Chem. 269, 232-237, 1994
A/Title: Cloning of a human seven-transmembrane domain receptor, LESTR, that is highly e
A/Reference number: A53103; MUID:94103215
A/Accession: A53103
A/Molecule type: mRNA
A/Residues: 1-352 <LO>
A/Cross-references: EMBL:X71635; NID:q297099; PIDN:CAA50641.1; PID:g297100
R/Herzog, H.; Hort, Y.J.; Shine, J.; Selbie, L.A.
DNA Cell Biol. 12, 465-471, 1993
A/Title: Molecular cloning, characterization, and localization of the human homolog to t
A/Reference number: I53006; MUID:93319629
A/Accession: I53006
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-352 <HE>
A/Cross-references: GB:L06797; PIDN:AAA03209.1; PID:g414928
R/Jazin, E.E.; Yoo, H.; Blomqvist, A.G.; Yee, F.; Weng, G.; Walker, M.W.; Salton, J.; Lar

Regul. Pept. 47, 247-258, 1993
A:Title: A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its human hom
A:Reference number: 159444; MUID:94052833
A:Accession: I59444
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-352 <RE2>
A:Cross-references: GB:I189313; NID:g189314; PIDN:AAAL6594.1; PID:g189314
R:Nomura, H.; Nielsen, B.W.; Matsushima, K.
Int. Immunol. 5, 1239-1249, 1993
A:Title: Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte c
A:Reference number: 154751; MUID:94092629
A:Accession: I69203

A:Status: preliminary: translated from GB/EMBL/DBET

A: Molecula tipa: mPNA

A: Molecule type: mRNA
A: Residues: 1-352 <RES>
A: Cross-references: GB:D10924; NID:g219868; PIDN:BAA01722.1; PID:g219869
C: Genetics:

A: Gene: CDP

A; Gene: GDB:NPY3R; NPY3

A;Cross-references: GDB:230002; OMIM:162643

A;Map position: 2q21-2q21

C:Superfamily: vertebrate rhodopsin

C; Keywords: G protein-coupled receptor; tra

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Query Match 68.4%: Score 39: DB 2: Length 352:

Query Match	08.4%	SCORE 33, DB 2; Length 332;
Best Local Similarity	80.0%	Pred NC 33.

Best Local Match	Similarity	Pred. No.	3.3;	Trade
8. Concentrative	80.0%	0. Mismatch	3.3;	Trade

Ov 2 KKARSMTDVY 11

[illegible]

RESULT

neuropeptide Y/peptide YY receptor Y3 - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 26-Aug-1999
C:Accession: S28787
R:Rimland, J.; Xin, W.; Sweetnam, P.; Saijoh, K.; Nestler, E.J.; Duman, R.S.
Mol. Pharmacol. 40, 869-875, 1991
A:Title: Sequence and expression of a neuropeptide Y receptor cDNA.
A:Reference number: S28787; MUID:92100053
A:Accession: S28787
A:Molecule type: mRNA
A:Residues: 1-353 <RIM>
A:Cross-references: EMBL:M86739
C:Superfamily: vertebrate rhodopsin
C:Keywords: appetite; G protein-coupled receptor; transmembrane protein

Query Match

	Query Match	68.4%	Score 39;	DB 2;	Length 353;
DNA	Folded	Coding	Match	78.4%	Score 23;
DNA	Folded	Coding	Match	78.4%	Score 23;

Best Local Similarity	80.0%	Pred. No.	3.4;

QY 2 K K A P S M T D V V 11

QY 2 AKARSMIDVY II
|| || || || ||

RESULTS

RESULT 9
 A43113
 chemokine (C-C) receptor 5 - human
 N:Alternate names: C-C CKR-5; CCR5
 C:Species: Homo sapiens (man)
 C:Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 20-Jun-2000
 C:Accession: A43113; S71808; A58834; A58832; G02653; A58833
 R:Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.
 Biochemistry 35, 3362-3367, 1996
 A:Title: Molecular cloning and functional expression of a new human CC-chemokine rece
 A:Reference number: A43113; MUID:96241590
 A:Accession: A43113

A:Molecule type: mRNA
A:Residues: 1-352 <SAM1>
A:Cross-references: GB:J91492; NID:gl1262810; PIDN:CAA62796.1; PID:gl1262811
R:Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Saragosth
M.; Imal, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Pa
Nature 382, 722-725, 1996
A:Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles o
A:Reference number: S71808; MUID:96345670
A:Accession: S71808
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 182-206; 207-230 <SAM2>
A:Accession: A58834
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-184, 'IKDSHLGAGPAACHGHLGNPKNSASVSK' <SAM3>
A:Cross-references: GB:X99393; NID:gl1524062; PIDN:CAA67767.1; PID:gl1524063
A:Note: this frameshift mutation results in a non-functional receptor but confers a deg
nd may have had a selective advantage by conferring resistance to Yersinia plague infect
R:Combadiere, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.
J. Leukoc. Biol. 60, 147-152, 1996
A:Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine rec
A:Reference number: A58832; MUID:96295970
A:Accession: A58832
A:Molecule type: mRNA
A:Residues: 1-352 <COM1>
A:Cross-references: GB:U57840; NID:gl1502408; PIDN:AAB17071.1; PID:gl1502409
A:Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes
R:Combadiere, C.
submitted to the EMBL Data Library, May 1996
A:Reference number: H01541
A:Accession: G02653
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-89, 'L', 91-352 <COM2>
A:Cross-references: EMBL:U057840
R:Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
J. Biol. Chem. 271, 17161-17166, 1996
A:Title: Molecular cloning and functional characterization of a novel human CC chemokine
A:Reference number: A58833; MUID:96291862
A:Accession: A58833
A:Molecule type: mRNA
A:Residues: 1-352 <RAP>
A:Cross-references: GB:U54994; NID:gl157945; PIDN:AAC50598.1; PID:gl157946
C:Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-1beta (see
C:Comment: Macrophage- and dual-tropic strains of HIV-1 bind to a complex of chemokine (C
C:Genetics:
A:Gene: GDB:CMKBR5; CCR5; CKR-5; CC-CKR-5; CKR5; ChemR13
A:Cross-references: GDB:1230510; OMIM:601373
A:Map position: 3p21-3p21
C:Function:
A:Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RANTR
A:Note: probably acts to control granulocyte proliferation and differentiation
C:Superfamily: vertebrate rhodopsin
C:Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembran
F:32-56/Domain: transmembrane #status predicted <TM1>
F:67-87/Domain: transmembrane #status predicted <TM2>
F:103-124/Domain: transmembrane #status predicted <TM3>
F:142-166/Domain: transmembrane #status predicted <TM4>
F:193-218/Domain: transmembrane #status predicted <TM5>
F:236-257/Domain: transmembrane #status predicted <TM6>
F:285-300/Domain: transmembrane #status predicted <TM7>
F:20-269, 101-178/disulfide bonds: #status predicted
F:268/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:336,337,342/Binding site: phosphate (Ser) (covalent) #status predicted
F:340,343/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 66.7%; Score 38; DB 2; Length 352;
Best Local Similarity 60.0%; Pred. No. 5.4;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 KKARSMTDVIY 11

Db 59 KRLKSMTDIY 68

RESULT 10

F71605

hypothetical protein PFB0820c - malaria parasite (Plasmodium falciparum)

C:Species: Plasmodium falciparum
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000

C:Accession: F71605
R:Gardner, M.J.; Rettel, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.;
Perte, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H
Science 282, 1126-1132, 1998

A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.

A:Reference number: A71600; MUID:99021743

A:Accession: F71605

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-273 <GAR>

A:Cross-references: GB:AE001419; GB:AE001362; NID:g3845281; PIDN:AAC71953.1; PID:g384

A:Experimental source: clone 3D7

C:Genetics:

A:Gene: PFB0820c

Query Match 64.9%; Score 37; DB 2; Length 273;

Best Local Similarity 63.6%; Pred. No. 6.6;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YKARSMTDVIY 11

Db 188 KYASSTTDIY 198

RESULT 11

JC4304

orphan G protein-coupled receptor - human

N:Alternate names: V28 protein

C:Species: Homo sapiens (man)

C:Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 19-May-2000

C:Accession: JC4304

R:Raport, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.

Gene 163, 295-299, 1995

A:Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely related t

A:Reference number: JC4304; MUID:96011651

A:Accession: JC4304

A:Molecule type: mRNA

A:Residues: 1-355 <RAP>

A:Cross-references: GB:U20350; NID:g665580; PIDN:AAA91783.1; PID:g665581

A:Experimental source: peripheral blood mononuclear cell

C:Comment: This protein is a cell-surface receptor which recognizes extracellular sig

C:Comment: This protein is a key regulator of many immune and homeostatic responses,

C:Genetics:

A:Gene: V28

A:Map position: 3pter-p21

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; lymphokine; transmembrane protein

F:33-57/Domain: transmembrane #status predicted <TM1>

F:66-88/Domain: transmembrane #status predicted <TM2>

F:104-125/Domain: transmembrane #status predicted <TM3>

F:146-165/Domain: transmembrane #status predicted <TM4>

F:197-217/Domain: transmembrane #status predicted <TM5>

F:230-254/Domain: transmembrane #status predicted <TM6>

F:275-296/Domain: transmembrane #status predicted <TM7>

Query Match 64.9%; Score 37; DB 2; Length 355;

Best Local Similarity 60.0%; Pred. No. 8.7;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 KKARSMTDVIY 11

Db 60 KKPKSVTDIY 69

RESULT 12

B70385 hypothetical protein aq_983 - Aquifex aeolicus

C:Species: Aquifex aeolicus

C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 18-Aug-2000

C:Accession: B70385

R:Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'V.

V. Nature 392, 353-358, 1998

A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A:Reference number: A70300; MUID:98196666

A:Accession: B70385

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-292 <AQP>

A:Cross-references: GB:AF000717; NID:g2983492; PIDN:AAC07075.1; PID:g2983497; GB:AE00065

A:Experimental source: strain VF5

C:Genetics:

C:Superfamily: Aquifex aeolicus hypothetical protein aq_983

Query Match 63.2%; Score 36; DB 2; Length 292;

Best Local Similarity 54.5%; Pred. No. 11;

Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 YKARSMTDVI 11

I : I : I : I : I

Db 223 YRKEKSLHDVI 233

RESULT 13

I58186

probable G protein-coupled receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000

C:Accession: I58186

R:Harrison, J.K.; Barber, C.M.; Lynch, K.R.

Neurosci. Lett. 169, 85-89, 1994

A:Title: cDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord and b

A:Reference number: I58186; MUID:94323113

A:Accession: I58186

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-354 <RES>

A:Cross-references: EMBL:U04808; NID:g2558635; PIDN:AAB87093.1; PID:g439861

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor

Query Match

Best Local Similarity 63.2%; Score 36; DB 2; Length 354;

Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKARSMTDVI 11

I : I : I : I : I

Db 61 RKRSITDIY 70

RESULT 14

A45177

chemokine (C-C) receptor 1 - human

N:Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999

C:Accession: A45177; I55671

R:Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.

Cell 72, 415-425, 1993

A:Title: Molecular cloning, functional expression, and signaling characteristics of a C-

A:Reference number: A45177; MUID:93161416

A:Accession: A45177

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-355 <NEO>

A:Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417

A:Experimental source: HL60 cells

A:Note: sequence extracted from NCBI backbone (NCBIP:124876)

R:Gao, J.

J. Exp. Med. 177, 1421-1427, 1993

A:Title: Structure and functional expression of the human macrophage inflammatory 1 a

A:Reference number: I55671; MUID:93240122

A:Accession: I55671

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-355 <RES>

A:Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417

C:Genetics:

A:Gene: GDB:CMKRL1; CMKR-1

A:Cross-references: GDB:I38446; OMIM:601159

A:Map position: 3p21-3p21

C:Superfamily: vertebrate rhodopsin

C:Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein;

F:35-60/Domain: transmembrane #status predicted <TM1>

F:71-91/Domain: transmembrane #status predicted <TM2>

F:108-129/Domain: transmembrane #status predicted <TM3>

F:147-171/Domain: transmembrane #status predicted <TM4>

F:205-223/Domain: transmembrane #status predicted <TM5>

F:240-264/Domain: transmembrane #status predicted <TM6>

F:288-305/Domain: transmembrane #status predicted <TM7>

F:5/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:24-273,106-183/Disulfide bonds: #status predicted

F:345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predi

Query Match 63.2%; Score 36; DB 2; Length 355;

Best Local Similarity 45.5%; Pred. No. 14;

Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 YKARSMTDVI 11

I : I : I : I : I

Db 62 YKRLNMTSIY 72

RESULT 15

T47727

hypothetical protein F18021.60 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000

C:Accession: T47727

R:Benes, V.; Wurmbach, E.; Drzonek, H.; Ansorge, W.; Mewes, H.W.; Rudd, S.; Lemcke, K

submitted to the Protein Sequence Database, April 2000

A:Reference number: Z24474

A:Accession: T47727

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-719 <BEN>

A:Cross-references: EMBL:ATF18021

A:Experimental source: cultivar Columbia; BAC clone F18021

C:Genetics:

A:Map position: 3

A:Introns: 244/2; 491/1; 511/1

A:Note: F18021.60

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

Query Match

Best Local Similarity 63.2%; Score 36; DB 2; Length 719;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 KKARSMTDVI 11

I : I : I : I : I

Db 598 KKANTKTDVI 607

Search completed: May 23, 2001, 15:31:59
Job time: 506 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 23, 2001, 15:36:17 ; Search time 62.39 Seconds
(without alignments)
6.040 Million cell updates/sec

Title: US-08-887-977-10_COPY_65_75
Perfect score: 57
Sequence: 1 YKARSMTDVI 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	100.0	367	1	CCR6_MOUSE
2	57	100.0	374	1	CCR6_MOUSE
3	49	86.0	360	1	CCR4_HUMAN
4	46	80.7	360	1	CCR4_MOUSE
5	43	75.4	350	1	GUSB_BOVIN
6	41	71.9	354	1	CCR5_RAT
7	41	71.9	355	1	CCR8_HUMAN
8	41	71.9	373	1	CCR2_MOUSE
9	41	71.9	373	1	CCR2_RAT
10	40	70.2	353	1	CCR8_MOUSE
11	39	68.4	192	1	CCR4_SHEEP
12	39	68.4	349	1	CCR4_RAT
13	39	68.4	352	1	CCR4_CERTO
14	39	68.4	352	1	CCR4_HUMAN
15	39	68.4	352	1	CCR4_MACFA
16	39	68.4	352	1	CCR4_MACMU
17	39	68.4	352	1	CCR4_PAPAN
18	39	68.4	353	1	CCR4_BOVIN
19	39	68.4	353	1	CCR4_FELCA
20	39	68.4	359	1	CCR4_MOUSE
21	38	66.7	352	1	CCR5_CERAE
22	38	66.7	352	1	CCR5_CERTO
23	38	66.7	352	1	CCR5_GORGO
24	38	66.7	352	1	CCR5_HUMAN
25	38	66.7	352	1	CCR5_HYLLE
26	38	66.7	352	1	CCR5_MACMU
27	38	66.7	352	1	CCR5_PANTR
28	38	66.7	352	1	CCR5_PAPHA
29	38	66.7	352	1	CCR5_PONFI
30	38	66.7	352	1	CCR5_PYGNI
31	38	66.7	352	1	CCR5_PYGNI
32	38	66.7	352	1	CCR5_TRAFR
33	38	66.7	352	1	CCR5_TRAPH

34	37	64.9	354	1	CCR5_MOUSE	P51682 mus musculu
35	37	64.9	355	1	C3X1_HUMAN	P49238 homo sapien
36	37	64.9	355	1	CCR1_MACMU	P56482 macaca mula
37	37	64.9	356	1	CCR8_MACMU	O97665 macaca mula
38	36	63.2	349	1	IL8A_RAT	P70612 rattus norv
39	36	63.2	354	1	C3X1_RAT	P35411 rattus norv
40	36	63.2	355	1	CCR1_HUMAN	P32246 homo sapien
41	36	63.2	370	1	VK02_SPVKA	Q08520 swinepox vi
42	36	63.2	636	1	F73_HUMAN	O15350 homo sapien
43	36	63.2	916	1	TOP1_ARATH	P30181 arabidopsis
44	35	61.4	342	1	BONZ_CERAE	O18983 cercopithec
45	35	61.4	342	1	BONZ_HUMAN	O00574 homo sapien

ALIGNMENTS

RESULT 1

ID	CCR6_MOUSE	STANDARD;	PRT;	367 AA.
AC	O54689;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CCR-6) (CCR-6) (KY411).			
GN	CCR6 OR CMKBR6.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Yanagihara S., Komura E., Yamaguchi Y.;			
RT	"Mouse G protein-coupled receptor KY411.";			
RL	Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99077268; PubMed=9862452;			
RA	Varona R., Zaballou A., Gutierrez J., Martin P., Roncal F.,			
RT	Albar J.P., Ardavin C., Marquez G.;			
RT	"Molecular cloning, functional characterization and mRNA expression			
RT	analysis of the murine chemokine receptor CCR6 and its specific ligand			
RL	MIP-3alpha.";			
FEBS	Lett. 440:188-194(1998).			
CC	-!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-			
CC	INTRACELLULAR AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE			
CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
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CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	EMBL; AB009369; BAA23776.1;			
DR	EMBL; AJ222714; CAA10956.1;			
DR	MGI; MGI:1333797; Cmkbr6.			
DR	InterPro; IPR000276;			
DR	Prfam; PF00001; 7tm_1; 1.			
DR	PRINTS; PR00237; GPCRHOOPS.			
DR	PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.			
DR	PROSITE; PS00262; G_PROTEIN_RECEPTOR_F1_2; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein.			
FT	DOMAIN 1 39			
FT	TRANSMEM 40 66			
FT	TRANSMEM 67 75			
FT	TRANSMEM 76 96			
FT	DOMAIN 97 111			
FT	TRANSMEM 112 133			
FT	TRANSMEM 133 133			


```
RESULT 3
CKR4_HUMAN
ID CKR4_HUMAN STANDARD; PRT; 360 AA.
AC P51679;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 4 (C-CR-4) (CCR-4) (CCR4)
DE (K5-5).
GN CCR4 OR CMKBR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95370289; PubMed=7642634;
RA Power C.A., Meyer A., Nemeth K., Bacon K.B., Hoogewerf A.J.,
RA Proudfoot A.E.I., Wells T.N.C.;
RT "Molecular cloning and functional expression of a novel CC chemokine
RT receptor cDNA from a human basophilic cell line.";
RL J. Biol. Chem. 270:19495-19500(1995).
RN [2]
RP FUNCTION.
RX MEDLINE=97313486; PubMed=9169480;
RA Inai T., Baba M., Nishimura M., Kakizaki M., Takagi S., Yoshie O.;
RT "The T cell-directed CC chemokine TARC is a highly specific
RT biological ligand for CC chemokine receptor 4.";
RL J. Biol. Chem. 272:15036-15042(1997).
CC -!- FUNCTION: RECEPTOR FOR C-C TYPE CHEMOKINE. BINDS TO TARC, MIP-1-
CC ALPHA, RANTES, AND MCP-1. SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: EXPRESSED STRONGLY IN PERIPHERAL BLOOD T CELLS
CC BUT NOT IN B CELLS, NATURAL KILLER CELLS, MONOCYTES, OR
CC GRANULOCYTES.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X85740; CAA59743.1; -
DR MIM; 604836; -
DR GCRDB; GCR_2115; -
DR InterPro; IPR000276; -
DR InterPro; IPR000355; -
DR InterPro; IPR002239; -
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00657; CCHEMOKINER4.
DR PRINTS; PR01109; CHEMOKINER4.
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR_F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN_RECEPTOR_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 40 67 1 (POTENTIAL)
FT DOMAIN 68 77 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 78 98 2 (POTENTIAL).
FT DOMAIN 99 111 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 112 133 3 (POTENTIAL).
FT DOMAIN 134 150 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 151 175 4 (POTENTIAL).
FT DOMAIN 176 206 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 207 226 5 (POTENTIAL).
FT DOMAIN 227 242 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 243 267 6 (POTENTIAL).
FT DOMAIN 268 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 284

FT TRANSMEM 285 308 7 (POTENTIAL).
FT DOMAIN 309 360 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 194 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 110 187 BY SIMILARITY.
SQ SEQUENCE 360 AA; 41402; 51EBE12AD1FAFBF CRC64;

Query Match 86.0%; Score 49; DB 1; Length 360;
Best Local Similarity 81.8%; Pred. No. 0.016;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YKARSMTDYY 11
DB 67 YKRLRSMTDYY 77

RESULT 4
CKR4_MOUSE
ID CKR4_MOUSE STANDARD; PRT; 360 AA.
AC P51680;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 4 (C-CR-4) (CCR-4) (CCR4).
GN CCR4 OR CMKBR4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
RX MEDLINE=96136324; PubMed=8573157;
RA Hoogewerf A.J., Black D., Proudfoot A.E.I., Wells T.N.C., Power C.A.;
RT "Molecular cloning of murine CC CR-4 and high affinity binding of
RT chemokines to murine and human CC CR-4.";
RL Biochem. Biophys. Res. Commun. 218:337-343(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
RX MEDLINE=96136324; PubMed=8573157;
RA Hoogewerf A.J., Black D., Proudfoot A.E.I., Wells T.N.C., Power C.A.;
RT "Molecular cloning of murine CC CR-4 and high affinity binding of
RT chemokines to murine and human CC CR-4.";
RL Biochem. Biophys. Res. Commun. 218:337-343(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6; TISSUE=Spleen;
RX MEDLINE=97335974; PubMed=9192769;
RA Youn B.-S., Kim S.-H., Lyu M.-S., Kozak C.A., Taub D.D., Kwon B.S.;
RT "Molecular cloning and characterization of a cDNA, CHEM1, encoding a
RT chemokine receptor with a homology to the human C-C chemokine
RT receptor, CCR-4.";
RL Blood 89:4448-4460(1997).
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO TARC AND
CC SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR
CC CALCIUM IONS LEVEL (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: DETECTED IN THE THYMUS AND T-CELLS.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; X90862; CAA62372.1; -
DR EMBL; U15208; AAA92582.1; -
DR GCRDB; GCR_1714; -
DR MGD; MGI:107824; Cmkbr4.
DR InterPro; IPR000276; -
DR InterPro; IPR000355; -
DR InterPro; IPR002239; -
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01109; CHEMOKINER4.
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DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 KW PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 FT DOMAIN 1 39
 FT TRANSMEM 40 67
 FT DOMAIN 68 77
 FT TRANSMEM 78 98
 FT DOMAIN 99 111
 FT TRANSMEM 112 133
 FT DOMAIN 134 150
 FT TRANSMEM 151 175
 FT DOMAIN 176 206
 FT TRANSMEM 207 226
 FT DOMAIN 227 242
 FT TRANSMEM 243 267
 FT DOMAIN 268 284
 FT TRANSMEM 285 308
 FT DOMAIN 309 360
 FT CARBOHYD 2 2
 FT CARBOHYD 183 183
 FT CARBOHYD 194 194
 FT DISULFID 110 187
 FT CONFLICT 4 4
 FT CONFLICT 145 145
 FT CONFLICT 181 181
 FT CONFLICT 205 205
 FT CONFLICT 221 221
 FT CONFLICT 241 241
 FT CONFLICT 246 246
 FT CONFLICT 293 293
 FT CONFLICT 311 311
 SQ SEQUENCE 360 AA; 41462 MW; 97BDB8C96D259AE3 CRC64;

Query Match 80.7%; Score 46; DB 1; Length 360;
 Best Local Similarity 72.7%; Pred. No. 0.066;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YKARSMTDVI 11
 |||:|||||

Db 67 YKRLKSMTDVI 77

RESULT 5
 GUSB_BOVIN STANDARD; PRT; 350 AA.
 ID GUSB_BOVIN
 AC P35350;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE POSSIBLE GUSTATORY RECEPTOR TYPE B (PPRI PROTEIN).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=Tongue;
 RX MEDLINE=93326166; PubMed=8392843;
 RA Matsuoka I., Mori T., Aoki J., Sato T., Kurihara K.;
 RT "Identification of novel members of G-protein coupled receptor
 superfamily expressed in bovine taste tissue";
 RL Biochem. Biophys. Res. Commun. 194:504-511(1993).
 CC -!- FUNCTION: POSSIBLE TASTE RECEPTOR. MAY ALSO BE A RECEPTOR FOR
 PEPTIDE LIGANDS.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN CIRCUMVALLATE AND FUNGIFORM
 PAPILLAE, OLFACTORY EPITHELIUM AND LUNG. LOWER EXPRESSION IN
 LIVER, KIDNEY AND TONGUE EPITHELIUM BEARING NO TASTE PAPILLAE.
 CC VERY LOW EXPRESSION IN THE CEREBRAL CORTEX OF THE BRAIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-18 IS THE INITIATOR.

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 CC -----
 DR EMBL; S63848; AAB27547.1; -
 DR PIR; JN0621; JN0621.
 DR GCRdb; GCR_0757; -
 DR InterPro; IPR000276; -
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Phosphorylation.
 FT DOMAIN 1 41 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 42 66 1 (POTENTIAL).
 FT DOMAIN 67 79 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 80 99 2 (POTENTIAL).
 FT DOMAIN 100 113 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 114 135 3 (POTENTIAL).
 FT DOMAIN 136 153 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 154 175 4 (POTENTIAL).
 FT DOMAIN 176 199 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 200 222 5 (POTENTIAL).
 FT DOMAIN 223 241 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 242 265 6 (POTENTIAL).
 FT DOMAIN 266 283 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 284 306 7 (POTENTIAL).
 FT DOMAIN 307 350 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 6 6 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 19 19 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT DISULFID 112 184 BY SIMILARITY.
 SQ SEQUENCE 350 AA; 40008 MW; E46BF942F3919C82 CRC64;

Query Match 75.4%; Score 43; DB 1; Length 350;
 Best Local Similarity 72.7%; Pred. No. 0.26;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YKARSMTDVI 11
 |||:|||||

Db 69 YKRRRTKTDVI 79

RESULT 6

CKR5_RAT STANDARD; PRT; 354 AA.
 ID CKR5_RAT
 AC O08556;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CCR-5) (MIP-1
 DE ALPHA RECEPTOR).
 DE CCR5 OR CMKBR5.
 OS Rattus norvegicus (Rat).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; Tissue=Brain;
 RX MEDLINE=98334064; PubMed=9670989;
 RA Speiss O., Gourmala N., Bodde H.W.G.M., Sauter A., Fiebich B.L.,
 RA Berger M., Gebicke-Haerter P.J.;
 RT "Cloning of rat HIV-1-chemokine coreceptor CKR5 from microglia and
 RT upregulation of its mRNA in ischemic and endotoxemic rat brain";
 RL J. Neurosci. Res. 53:16-28(1998).
 RN [2]

```

RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RX MEDLINE=98318173; PubMed=9655467;
RA Jiang Y., Salfraanca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
RA Defebvre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
RT "Chemokine receptor expression in cultured glia and rat experimental
RT allergic encephalomyelitis.";
RL J. Neuroimmunol. 86:1-12(1998).
CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Y12009; CAA72737.1; -
DR GCRDB; GCR_1470; -
DR InterPro; IPR000276; -
DR InterPro; IPR000355; -
DR InterPro; IPR002240; -
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GCRHDDOPSN.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01110; CHEMOKINER5.
DR PROSITE; PS00237; G-PROTEIN_RECP_FL_1; 1.
DR PROSITE; PS50262; G-PROTEIN_RECP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 32
FT TRANSMEM 33 60
FT DOMAIN 61 70
FT TRANSMEM 71 91
FT DOMAIN 92 104
FT TRANSMEM 105 126
FT DOMAIN 127 143
FT TRANSMEM 144 168
FT DOMAIN 169 200
FT TRANSMEM 201 220
FT TRANSMEM 221 237
FT DOMAIN 238 262
FT TRANSMEM 263 279
FT DOMAIN 280 303
FT TRANSMEM 304 354
FT DISULFID 103 180
FT CARBOHYD 270 270
SQ SEQUENCE 354 AA; 41030 MW; 77EDB368AA4C868D CRC64;

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Query Match 71.9%; Score 41; DB 1; Length 354;
 Best Local Similarity 70.0%; Pred. No. 0.67;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KKARSMTDQV 11
 ||:||||:|
 DB 61 KKLKASMTDIY 70

RESULT 7
 CCR8_HUMAN
 ID CCR8_HUMAN STANDARD; PRT; 355 AA.
 AC P51685;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 8 (C-C CCR-8) (CCR-8) (GPR-CY6)
 DE (GPCY6) (CHEMOKINE RECEPTOR-LIKE 1) (CCR-L1) (TER1) (CMKBR12) (CC-

DE CHEMOKINE RECEPTOR CHEMRL1).
 GN CCR8 OR CMKBR8 OR CKRL1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97351133; PubMed=9207005;
 RA Tiffany H.L., Lautens L.L., Gao J.-L., Pease J., Locati M.,
 RA Combadiere C., Modi W., Bonner T.I., Murphy P.M.;
 RT "Identification of CCR8: a human monocyte and thymus receptor for the
 RT CC chemokine I-309.";
 RL J. Exp. Med. 186:165-170(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98129363; PubMed=9469461;
 RA Goya I., Gutierrez J., Varona R., Kremer L., Zaballos A., Marquez G.;
 RT "Identification of CCR8 as the specific receptor for the human beta-
 RT chemokine I-309: cloning and molecular characterization of murine
 RT CCR8 as the receptor for TCA-3.";
 RL J. Immunol. 160:1975-1981(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97040707; PubMed=8886020;
 RA Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G.;
 RT "Molecular cloning and RNA expression of two new human chemokine
 RT receptor-like genes.";
 RL Biochem. Biophys. Res. Commun. 227:846-853(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97131825; PubMed=8977299;
 RA Samson M., Stordeur P., Labbe O., Soularue P., Vassart G.,
 RA Parmentier M.;
 RT "Molecular cloning and chromosomal mapping of a novel human gene,
 RT ChemRL, expressed in T lymphocytes and polymorphonuclear cells and
 RT encoding a putative chemokine receptor.";
 RL Eur. J. Immunol. 26:3021-3028(1996).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX Nakajima T., Yoshida R., Harada S.;
 RA Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP LIGAND BINDING.
 RX MEDLINE=98180363; PubMed=9521068;
 RA Bernardini G., Hedrick J., Sozzani S., Luini W., Spinetti G.,
 RA Weiss M., Menon S., Zlotnik A., Mantovani A., Santoni A.,
 RA Napolitano M.;
 RT "Identification of the CC chemokines TARC and macrophage inflammatory
 RT protein-1 beta as novel functional ligands for the CCR8 receptor.";
 RL Eur. J. Immunol. 28:582-588(1998).
 CC -1- FUNCTION: RECEPTOR FOR THE CHEMOKINES SCY1/I-309, SCY44/MIP-1-
 CC BETA AND SCY41/TARC. MAY REGULATE MONOCYTE CHEMOTAXIS AND THYMIC
 CC CELL LINE APOPTOSIS.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 DR EMBL; U45983; AAB61962.1; -
 DR EMBL; U62556; AAB05542.1; -
 DR EMBL; Z79782; CAB02142.1; -
 DR EMBL; Y08456; CAA69712.1; -
 DR EMBL; D49919; BAA23387.1; -
 DR EMBL; AF005210; AAB62547.1; -
 DR GCRDB; GCR_1333; -
 DR GCRDB; GCR_1915; -

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DR GCRDb; GCR_2111; -
DR GCRDb; GCR_2611; -
DR GCRDb; GCR_2619; -
DR MIM: 601834; -
DR InterPro; IPR000276; -
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECF_FL_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECF_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 35
FT TRANSMEM 36 63
FT DOMAIN 64 73
FT TRANSMEM 74 93
FT DOMAIN 94 107
FT TRANSMEM 108 129
FT DOMAIN 130 146
FT TRANSMEM 147 171
FT DOMAIN 172 202
FT TRANSMEM 203 222
FT DOMAIN 223 238
FT TRANSMEM 239 263
FT DOMAIN 264 280
FT TRANSMEM 281 304
FT DOMAIN 305 355
FT DISULFID 106 183
SQ SEQUENCE 355 AA; 40844 MW; BC14A153CF695361 CRC64;

Query Match 71.9%; Score 41; DB 1; Length 355;
Best Local Similarity 80.0%; Pred. No. 0.67;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KKARSMTDVIY 11
Db 64 KKLRSITDVIY 73

RESULT 8
ID CKR2_MOUSE STANDARD; PRT; 373 AA.
AC P51683; Q611172;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 2 (C-C CKR-2) (CCR-2) (CCR2)
DE (JE/FIC RECEPTOR) (MCP-1 RECEPTOR).
GN CKR2 OR CMKBR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96205938; PubMed=86311787;
RA Boring L., Gosling J., Montecarlo F.S., Lusis A.J., Tsou C.-L.,
RA Charo I.F.;
RT "Molecular cloning and functional expression of murine JE (monocyte
RT chemoattractant protein 1) and murine macrophage inflammatory protein
RT alpha receptors: evidence for two closely linked C-C chemokine
RT receptors on chromosome 9."
RL J. Biol. Chem. 271:7551-7558(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-BALB/C;
RA Kurihara T., Bravo R.;
RT "Cloning and functional expression of mCCR2, a murine receptor for
RT the C-C chemokines JE and FIC."
RL J. Biol. Chem. 271:11603-11606(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97026720; PubMed=8872898;

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Heesen M., Tanabe S., Berman M.A., Yoshizawa I., Luo Y., Kim R.,
Post T.W., Gerard C., Dorf M.E.;
"Mouse astrocytes respond to the chemokines MCP-1 and KC, but reverse
transcriptase-polymerase chain reaction does not detect mRNA for the
KC or new MCP-1 receptor.";
J. Neurosci. Res. 45:382-391(1996).
-!- FUNCTION: RECEPTOR FOR THE MCP-1 (JE), MCP-3 (FIC) AND MCP-5
CHEMOKINES. TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR
CALCIUM IONS LEVEL.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: DETECTED IN MONOCYTE/MACROPHAGE CELL LINES,
BUT NOT IN NONHEMATOPOIETIC CELL LINES.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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EMBL; U47035; AAC52453.1; -
EMBL; U51717; AAC52557.1; -
EMBL; U56819; AAC52784.1; -
GCRDb; GCR_1649; -
GCRDb; GCR_1651; -
GCRDb; GCR_1657; -
MGD; MGI:106185; Cmkbr2.
InterPro; IPR000276; -
InterPro; IPR000355; -
InterPro; IPR002237; -
Pfam; PF00001; 7tm.1; 1.
PRINTS; PR00237; GPCRHHODOPSN.
PRINTS; PR00657; CCEMOKINER2.
PRINTS; PR01107; CHEMOKINER2.
PROSITE; PS00237; G_PROTEIN_RECF_FL_1; 1.
PROSITE; PS0262; G_PROTEIN_RECF_FL_2; 1.
G-protein coupled receptor; Transmembrane.
DOMAIN 1 55
TRANSMEM 56 83
DOMAIN 84 93
TRANSMEM 94 114
DOMAIN 115 127
TRANSMEM 128 149
DOMAIN 150 166
TRANSMEM 167 191
DOMAIN 192 219
TRANSMEM 220 239
DOMAIN 240 256
TRANSMEM 257 281
DOMAIN 282 298
TRANSMEM 299 322
DOMAIN 323 373
DISULFID 126 203
CONFLICT 39 39
CONFLICT 184 184
CONFLICT 264 264
SEQUENCE 373 AA; 42782 MW; FA012C10F4C9325A CRC64;
Query Match 71.9%; Score 41; DB 1; Length 373;
Best Local Similarity 70.0%; Pred. No. 0.7;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 2 KKARSMTDVIY 11
Db 84 KKLKLSMTDVIY 93
RESULT 9
CKR2_RAT
ID CKR2_RAT STANDARD; PRT; 373 AA.

AC Q28553;
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 15-JUL-1998 (Rel. 36, Last sequence update)
DE 15-JUL-1998 (Rel. 36, Last sequence update)
DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (SDF-1 RECEPTOR)
DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LEUKOCYTE-DERIVED
DE SEVEN TRANSMEMBRANE DOMAIN RECEPTOR) (LESTR) (FRAGMENT).
GN CXCR4 OR LESTR.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Hypothalamus;
RA Dyer C.J., Matteri R.L., Keisler D.H.;
RT "Development of an ovine Y3 cDNA and expression of the Y3 receptor
mRNA in the ovine hypothalamus and pituitary.";
RL Abstr. - Soc. Neurosci. 21:1890-1890(1995).
CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -1- CAUTION: WAS ORIGINALLY THOUGHT TO BE A RECEPTOR FOR NEUROPEPTIDE
CC Y, TYPE 3 (NPY3-R).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U38942; AAA81347.1;
CC GCRDB; GCR1581;
CC InterPro; IPR000276;
CC Pfam; PF00001; 7tm.1; 1.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
KW NON_TER 1
FT DOMAIN <1 29
FT TRANSMEM 30 53
FT DOMAIN 54 69
FT TRANSMEM 70 89
FT DOMAIN 90 100
FT TRANSMEM 101 122
FT DOMAIN 123 144
FT TRANSMEM 145 165
FT DOMAIN 166 190
FT TRANSMEM 191 >192
FT DISULFID 99 176
FT NON_TER 192 192
SQ SEQUENCE 192 AA; 22178 MW; A8BCFE303C52BD98 CRC64;

Query Match 68.4%; Score 39; DB 1; Length 192;
Best Local Similarity 80.0%; Pred. No. 0.88;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KKARMTDQV 11
||| |||||
DB 57 KKLRSMTDKY 66

RESULT 12
CCRA_RAT STANDARD; PRT; 349 AA.
AC O08565;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (SDF-1 RECEPTOR)
DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LEUKOCYTE-DERIVED
DE SEVEN TRANSMEMBRANE DOMAIN RECEPTOR) (LESTR).
GN CXCR4 OR CXKRA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Wistar; TISSUE-Spleen;
RA Harrison J.K., Salafranca M.N.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
CC EMBL: U50610; AAB50408.1;
CC GCRDB; GCR1401;
CC InterPro; IPR000276;
CC InterPro; IPR001277;
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHHODOPS.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
KW DOMAIN 1 36
FT TRANSMEM 37 60
FT DOMAIN 61 76
FT TRANSMEM 77 96
FT DOMAIN 97 107
FT TRANSMEM 108 129
FT DOMAIN 130 151
FT TRANSMEM 152 172
FT DOMAIN 173 197
FT TRANSMEM 198 217
FT DOMAIN 218 237
FT TRANSMEM 238 258
FT DOMAIN 259 282
FT TRANSMEM 283 302
FT DOMAIN 303 349
FT DISULFID 106 183
FT CARBOHYD 8 8
SQ SEQUENCE 349 AA; 39334 MW; 7E0789A605C60C09 CRC64;

Query Match 68.4%; Score 39; DB 1; Length 349;
Best Local Similarity 80.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KKARMTDQV 11
||| |||||
DB 64 KKLRSMTDKY 73

RESULT 13
CCRA_CERTO STANDARD; PRT; 352 AA.
AC O62747;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (CXCR-4) (SDF-1 RECEPTOR)
DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LESTR).
GN CXCR4.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98321155; PubMed=9565999;
RA Chen Z., Gettie A., Ho D.D., Marx P.A.;
RT "Primary SIVsm isolates use the CCR5 coreceptor from sooty mangabeys
naturally infected in west Africa: a comparison of coreceptor usage
of primary SIVsm, HIV-2, and SIVmac.";
RL Virology 246:113-124(1998).
CC -!- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL; AF051906; AAC39834.1;
DR InterPro; IPR000276;
DR InterPro; IPR001277;
DR Pfam; PF00001; 7tm.1.1;
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR00645; LCRORPHANR.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_FL2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 39
FT TRANSEM 40 63
FT DOMAIN 64 79
FT TRANSEM 80 99
FT DOMAIN 100 110
FT TRANSEM 111 132
FT DOMAIN 133 154
FT TRANSEM 155 175
FT DOMAIN 176 200
FT TRANSEM 201 220
FT DOMAIN 221 240
FT TRANSEM 241 261
FT DOMAIN 262 285
FT TRANSEM 286 305
FT DOMAIN 306 352
FT CARBOHYD 11 11
FT DISULFID 109 186
SQ SEQUENCE 352 AA; 39648 MW; 4027432B8032F87E CRC64;

Query Match 68.4%; Score 39; DB 1; Length 352;
Best Local Similarity 80.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KKARSMTDVIY 11
||| |||||
Db 67 KKLRSMTDKY 76

RESULT 14
CCR4_HUMAN STANDARD; PRT; 352 AA.
AC P30991; P56438;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (CXCR-4) (SDF-1 RECEPTOR)
DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LEUKOCYTE-DERIVED
DE SEVEN TRANSMEMBRANE DOMAIN RECEPTOR) (LESTR) (LCR1) (FB22) (NPYRL)
DE (HM89).
GN CXCR4.
OS Homo sapiens (Human), and Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606, 9598;
RN [1]
RP SEQUENCE FROM N.A.
RX SPECIES=Human; TISSUE=Lung;
RA MEDLINE=93319629; PubMed=8329116;
RA Herzog H., Hort Y.J., Shine J., Selbie L.A.;
RT "Molecular cloning, characterization, and localization of the human
RT homolog to the reported bovine NPY Y3 receptor: lack of NPY binding
RT and activation.";
RL DNA Cell Biol. 12:465-471(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX SPECIES=Human; TISSUE=Brain;
RA MEDLINE=94052833; PubMed=8234909;
RA Jazin E.E., Yoo H., Blomqvist G., Yee F., Weng G., Walker M.W.,
RA Salon J., Larhammar D., Wahlestedt C.R.;
RT "A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its
RT human homologue, confers neither NPY binding sites nor NPY
RT responsiveness on transfected cells.";
RL Regul. Pept. 47:247-258(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX SPECIES=Human; TISSUE=Spleen;
RA MEDLINE=93315164; PubMed=8325644;
RA Federspiel B., Delaney A.D., Clark-Lewis I., Jirik F., Duncan A.M.,
RA Schappert K.T., Melhado I.;
RT "Molecular cloning of the cDNA and chromosomal localization of the
RT gene for a putative seven-transmembrane segment (7-TMS) receptor
RT isolated from human spleen.";
RL Genomics 16:707-712(1993).
RN [4]
RP SEQUENCE FROM N.A.
RX SPECIES=Human; TISSUE=Leukocyte;
RA MEDLINE=94103215; PubMed=8276799;
RA Loetscher M., Geiser T., O'Reilly T., Zwaalen R., Baggiolini M.,
RA Moser B.;
RT "Cloning of a human seven-transmembrane domain receptor, LESTR, that
RT is highly expressed in leukocytes.";
RL J. Biol. Chem. 269:232-237(1994).
RN [5]
RP SEQUENCE FROM N.A.
RX SPECIES=Human; TISSUE=Monocytes;
RA MEDLINE=94092629; PubMed=7505609;
RA Nomura H., Nielsen B.W., Matsushima K.;
RT "Molecular cloning of cDNAs encoding a LD78 receptor and putative
RT leukocyte chemotactic peptide receptors.";
RL Int. Immunol. 5:1239-1249(1993).
RN [6]
RP SEQUENCE FROM N.A.
RX SPECIES=Human;
RA Wegner S.A., Ehrenberg P.K., Chang G., Dayhoff D.E., Michael N.L.;
RA Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RX SPECIES=Human;
RA MEDLINE=98258970; PubMed=9599023;
RA Caruz A., Samsom M., Alonso J.M., Alcamí J., Baluev F.,
RA Virelizier J.L., Parmentier M., Arenzana-Seisdedos F.;
RT "Genomic organization and promoter characterization of human CXCR4
RT gene.";
RL FEBS Lett. 426:271-278(1998).
RN [8]
RP SEQUENCE FROM N.A.
RX SPECIES=Human;

RA Xiao L., Weiss S., Qari S., Rudolph D., Hodge T., Lal R.;
 RT "Partial resistance to infection by syncytium-inducing primary HIV-1
 RT in exposed uninfected individuals homozygous for CCR5 32bp
 RL deletion.";
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human; TISSUE=Blood;
 RA Frodl R., Moeppps B., Gierschik P.;
 RT "Genomic organization and expression pattern of the human chemokine
 RT receptor CXCR4.";
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RN [10]
 RP SEQUENCE FROM N.A.
 RC SPECIES=P.troglodytes;
 RA Pretet J.-L., Zerbib A., Girard M., Guillet J.-G., Butor C.;
 RT "Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1.";
 RL AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
 RN [11]
 RP FUNCTION.
 RA MEDLINE=96351077; PubMed=8752280;
 RA Bleul C.C., Farzan M., Choe H., Parolin C., Clark-Lewis I.,
 RA Soderliski J., Springer T.A.;
 RT "The lymphocyte chemoattractant SDF-1 is a ligand for LESTR/fusin and
 RT blocks HIV-1 entry.";
 RL Nature 382:829-833(1996).
 RN [12]
 RP FUNCTION.
 RA MEDLINE=96351078; PubMed=8752281;
 RA Oberlin E., Amara A., Bachevalier F., Bessia C., Virelizier J.-L.,
 RA Arenzana-Seisdedos F., Schwartz O., Heard J.-M., Clark-Lewis I.,
 RA Legler D.F., Loetscher M., Baggiolini M., Moser B.;
 RT "The CXCR chemokine SDF-1 is the ligand for LESTR/fusin and prevents
 RT infection by T-cell-line-adapted HIV-1.";
 RL Nature 382:833-835(1996).
 RN [13]
 RP ERRATUM.
 RA Oberlin E., Amara A., Bachevalier F., Bessia C., Virelizier J.-L.,
 RA Arenzana-Seisdedos F., Schwartz O., Heard J.-M., Clark-Lewis I.,
 RA Legler D.F., Loetscher M., Baggiolini M., Moser B.;
 RL Nature 384:288-288(1996).
 RN [14]
 RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
 RA MEDLINE=96217947; PubMed=8629022;
 RA Feng Y., Broder C.C., Kennedy P.E., Berger E.A.;
 RT "HIV-1 entry cofactor: functional cDNA cloning of a
 RT seven-transmembrane, G protein-coupled receptor.";
 RL Science 272:872-877(1996).
 CC -!- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
 CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. ACTS AS
 CC A CO-RECEPTOR WITH CD4 FOR SYNCYTIIUM-INDUCING STRAINS (SI) (1-
 CC CELL-LINE-ADAPTED) OF HIV-1 VIRUS. IT PROMOTES ENV-MEDIATED FUSION
 CC OF THE VIRUS.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -!- CAUTION: WAS ORIGINALLY THOUGHT TO BE A RECEPTOR FOR NEUROPEPTIDE
 CC Y, TYPE 3 (NPY3-R).
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 CC -----
 DR EMBL; L01639; AAA16594.1; -;
 DR EMBL; M99293; AAA16617.1; -;
 DR EMBL; X71635; CAA50641.1; -;
 DR EMBL; L06797; AAA03209.1; -;
 DR EMBL; D10924; BAA01722.1; -;
 DR EMBL; AF005058; AAB93982.1; -;

DR EMBL; AF052572; AAC34581.1; -;
 DR EMBL; AF025375; AAB81970.1; -;
 DR EMBL; Y14739; CAA75034.1; -;
 DR EMBL; U89798; AAC03718.1; -;
 DR PIR; S32761; S32761.
 DR PIR; A45747; A45747.
 DR GCRDB; GCR_0438; -;
 DR GCRDB; GCR_0448; -;
 DR GCRDB; GCR_0475; -;
 DR GCRDB; GCR_0529; -;
 DR GCRDB; GCR_0903; -;
 DR GCRDB; GCR_2433; -;
 DR GCRDB; GCR_2568; -;
 DR MIM; 162643; -;
 DR InterPro; IPR000276; -;
 DR InterPro; IPR001277; -;
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODOPS.
 DR PRINTS; PR00645; LCR1ORPHAN.
 DR PROSITE; PS00237; G_PROTEIN_RECPT_FL_2; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECPT_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 39
 FT TRANSMEM 40 63
 FT DOMAIN 64 79
 FT TRANSMEM 80 99
 FT DOMAIN 100 110
 FT TRANSMEM 111 132
 FT DOMAIN 133 154
 FT TRANSMEM 155 175
 FT DOMAIN 176 200
 FT TRANSMEM 201 220
 FT DOMAIN 221 240
 FT TRANSMEM 241 261
 FT DOMAIN 262 285
 FT TRANSMEM 286 305
 FT DOMAIN 306 352
 FT CARBOHYD 109 186
 FT DISULFID 109 186
 FT SEQUENCE 352 AA; 39745 MW; 8C8476A186786B83 CRC64;
 Query Match 68.4%; Score 39; DB 1; Length 352;
 Best Local Similarity 80.0%; Pred. No. 1.7;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 KKARSMTDYY 11
 || |||||
 Db 67 KKLRSMTDKY 76
 RESULT 15
 CCR4_MACFA STANDARD; PRT; 352 AA.
 ID CCR4_MACFA AC Q28474;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (CXCR-4) (SDF-1 RECEPTOR)
 DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LESTR).
 GN CXCR4
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tatsumi M., Takahashi H.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
 CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL; D86579; BAA13126.1; -;
DR GCRDB; GCR_1143; -;
DR InterPro; IPR000276; -;
DR InterPro; IPR001277; -;
DR Pfam; PF00001; 7tm.1; 1;
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PRINTS; PR00645; LCKRIORPHANR.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1;
DR PROSITE; PS50262; G_PROTEIN_RECEP_FL_2; 1;
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 40 63 1 (POTENTIAL).
FT DOMAIN 64 79 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 80 99 2 (POTENTIAL).
FT DOMAIN 100 110 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 111 132 3 (POTENTIAL).
FT DOMAIN 133 154 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 155 175 4 (POTENTIAL).
FT DOMAIN 176 200 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 201 220 5 (POTENTIAL).
FT DOMAIN 221 240 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 241 261 6 (POTENTIAL).
FT DOMAIN 262 285 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 286 305 7 (POTENTIAL).
FT DOMAIN 306 352 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 109 186 BY SIMILARITY.
SQ SEQUENCE 352 AA; 39753 MW; 432DA6C11859EF8A CRC64;

Query Match 68.4%; Score 39; DB 1; Length 352;
Best Local Similarity 80.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KKASMTDGY 11
Db 1111111111
67 KLRSMTDKY 76

Search completed: May 23, 2001, 15:36:17
Job time: 648 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:35:12 ; Search time 189.03 Seconds
(without alignments)
6.821 Million cell updates/sec

Title: US-08-887-977-10_COPY_65_75
Perfect score: 57
Sequence: 1 YKKARSMTDVY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_15:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rodent:
12: sp_unclassified:
13: sp_vertebrate:
14: sp_virus:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB ID	Description
1	57	100.0	367	11	Q91V0 mus musculus
2	49	86.0	360	4	Q9ULY7 homo sapien
3	49	86.0	360	4	Q9ULY6 homo sapien
4	43	75.4	350	4	Q9NPB9 homo sapien
5	42	73.7	351	6	Q9MYJ9 oryctolagus
6	41	71.9	334	6	Q97724 felis silve
7	41	71.9	339	6	Q9TUS4 lemur varie
8	41	71.9	339	6	Q9TUS3 lemur catta
9	41	71.9	339	6	Q9TUS2 lemur catta
10	41	71.9	339	6	Q9TUS1 lemur varie
11	41	71.9	339	6	Q9TUS0 lemur varie
12	41	71.9	339	6	Q9TUS3 lemur catta
13	41	71.9	351	6	Q97774 felis silve
14	41	71.9	373	11	O55193 rattus norv
15	39	68.4	332	11	Q62973 rattus norv
16	39	68.4	334	6	Q9N1P4 cercopithec
17	39	68.4	334	6	Q9N1P2 saquinus oe
18	39	68.4	334	6	Q9N130 saimiri bol
19	39	68.4	346	6	Q9MZM4 nycticebus

20	39	68.4	346	6	Q9MZM3
21	39	68.4	346	6	Q9MZM2
22	39	68.4	347	6	Q9MZQ3
23	39	68.4	347	6	Q9MZQ2
24	39	68.4	347	6	Q9MZQ1
25	39	68.4	347	6	Q9MZQ0
26	39	68.4	347	6	Q9MZP9
27	39	68.4	347	6	Q9MZP8
28	39	68.4	347	6	Q9MZP7
29	39	68.4	347	6	Q9MZP6
30	39	68.4	347	6	Q9MZP5
31	39	68.4	347	6	Q9MZP4
32	39	68.4	347	6	Q9MZP3
33	39	68.4	347	6	Q9MZP2
34	39	68.4	347	6	Q9MZP1
35	39	68.4	347	6	Q9MZP0
36	39	68.4	347	6	Q9MZN9
37	39	68.4	347	6	Q9MZN8
38	39	68.4	347	6	Q9MZN7
39	39	68.4	347	6	Q9MZN6
40	39	68.4	347	6	Q9MZN5
41	39	68.4	347	6	Q9MZN4
42	39	68.4	347	6	Q9MZN3
43	39	68.4	347	6	Q9MZN2
44	39	68.4	347	6	Q9MZN1
45	39	68.4	347	6	Q9MZN0

ALIGNMENTS

RESULT 1

Q9R1V0 Q9R1V0 PRELIMINARY; PRT; 367 AA.
AC Q9R1V0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE CC_CHEMOKINE_LARC_SPECIFIC_RECEPTOR.
GN MCCR6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Tanaka Y.;
RT "Molecular Cloning of Murine Homologue of CCR6, the Specific Receptor for CC Chemokine LARC."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB016031; BAA82443.1;
DR INTERPRO; IPR000190;
DR INTERPRO; IPR000276;
DR INTERPRO; IPR000355;
DR PFAM; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR8RHODOPN.
DR PRINTS; PR00635; ANGIOTENSINR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 367 AA; 42082 MW; 207FD98B2F7A6DD3 CRC64;

Query Match 100.0%; Score 57; DB 11; Length 367;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YKKARSMTDVY 11
|||||
Db 66 YKKARSMTDVY 76

RESULT 2

Q9ULY7
ID Q9ULY7 PRELIMINARY; PRT; 360 AA.
AC Q9ULY7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE B-CHEMOKINE RECEPTOR CCR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kato H., Tsuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki H.,
RA Hirai K., Tokunaga K.;
RT "New variations of human CC-chemokine receptors CCR3 and CCR4.";
RL Genes Immun. 1:97-104(1999).
DR EMBL; AB023889; BAA86966.1; -;
DR INTERPRO; IPR000190; -;
DR INTERPRO; IPR000248; -;
DR INTERPRO; IPR000276; -;
DR INTERPRO; IPR000355; -;
DR INTERPRO; IPR001277; -;
DR INTERPRO; IPR002236; -;
DR INTERPRO; IPR002239; -;
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR00241; ANGIOTENSINR.
DR PRINTS; PR00635; ANGIOTENSINR.
DR PRINTS; PR00645; LCRIORPHANR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01106; CHEMOKINER1.
DR PRINTS; PR01109; CHEMOKINER4.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT VARIANT 130 130 V -> L.
SQ SEQUENCE 360 AA; 41388 MW; F52DA1A8D9DA7DDB CRC64;

Query Match 86.0%; Score 49; DB 4; Length 360;
Best Local Similarity 81.8%; Pred. No. 0.078; 1; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YKARSMTDVI 11
II: |||||
Db 67 YKRLSMTDVI 77

RESULT 3
ID Q9ULY6 PRELIMINARY; PRT; 360 AA.
AC Q9ULY6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE B-CHEMOKINE RECEPTOR CCR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kato H., Tsuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki H.,
RA Hirai K., Tokunaga K.;
RT "New variations of human CC-chemokine receptors CCR3 and CCR4.";
RL Genes Immun. 1:97-104(1999).
DR EMBL; AB023891; BAA86968.1; -;
DR INTERPRO; IPR000190; -;
DR INTERPRO; IPR000248; -;
DR INTERPRO; IPR000276; -;
DR INTERPRO; IPR000355; -;
DR INTERPRO; IPR001277; -;
DR INTERPRO; IPR002236; -;

DR INTERPRO; IPR002239; -;
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR00241; ANGIOTENSINR.
DR PRINTS; PR00635; ANGIOTENSINR.
DR PRINTS; PR00645; LCRIORPHANR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01106; CHEMOKINER1.
DR PRINTS; PR01109; CHEMOKINER4.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT VARIANT 178 178 S -> C.
SQ SEQUENCE 360 AA; 41386 MW; AAF0EA3AD1EAF6D2 CRC64;

Query Match 86.0%; Score 49; DB 4; Length 360;
Best Local Similarity 81.8%; Pred. No. 0.078; 1; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YKARSMTDVI 11
II: |||||
Db 67 YKRLSMTDVI 77

RESULT 4
ID Q9NPB9 PRELIMINARY; PRT; 350 AA.
AC Q9NPB9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE CHEMOKINE RECEPTOR (CC CHEMOKINE RECEPTOR) (ORPHAN SEVEN-TRANSMEMBRANE RECEPTOR).
DE RECEPTOR.
GN CCR11 OR CCBP2 OR VSHK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Schweickart V.L., Epp A., Raport C.J., Gray P.W.;
RT "CCR11 is a Functional Receptor for the Monocyte Chemoattractant Protein Family of Chemokines.";
RL J. Biol. Chem. 275:9550-9556(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20171478; PubMed=10706668;
RA Gosling J., Dairaghi D.J., Wang Y., Hanley M., Talbot D., Miao Z.,
RA Schall T.J.;
RT "Cutting edge: identification of a novel chemokine receptor that binds dendritic cell- and T cell-active chemokines including ELC, SLC, and TECK.";
RT J. Immunol. 164:2851-2856(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Khoja H., Wang G., Lee Ng C.-T., Tucker J., Brown T., Shymala V.;
RT "Cloning of CCR11, an orphan seven transmembrane receptor related to chemokine receptors, expressed abundantly in heart.";
RL Gene 246:229-238(2000).
RN [4]
RP SEQUENCE FROM N.A.
RA Shymala V., Khoja H.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AF193507; AAF61299.1; -;
DR EMBL; AF233281; AAF44751.1; -;
DR EMBL; AF110640; AAF59827.1; -;
KW Receptor; Transmembrane.
SQ SEQUENCE 350 AA; 39913 MW; 8E26049D2D5757C8 CRC64;

Query Match 75.4%; Score 43; DB 4; Length 350;
Best Local Similarity 72.7%; Pred. No. 1.2;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OC oryctoideus cuniculus (rabbit).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 NCBI_TaxID=9986;
 [1]
 RN SEQUENCE FROM N. A.
 RP MEDLINE=20153429; PubMed=10686294;
 RX Liang M., Rosser M.P., Ng H.P., May K., Bauman J.G., Islam I.,
 RA Ghanam A., Kretschmer P.J., Pu H., Dunning L., Snider R.M.,
 RA Morrissey M.M., Hesselgesser J., Perez H.D., Horuk R.;
 RT "Species selectivity of a small molecule antagonist for the CCR1
 RT chemokine receptor".
 RL Eur. J. Pharmacol. 389:41-49(2000).
 RL EMBL; AF127521; AAF36452.1; -.
 SQ SEQUENCE 351 AA; 40534 MW; B3FED6117A141552 CRC64;
 KW Receptor.

DT	01-MAY-2000	(TEMBLrel. 13, Created)
DT	01-MAY-2000	(TEMBLrel. 13, Last sequence update)
DT	01-OCT-2000	(TEMBLrel. 15, Last annotation update)
DE	C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).	
GN	CCR5.	
OS	Lemur variegatus (Ruffed lemur) (Varecia variegata).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Strepsirhini; Lemuridae; Varecia.	
OX	NCBI_TaxID=9455;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,	
RA	Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;	
RT	"Sequences of the CCR5 genes from diverse simian and prosimian	
RT	species.";	
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.	

RA	"Sequences of the CCR5 genes from diverse simian and primate species";
RT	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RL	EMBL; AF162009; AAD47764.1; -;
DR	INTERPRO: IPR000248; -;
DR	INTERPRO: IPR000376; -;
DR	INTERPRO: IPR000355; -;
DR	INTERPRO: IPR001277; -;
DR	INTERPRO: IPR002236; -;
DR	INTERPRO: IPR002237; -;
DR	INTERPRO: IPR002238; -;
DR	INTERPRO: IPR002240; -;
DR	PFAM; PF00001.7 tm1.1;
DR	PRINTS; PR00237; GPCRRHODOPSIN.
DR	PRINTS; PR00241; ANGIOTENSINR.
DR	PRINTS; PR00645; LCRIPORPHAN.
DR	PRINTS; PR00657; CCHEMOKINER.
DR	PRINTS; PR01106; CHEMOKINER1.
DR	PRINTS; PR01107; CHEMOKINER2.
DR	PRINTS; PR01108; CHEMOKINER3.
DR	PRINTS; PR01110; CHEMOKINERS.
DR	PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW	Receptor.
FT	NON_TER 1
FT	NON_TER 339
FT	SEQUENCE 339 AA; B53CFE4F65B09E1A CRC64;
SQ	

Query Match	71.9%;	Score 41;	DB 6;	Length 339;
Best Local Similarity	70.0%;	Pred. No. 3;		
Matches	7:	Conservative	2:	Mismatches
				1: Idels

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QY      2 KKARSMTDVY 11
DB      52 KKLKSMTDIY 61

RESULT 8
Q9TUS3
ID Q9TUS3 PRELIMINARY; PRT; 339 AA.
AC Q9TUS3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN CCR5.
OS Lemur catta (Ring-tailed lemur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirrhini; Lemnridae; Lemur.
OX NCBI_TaxID=9447;
RN [1]
RP KUNSTMAN K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162010; AAD47765.1; -
DR INTERPRO; IPR000248; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR000355; -
DR INTERPRO; IPR001277; -
DR INTERPRO; IPR002236; -
DR INTERPRO; IPR002237; -
DR INTERPRO; IPR002238; -
DR INTERPRO; IPR002240; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00241; ANGIOTENSINR.
DR PRINTS; PR00645; LCR1ORPHANR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01106; CHEMOKINER1.
DR PRINTS; PR01107; CHEMOKINER2.
DR PRINTS; PR01108; CHEMOKINER3.
DR PRINTS; PR01110; CHEMOKINER5.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 38678 MW; 4CF60C5648C8DC1 CRC64;

Query Match 71.9%; Score 41; DB 6; Length 339;
Best Local Similarity 70.0%; Pred. No. 3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 KKARSMTDVY 11
DB      52 KKLKSMTDIY 61

RESULT 9
Q9TUS2
ID Q9TUS2 PRELIMINARY; PRT; 339 AA.
AC Q9TUS2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN CCR5.
OS Lemur catta (Ring-tailed lemur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirrhini; Lemnridae; Lemur.
OX NCBI_TaxID=9447;

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RN [1]
RP KUNSTMAN K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162012; AAD47767.1; -
DR INTERPRO; IPR000248; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR000355; -
DR INTERPRO; IPR001277; -
DR INTERPRO; IPR002236; -
DR INTERPRO; IPR002237; -
DR INTERPRO; IPR002238; -
DR INTERPRO; IPR002240; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00241; ANGIOTENSINR.
DR PRINTS; PR00645; LCR1ORPHANR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01106; CHEMOKINER1.
DR PRINTS; PR01107; CHEMOKINER2.
DR PRINTS; PR01108; CHEMOKINER3.
DR PRINTS; PR01110; CHEMOKINER5.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 38646 MW; BA7E73C6F05E2CA4 CRC64;

Query Match 71.9%; Score 41; DB 6; Length 339;
Best Local Similarity 70.0%; Pred. No. 3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 KKARSMTDVY 11
DB      52 KKLKSMTDIY 61

RESULT 10
Q9TUS1
ID Q9TUS1 PRELIMINARY; PRT; 339 AA.
AC Q9TUS1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN CCR5.
OS Lemur variegatus (Ruffed lemur) (Varecia variegata).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirrhini; Lemnridae; Varecia.
OX NCBI_TaxID=9455;
RN [1]
RP KUNSTMAN K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162013; AAD47768.1; -
DR INTERPRO; IPR000248; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR000355; -
DR INTERPRO; IPR001277; -
DR INTERPRO; IPR002236; -
DR INTERPRO; IPR002237; -
DR INTERPRO; IPR002238; -
DR INTERPRO; IPR002240; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00241; ANGIOTENSINR.

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DR PRINTS; PR00645; LCR1ORPHANR.
DR PRINTS; PR00657; CCHEMOKINER1.
DR PRINTS; PR01106; CHEMOKINER1.
DR PRINTS; PR01107; CHEMOKINER2.
DR PRINTS; PR01108; CHEMOKINER3.
DR PRINTS; PR01110; CHEMOKINER5.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 38682 MW; 6A770AFCA7E02F6 CRC64;

Query Match 71.9%; Score 41; DB 6; Length 339;
Best Local Similarity 70.0%; Pred. No. 3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 KKLSMTDVIY 11
|| :||||:|
Db 52 KKLSMTDIY 61

RESULT 11
OYTUSO PRELIMINARY; PRT; 339 AA.
AC OYTUSO;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN CCR5.
OS Lemur variegatus (Ruffed lemur) (Varecia variegata).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Lemuridae; Varecia.
OX NCBI_TaxID=9455;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162014; AAD47769.1; -
DR INTERPRO; IPR00248; -
DR INTERPRO; IPR00276; -
DR INTERPRO; IPR00355; -
DR INTERPRO; IPR001277; -
DR INTERPRO; IPR00236; -
DR INTERPRO; IPR00237; -
DR INTERPRO; IPR002240; -
DR INTERPRO; IPR002238; -
DR INTERPRO; IPR002238; -
DR INTERPRO; IPR002240; -
DR PFAM; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHDOPSN.
DR PRINTS; PR00241; ANGIOTENSINR.
DR PRINTS; PR00645; LCR1ORPHANR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01106; CHEMOKINER1.
DR PRINTS; PR01107; CHEMOKINER2.
DR PRINTS; PR01108; CHEMOKINER3.
DR PRINTS; PR01110; CHEMOKINER5.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 38713 MW; 77DCE451AA3A4CB6 CRC64;

Query Match 71.9%; Score 41; DB 6; Length 339;
Best Local Similarity 70.0%; Pred. No. 3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 KKLSMTDVIY 11
|| :||||:|

Db 52 KKLSMTDIY 61
RESULT 12
OYTQUS PRELIMINARY; PRT; 339 AA.
AC OYTQUS;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN CCR5.
OS Lemur catta (Ring-tailed lemur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Lemuridae; Lemur.
OX NCBI_TaxID=9447;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162011; AAD47766.1; -
DR EMBL; AF162008; AAD47763.1; -
DR INTERPRO; IPR000248; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR000355; -
DR INTERPRO; IPR001277; -
DR INTERPRO; IPR002236; -
DR INTERPRO; IPR002237; -
DR INTERPRO; IPR002238; -
DR INTERPRO; IPR002240; -
DR PFAM; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHDOPSN.
DR PRINTS; PR00241; ANGIOTENSINR.
DR PRINTS; PR00645; LCR1ORPHANR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01106; CHEMOKINER1.
DR PRINTS; PR01107; CHEMOKINER2.
DR PRINTS; PR01108; CHEMOKINER3.
DR PRINTS; PR01110; CHEMOKINER5.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 38712 MW; 8A2D0D74093A56AE CRC64;

Query Match 71.9%; Score 41; DB 6; Length 339;
Best Local Similarity 70.0%; Pred. No. 3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 KKLSMTDVIY 11
|| :||||:|
Db 52 KKLSMTDIY 61

RESULT 13
OY7774 PRELIMINARY; PRT; 351 AA.
AC OY7774;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE CCR5.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Lerner D.L., Elder J.H.;

"Feline CCR5";
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U92796; AAD00729.1; -
 DR INTERPRO; IPR000248; -
 DR INTERPRO; IPR000276; -
 DR INTERPRO; IPR000355; -
 DR INTERPRO; IPR000923; -
 DR INTERPRO; IPR002236; -
 DR INTERPRO; IPR002237; -
 DR INTERPRO; IPR002240; -
 DR PFAM; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00241; ANGIOTENSINR.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01106; CHEMOKINER1.
 DR PRINTS; PR01107; CHEMOKINER2.
 DR PRINTS; PR01110; CHEMOKINER5.
 DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 SQ SEQUENCE 351 AA; 39601 MW; 14EAE1C32D42B7FB CRC64;

Query Match 71.9%; Score 41; DB 6; Length 351;
 Best Local Similarity 80.0%; Pred. No. 3.1; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 2;

QY 2 KKARSMTDVIY 11
 ||| |
 DB 59 KKLKGMTDVIY 68

RESULT 14
 ID 055193 PRELIMINARY; PRT; 373 AA.
 AC 055193;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 2 (C-C CCR-2) (CCR-2) (CCR2).
 GN CMKR2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE DAWLEY;
 RX MEDLINE=98318173; PubMed=9655467;
 RA Jiang Y., Salafranca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
 RA defiebre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
 RT "Chemokine receptor expression in cultured glia and rat experimental
 RT allergic encephalomyelitis";
 RL J. Neuroimmunol. 86:1-12(1998).
 CC -!- FUNCTION: RECEPTOR FOR THE MCP-1 (JE), MCP-3 (FIC) AND MCP-5
 CC CHEMOKINES. TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR
 CC CALCIUM IONS LEVEL (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN LUNG, SPLEEN, KIDNEY, THYMUS AND
 CC MACROPHAGES.
 CC -!- INDUCTION: IN ANIMALS IN WHICH EXPERIMENTAL ALLERGIC
 CC ENCEPHALOMYELITIS (EAE) HAS BEEN INDUCED.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; U77349; AAC03242.1; -
 DR INTERPRO; IPR000276; -
 DR INTERPRO; IPR000355; -
 DR INTERPRO; IPR002237; -
 DR PFAM; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01107; CHEMOKINER2.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 KW G-protein coupled receptor; Transmembrane.
 FT DOMAIN 1 60 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 61 81
 FT DOMAIN 82 91 POTENTIAL.
 FT TRANSMEM 92 112 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 113 128 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 129 149 POTENTIAL.
 FT DOMAIN 150 170 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 171 191 POTENTIAL.
 FT DOMAIN 192 220 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 221 241 POTENTIAL.
 FT DOMAIN 242 256 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 257 277 POTENTIAL.
 FT DOMAIN 278 301 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 302 322 POTENTIAL.
 FT DOMAIN 323 373 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 126 203 BY SIMILARITY.
 SQ SEQUENCE 373 AA; 42763 MW; 2E7BB012F5D6FD09 CRC64;

Query Match 71.9%; Score 41; DB 11; Length 373;
 Best Local Similarity 70.0%; Pred. No. 3.3;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KKARSMTDVIY 11
 ||| |
 DB 84 KKLKSMTDIY 93

RESULT 15
 ID 062973 PRELIMINARY; PRT; 332 AA.
 AC 062973;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE CHEMOKINE RECEPTOR LCRI.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE DAWLEY;
 RA Wong M., Xin W.W., Duman R.S.;
 RA Mol. Psych. 0:0-0(0).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; U54791; AAB01981.1; -
 DR INTERPRO; IPR000276; -
 DR INTERPRO; IPR001277; -
 DR INTERPRO; IPR003006; -
 DR PFAM; PF00001; 7tm_1; 2.
 DR PRINTS; PR00845; LCRIORPHANR.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 SQ SEQUENCE 332 AA; 37442 MW; 0FFED9BF8C7150BE CRC64;

Query Match 68.4%; Score 39; DB 11; Length 332;
 Best Local Similarity 80.0%; Pred. No. 7.4;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KKARSMTDVIY 11
 ||| |
 DB 64 KKLKSMTDKY 73

Search completed: May 23, 2001, 15:35:12
 Job time: 618 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:28:27 ; Search time 184.73 Seconds
(without alignments)
5.570 Million cell updates/sec

Title: US-08-887-977-10_COPY_79_96

Perfect score: 90

Sequence: 1 MATADILFVLTLPFWA18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_0401.*
1: /SID56/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID56/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID56/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SID56/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SID56/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SID56/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SID56/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SID56/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SID56/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SID56/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SID56/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SID56/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SID56/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SID56/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SID56/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SID56/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SID56/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SID56/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SID56/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SID56/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID56/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID56/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	90	100.0	365	19 W48086	Human dendritic ce
2	90	100.0	365	21 Y97077	Primate (human) ch
3	78	86.7	40	19 W56165	Partial amino acid
4	78	86.7	358	15 R53745	Partial sequence o
5	78	86.7	358	21 B21689	Human 7TM recepto
6	78	86.7	361	20 W97348	An Epstein-barr vi
7	78	86.7	378	15 R54079	Epstein Barr virus
8	78	86.7	378	15 R53744	Putative seven tra
9	78	86.7	378	19 W48724	Human V31 seven tr
10	78	86.7	378	19 W56164	G-protein coupled
11	78	86.7	378	19 W53622	Epstein Barr virus

12	78	86.7	378	21 B21688	Human 7TM receptor
13	78	86.7	378	21 Y90629	Human G protein-co
14	78	86.7	378	21 Y90663	Human mutant G pro
15	78	86.7	378	22 B50859	Human CCR7. Homo
16	78	86.7	410	15 R53743	Putative seven tra
17	78	86.7	410	19 W48723	Polypeptide sequen
18	78	86.7	410	21 B21687	Genomic clone of 7
19	75	83.3	24	20 Y39273	G-protein coupled
20	75	83.3	32	20 Y39262	G-protein coupled
21	75	83.3	116	21 G01911	Human secreted pro
22	75	83.3	337	15 R53753	Seven transmembran
23	75	83.3	337	19 W48734	Human RM3 seven tr
24	75	83.3	337	21 B21698	Human 7TM receptor
25	75	83.3	352	13 R27792	New platelet facto
26	75	83.3	352	16 R68812	Human monocyte PF4
27	75	83.3	352	16 R80757	Chemokine superfam
28	75	83.3	352	20 Y39993	Human CXCR4 protei
29	75	83.3	352	21 Y52507	G-protein coupled
30	75	83.3	356	20 W97362	Human CXC-chemokin
31	75	83.3	357	21 B19605	G-protein coupled
32	75	83.3	357	21 Y90615	Human CC chemokine
33	75	83.3	357	21 Y90649	Human G protein-co
34	75	83.3	359	19 W64778	A murine CXC chemo
35	75	83.3	359	20 Y39994	Mouse CXCR4 protei
36	72	80.0	359	15 R53747	Seven transmembran
37	72	80.0	359	19 W48728	Murine V31 seven t
38	72	80.0	359	21 B21691	7TM receptor prote
39	72	80.0	378	21 B21699	Mouse CC-CRR5 prot
40	71	78.9	354	19 W54037	G-protein coupled
41	70	77.8	312	15 R48717	G-protein coupled
42	70	77.8	312	17 W02689	G-protein coupled
43	70	77.8	350	20 Y57291	Mouse BGCKr protei
44	70	77.8	355	13 R28272	Sequence in a high
45	70	77.8	355	16 R80950	Recombinant high a

ALIGNMENTS

RESULT 1

W48086
ID W48086 standard; Protein; 365 AA.

XX AC W48086;

XX DT 11-JUN-1998 (first entry)

XX XX Human dendritic cell chemokine receptor.

XX DE Human; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta;
XX KW receptor; dendritic cell; macrophage; inflammation; asthma.

XX OS Homo sapiens.

XX XX Key Location/Qualifiers

XX FH Misc-difference 193

XX FT /note= "encoded by CAN"

XX XX WO9801557-A2.

XX PN 15-JAN-1998.

XX PD 02-JUL-1997; 97WO-US10819.

XX PF 04-JUN-1997; 97US-0048593.

XX PR 05-JUL-1996; 96US-0675814.

XX PR 11-OCT-1996; 96US-0028329.

XX XX (SCHE) SCHERING CORP.

XX PA Gish KC, Schall TJ, Vicari A, Wang W, Zlotnik A;

XX PI WPI; 1998-101054/09.

DR N-PSDB; V15418.
 XX Novel chemokines, e.g. thymus expressed chemokine - used for
 PT treating inflammatory conditions including asthma.
 XX
 XX Claim 3: Page 94-95; 202pp; English.
 XX
 CC The present sequence represents human dendritic cell chemokine receptor.
 CC Antibodies which bind to the protein can be used in detecting or
 CC diagnosing various immunological conditions related to expression
 CC of the protein. The nucleic acid can be used for screening and
 CC isolating DNA clones for the chemokines, especially from other
 CC species. The chemokine can be used in the treatment of conditions
 CC associated with abnormal physiology or development, including
 CC inflammatory conditions such as asthma.
 XX
 XX Sequence 365 AA;

Query Match 100.0%; Score 90; DB 19; Length 365;
 Best Local Similarity 100.0%; Pred. No. 1.6e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPFWAVS 18
 DB 79 maiadilfvltlpfwavs 96
 |||||

RESULT 2
 Y97077
 ID Y97077 standard; Protein; 365 AA.
 XX
 AC Y97077;
 XX
 DT 04-DEC-2000 (first entry)
 XX
 DE Primate (human) chemokine receptor CCR6.
 XX
 KW MIP-3-alpha; chemokine; CCR6 receptor; ligand; cytostatic; agonist;
 KW antagonist; anti-psoriatic; dermatological; immunosuppressive;
 KW anti-inflammatory.
 XX

OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Misc-difference 193
 FT /note= "Encoded by CAN#"

XX WO200046248-A1.
 XX 10-AUG-2000.
 XX
 XX 02-FEB-2000; 2000WO-US00511.
 XX
 XX 03-FEB-1999; 99US-0244281.
 XX (SCHE) SCHERING CORP.
 XX
 XX Oldham ER, Honey B, Dieu-Nosjean M, Caux C, Zlotnik A;
 XX WPI; 2000-543477/49.
 XX N-PSDB; A51971.

PT Novel methods for modulating the migration of cells within or to the
 PT skin using MIP-3-alpha or CCR6 agonists or antagonists, useful for
 PT treating skin disorders, e.g. cancer
 XX
 XX Disclosure; Page 53-54; 61pp; English.

XX The MIP-3-alpha chemokine is expressed in inflamed skin cells. This
 CC chemokine is the ligand for the CCR6 receptor. MIP-3-alpha or CCR6
 CC agonists or antagonists can be used to modulate the migration of a cell
 CC within or to the skin of a mammal. MIP-3-alpha can be used to purify a

CC population of cells expressing a MIP-3-alpha receptor. The methods are
 CC useful for treating a mammalian subject with a skin disease or condition,
 CC e.g. cancer, metastasis, psoriasis, atopic or contact dermatitis,
 CC systemic lupus erythematosus and lichen ruber planus, or for treating
 CC skin transplants or grafts.
 XX

SQ Sequence 365 AA;

Query Match 100.0%; Score 90; DB 21; Length 365;
 Best Local Similarity 100.0%; Pred. No. 1.6e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPFWAVS 18
 DB 79 maiadilfvltlpfwavs 96
 |||||

RESULT 3
 W56165
 ID W56165 standard; Peptide; 40 AA.
 XX
 AC W56165;
 XX
 DT 20-JUL-1998 (first entry)
 XX
 DE Partial amino acid sequence of an opiate/opioid receptor protein.
 XX
 KW Lymphocyte R7G; EB11; G-protein coupled receptor;
 KW opiate/opioid recognition site; opiate; opioid; opioid binding protein;
 KW screening; lymphocyte receptor; compound; agonist; antagonist;
 KW lymphocyte receptor protein; immune-cell specific lymphocyte receptor;
 KW neuronal type opioid receptor.
 XX

OS Homo sapiens.

XX US5753516-A.

XX 19-MAY-1998.

XX 03-FEB-1995; 95US-0383751.

XX 03-FEB-1995; 95US-0383751.

XX (FINB/) FINBERG R W.

XX (HEAG/) HEAGY W E.

XX Finberg RW, Heagy WE;

XX WPI; 1998-311410/27.

XX Screening assay for lymphocyte opioid receptor ligands - using
 PT recombinant receptor protein

XX Disclosure; Fig 17; 70pp; English.

XX The present sequence represents the partial amino acid sequence in
 CC the second transmembrane region of an opiate/opioid receptor protein.
 CC The specification describes a novel lymphocyte R7G, termed EB11. R7G
 CC proteins are part of the G-protein coupled receptor superfamily. EB11 is
 CC a functional opiate/opioid recognition site that probably plays a major
 CC role in mediating the effects that opiate/opioids have on lymphocytes.
 CC The EB11 protein is an opioid binding protein that is displayed on the
 CC surface of lymphocytes. A process for screening a candidate substance for
 CC ability to interact with a lymphocyte receptor comprises selecting a
 CC candidate substance having a chemical structure or biological activity
 CC suggestive of an ability to mimic the biological activity of an
 CC opiate, opioid drug or opioid peptide having known binding affinity for
 CC EB11. The ability of the candidate substance is tested to interact with
 CC the lymphocyte receptor protein. This method can be used to screen for
 CC agonists or antagonists to the lymphocyte receptor protein. The method
 CC can be modified and used to screen for agonists or antagonists to the
 CC immune-cell specific lymphocyte receptor polypeptide or the neuronal type

CC opioid receptor polypeptide.

XX Sequence 40 AA;

Query Match 86.7%; Score 78; DB 19; Length 40;

Best Local Similarity 77.8%; Pred. No. 1.7e-06;

Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTPFWAVS 18

:|:|||||:|||||||

Db 20 lavadilfltltpfwavs 37

RESULT 4

R53745

ID R53745 standard; Protein; 358 AA.

XX

AC R53745;

XX

DT 02-FEB-1995 (first entry)

XX

DE Partial sequence of seven transmembrane receptor (V31).

XX

KW Primer; seven transmembrane receptor; receptor; amplification; PCR;

KW

polymerase chain reaction.

XX

OS Homo sapiens.

XX

PN W09412635-A.

XX

PD 09-JUN-1994.

XX

PF 17-NOV-1993; 93WO-US11153.

XX

PR 17-NOV-1992; 92US-0977452.

XX

PA (ICOS-) ICOS CORP.

XX

PI Godiska R, Gray PW, Schweickart VL;

XX

WPI; 1994-200264/24.

DR

N-PSDB; Q66162.

XX

PT DNA encoding seven transmembrane receptors - used to develop

PT

prods. for use as therapeutic or diagnostic agents for conditions

PT

involving the receptors.

XX

PS Example 3; Page 56-57; 100pp; English.

XX

CC Two primers (Q66148, Q66149) were used to amplify human genomic DNA

CC

purified from leukocytes. Approximately 1000 clones were isolated

CC

after the initial amplification reaction and probed with sequences

CC

specific for seven transmembrane receptors IL8R1, AT2R and R20.

CC

Clones which did not hybridise were then chosen for sequence

CC

analysis. Three new clones were identified that appeared to encode

CC

seven transmembrane receptor segments. Two more primers (Q66151,

CC

Q66152) were used to isolate a full length version of one of these

CC

clones designated V31 (See Q66153). This is the sequence encoded

CC

by exon 3 of the V31 genomic clone.

XX Sequence 358 AA;

Query Match 86.7%; Score 78; DB 15; Length 358;

Best Local Similarity 77.8%; Pred. No. 1.7e-05;

Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTPFWAVS 18

:|:|||||:|||||||

Db 80 lavadilfltltpfwavs 97

RESULT 5

B21689

ID B21689 standard; Protein; 358 AA.

XX

AC B21689;

XX

DT 26-JAN-2001 (first entry)

XX

DE Human 7TM receptor V31-B cDNA clone exon 1 protein.

XX

KW Seven transmembrane receptor; 7TM; heptahelical; serpentine;

KW

G-protein-coupled; V28; V31; V112; R20; R2; R12; Rm3; gene therapy;

KW cancer.

XX

OS Homo sapiens.

XX

PN US6107475-A.

XX

PD 22-AUG-2000.

XX

PF 26-APR-1999; 99US-0299843.

XX

PR 17-MAY-1994; 94US-0245242.

PR

01-JUN-1998; 98US-0088337.

PR

17-NOV-1992; 92US-0977452.

PR

17-NOV-1993; 93US-0153848.

XX

PA (ICOS-) ICOS CORP.

XX

PI Schweickart VL, Gray PW, Godiska R;

XX

WPI; 2000-571335/53.

DR

N-PSDB; A91709.

XX

PT Polynucleotide encoding seven transmembrane receptors, antibody

PT

specific to the receptor, agonist and antagonist of the receptor useful

PT

for treating inflammation in a mammal

XX

PS Example 3; Columns 49-52; 61pp; English.

XX

CC The present sequence is a novel seven transmembrane (7TM) receptors

CC

(also known as heptahelical, serpentine or G-protein-coupled receptors).

CC

The coding sequence for the present sequence may be used for gene

CC

therapy for diseases such as cancer.

XX

SQ Sequence 358 AA;

Query Match 86.7%; Score 78; DB 21; Length 358;

Best Local Similarity 77.8%; Pred. No. 1.7e-05;

Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTPFWAVS 18

:|:|||||:|||||||

Db 80 lavadilfltltpfwavs 97

RESULT 6

W97348

ID W97348 standard; Protein; 361 AA.

XX

AC W97348;

XX

DT 12-MAY-1999 (first entry)

XX

DE An Epstein-barr virus-induced G-protein coupled receptor.

XX

KW Epstein-barr virus-induced G-protein coupled receptor; EB1 3;

KW

splicing variant; EB1 1; vaccine; infection; HIV-1; HIV-2; pain;

KW

cancer; anorexia; bulimia; asthma; Parkinson's disease;

KW

acute heart failure; hypotension; hypertension; urinary retention;

KW

osteoporosis; angina pectoris; myocardial infarction; ulcer; allergy;

benign prostatic hypertrophy; psychotic disorder; neurological disorder;

KW anxiety; schizophrenia; manic depression; delirium; dementia;
 KW severe mental retardation; dyskinesias; Huntington's disease;
 KW Gilles de la Tourette's syndrome.

OS Homo sapiens.

XX EP894854-A2.

PN

XX 03-FEB-1999.

PD 04-DEC-1997; 97EP-0309791.

PF 29-JUL-1997; 97US-0902294.

PR (SMIK) SMITHKLINE BEECHAM CORP.

XX Zhu Y;

PI WPI; 1999-108346/10.

XX N-PSDB; X15857.

DR New Epstein-barr virus-induced G-protein coupled receptor (EBI 3)
 PT gene and protein - useful as diagnostic reagents and for prevention
 PT and treatment of HIV infections and cancer

XX Claim 2; Page 7; 20pp; English.

XX The present sequence represents a Epstein-barr virus-induced G-protein
 CC coupled receptor (EBI 3), which is a splicing variant of EBI 1. EBI 3
 CC antibodies are useful for inducing an immune response to immunize and
 CC prevent disease, and for isolating EBI 3 clones or purifying the
 CC polypeptides by affinity chromatography. EBI 3 polypeptides can be
 CC administered directly or as a vaccine to inoculate against disease.
 CC Diseases diagnosed, prevented and treated include: bacterial, fungal,
 CC viral and protozoan infections, particularly infections caused by HIV-1
 CC or HIV-2; pain; cancers; anorexia; bulimia; asthma; Parkinson's disease;
 CC acute heart failure; hypotension; hypertension; urinary retention;
 CC osteoporosis; angina pectoris; myocardial infarction; ulcers; allergies;
 CC benign prostatic hypertrophy; and psychotic and neurological disorders,
 CC including anxiety, schizophrenia, manic depression, delirium, dementia,
 CC severe mental retardation and dyskinesias, such as Huntington's disease
 CC or Gilles de la Tourette's syndrome.

XX Sequence 361 AA;

Query Match 86.7%; Score 78; DB 20; Length 361;
 Best Local Similarity 77.8%; Pred. No. 1.7e-05;
 Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 MAIADILFVLTLPFWAVS 18

Db 100 lavadilfvltpfwavs 117

RESULT 7

R54079 R54079 standard; Protein; 378 AA.

XX R54079;

XX 03-FEB-1995 (first entry)

DE Epstein Barr virus induced (EBI-1) polypeptide.

XX Epstein Barr virus; EBV; induction; detection; diagnosis;
 KW lymphocytes; antigen; growth; differentiation; mediator;
 KW infectious mononucleosis.

XX Homo sapiens.

XX OS

XX Key Location/Qualifiers

FT Region 1..24

FT /label= Hydrophobic region.
 FT /note= "Predicted to be a signal peptide for
 FT membrane translocation."
 FT 36
 FT Modified-site
 FT /note= "Potential N-linked glycosylation site."
 FT 60..86
 FT Region
 FT /label= Hydrophobic region.
 FT 96..116
 FT Region
 FT /label= Hydrophobic region.
 FT 131..152
 FT Region
 FT /label= Hydrophobic region.
 FT 151..159
 FT Region
 FT /note= "This sequences motif
 FT (S-[I/V]-D-R-[Y/F]-X-X-X-X) is highly
 FT conserved among a large number of G-protein
 FT coupled receptors."
 FT 171..191
 FT Region
 FT /label= Hydrophobic region.
 FT 220..247
 FT Region
 FT /label= Hydrophobic region.
 FT 264..289
 FT Region
 FT /label= Hydrophobic region.
 FT 292
 FT Modified-site
 FT /note= "Potential N-linked glycosylation site."
 FT 314..331
 FT Region
 FT /label= Hydrophobic region.

XX WO9412519-A.

PN 09-JUN-1994.

XX 08-OCT-1993; 93WO-US09636.

XX 25-NOV-1992; 92US-0980518.

XX (EGHM) BRIGHAM & WOMENS HOSPITAL.

XX Birkenbach M, Kieff E;

XX WPI; 1994-200183/24.

XX N-PSDB; Q64125.

XX DNA coding for Epstein Barr Virus induced (EBI) polypeptide(s)
 PT and antibodies to EBI1, 2 and 3 - useful for detecting EBV by
 PT hybridisation or by immunoassay

XX Claim 8; Page 54-56; 84pp; English.

XX EBV infected B lymphocytes recapitulate features of antigen
 CC stimulation in enlarging, increasing RNA synthesis, expressing
 CC activation antigens and adhesion molecules, secreting Ig and
 CC proliferating. Unlike antigen stimulated B lymphocytes, EBV
 CC infected B lymphocytes continue to proliferate (in vitro) as
 CC immortalised lymphoblastoid cell lines. Because of the similar
 CC effects of EBV and antigen, EBV induced genes are likely to include
 CC mediators of antigen induced B lymphocyte growth or differentiation.

XX Sequence 378 AA;

Query Match 86.7%; Score 78; DB 15; Length 378;
 Best Local Similarity 77.8%; Pred. No. 1.8e-05;
 Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 MAIADILFVLTLPFWAVS 18

Db 100 lavadilfvltpfwavs 117

RESULT 8

R53744

ID R53744 standard; Protein; 378 AA.

XX

AC R53744;
 XX
 DT 02-FEB-1995 (first entry)
 XX
 DE Putative seven transmembrane receptor (V31).
 XX
 KW Primer; seven transmembrane receptor; receptor; amplification; PCR;
 XX polymerase chain reaction.
 XX
 OS Homo sapiens.
 XX
 PN W09412635-A.
 XX
 PD 09-JUN-1994.
 XX
 XX 17-NOV-1993; 93WO-US11153.
 XX
 XX 17-NOV-1992; 92US-0977452.
 PR
 XX (ICOS-) ICOS CORP.
 XX
 PA Godiska R, Gray PW, Schweickart VL;
 XX
 PI WPI; 1994-200264/24.
 XX
 DR N-PSDB; Q66160.
 XX
 XX DNA encoding seven transmembrane receptors - used to develop
 PT prods. for use as therapeutic or diagnostic agents for conditions
 PT involving the receptors.
 PT
 XX Claim 1; Page 52-53; 100pp; English.
 PS
 XX A human cDNA encoding the seven transmembrane receptor V31 was
 CC isolated by first amplifying a partial cDNA clone from a human
 CC tonsil cDNA library using two primers (Q66154, Q66155). The resulting
 CC amplified products were probed using two radioactively labelled
 CC sequences (Q66156, Q66157). A hybridising band was isolated from the
 CC gel and cloned. The resulting clone was named pV31-5'end (Q66158). A
 CC full length cDNA clone was isolated from a peripheral blood
 CC mononuclear cell library using V31 specific primers (Q66159, Q66152).
 CC Clone pMC75 was isolated and the V31 cDNA insert in the clone was
 CC designated cDNA V31-B (Q66160).
 XX
 XX Sequence 378 AA;
 SQ

Query Match 86.7%; Score 78; DB 15; Length 378;
 Best Local Similarity 77.8%; Pred. No. 1.8e-05;
 Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLFPWAVS 18
 :|:||||:|||||
 Db 100 lavadilfvltpfwavs 117

RESULT 9
 W48724
 ID W48724 standard; Protein; 378 AA.
 XX
 AC W48724;
 XX
 DT 25-SEP-1998 (first entry)
 XX
 DE Human V31 seven transmembrane receptor.
 XX
 XX V28; placenta; seven transmembrane receptor; 7TM; signal transduction;
 KW immunology; inflammation; V31.
 KW
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH 58..86
 FT Domain /note= "Transmembrane domain 1"
 FT

FT Domain 96..119
 FT /note= "Transmembrane domain 2"
 FT 131..152
 FT /note= "Transmembrane domain 3"
 FT 171..196
 FT /note= "Transmembrane domain 4"
 FT 219..247
 FT /note= "Transmembrane domain 5"
 FT 264..285
 FT /note= "Transmembrane domain 6"
 FT 306..331
 FT /note= "Transmembrane domain 7"
 XX
 PN US5759804-A.
 XX
 PD 02-JUN-1998.
 XX
 XX 17-NOV-1993; 93US-0153848.
 PF
 XX 17-NOV-1992; 92US-0977452.
 PR
 XX (ICOS-) ICOS CORP.
 XX
 PA Godiska R, Gray PW, Schweickart VL;
 XX
 PI WPI; 1998-332132/29.
 XX
 DR N-PSDB; V18347.
 DR
 XX DNA encoding V28 seven transmembrane receptor polypeptide - useful
 PT for producing recombinant polypeptide and anti-V28 antibodies, and
 PT in screening assays for V28 agonists and antagonists
 PT
 XX Example 3; Columns 39-42; 56pp; English.
 PS
 XX The present sequence represents the V31 seven transmembrane (7TM)
 CC receptor encoded by the V31 cDNA (V18347). The invention claims for
 CC a full length V28 genomic DNA (V18343) and the V28 protein it
 CC encodes (W48722). V28 and V31 proteins are 7TM receptors which
 CC are probably involved in signal transduction. The invention also
 CC claims that cells transformed with V28 DNA can be used to produce the
 CC recombinant polypeptide, to produce anti-V28 antibodies or in screening
 CC assays for V28 agonists or antagonists. The antibodies, agonists and
 CC antagonists could then be used to modulate V28 receptor-ligand binding,
 CC for e.g. in immunological and/or inflammatory events in vivo.
 XX
 XX Sequence 378 AA;
 SQ

Query Match 86.7%; Score 78; DB 19; Length 378;
 Best Local Similarity 77.8%; Pred. No. 1.8e-05;
 Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLFPWAVS 18
 :|:||||:|||||
 Db 100 lavadilfvltpfwavs 117

RESULT 10
 W56164
 ID W56164 standard; Protein; 378 AA.
 XX
 AC W56164;
 XX
 DT 20-JUL-1998 (first entry)
 XX
 DE G-protein coupled receptor (R7G) designated EB11.
 XX
 KW Lymphocyte R7G; EB11; G-protein coupled receptor;
 KW opiate/opioid recognition site; opiate; opioid; opioid binding protein;
 KW screening; lymphocyte receptor; compound; agonist; antagonist;
 KW lymphocyte receptor protein; immune-cell specific lymphocyte receptor;
 KW neuronal type opioid receptor.
 XX

```

OS Homo sapiens.
XX US5753516-A.
XX
XX PD 19-MAY-1998.
XX
XX PF 03-FEB-1995; 95US-0383751.
XX
XX PR 03-FEB-1995; 95US-0383751.
XX
XX PA (FINB/) FINBERG R W.
XX (HEAG/) HEAGY W E.
XX
XX PI Finberg RW, Heagy WE;
XX
XX DR WPI; 1998-311410/27.
XX N-PSDB; V22684.
XX
XX PT Screening assay for lymphocyte opioid receptor ligands - using
XX recombinant receptor protein
XX
XX PS Claim 1; Columns 87-88; 70pp; English.
XX
XX CC The present sequence represents a novel lymphocyte R7G, termed EBI1. R7G
XX proteins are part of the G-protein coupled receptor superfamily. EBI1 is
XX a functional opiate/opioid recognition site that probably plays a major
XX role in mediating the effects that opiate/opioids have on lymphocytes.
XX The EBI1 protein is an opioid-binding protein that is displayed on the
XX surface of lymphocytes. A process for screening a candidate substance for
XX ability to interact with a lymphocyte receptor comprises selecting a
XX candidate substance having a chemical structure or biological activity
XX suggestive of an ability to mimic the biological activity of an
XX opiate, opioid drug or opioid peptide having known binding affinity for
XX EBI1. The ability of the candidate substance is tested to interact with
XX the lymphocyte receptor protein. This method can be used to screen for
XX agonists or antagonists to the lymphocyte receptor protein. The method
XX can be modified and used to screen for agonists or antagonists to the
XX immune-cell specific lymphocyte receptor polypeptide or the neuronal type
XX opioid receptor polypeptide.
XX
XX SQ Sequence 378 AA;

Query Match 86.7%; Score 78; DB 19; Length 378;
Best Local Similarity 77.8%; Pred. No. 1.8e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTPFWAVS 18
   :|:||||:|||||
Db 100 lavadilflitpways 117

RESULT 11
W53622
ID W53622 standard; Protein; 378 AA.
XX
XX AC W53622;
XX
XX DT 09-JUL-1998 (first entry)
XX
XX DE Epstein Barr virus induced protein 1 (EBI-1).
XX
XX KW Assessing; monitoring; foetal development; placental development;
XX Epstein Barr virus; EBV; induced gene 1; EBI-1.
XX
XX OS Homo sapiens.
XX
XX PN US5744301-A.
XX
XX PD 28-APR-1998.
XX
XX PF 02-FEB-1995; 95US-0383750.
XX

Query Match 86.7%; Score 78; DB 19; Length 378;
Best Local Similarity 77.8%; Pred. No. 1.8e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTPFWAVS 18
   :|:||||:|||||
Db 100 lavadilflitpways 117

RESULT 12
B21688
ID B21688 standard; Protein; 378 AA.
XX
XX AC B21688;
XX
XX DT 26-JAN-2001 (first entry)
XX
XX DE Human 7TM receptor V31-B cDNA clone protein.
XX
XX KW Seven transmembrane receptor; 7TM; heptahelical; serpentine;
XX G-protein-coupled; V28; V31; V112; R20; R2; R12; RM3; gene therapy;
XX cancer.
XX
XX OS Homo sapiens.
XX
XX PN US6107475-A.
XX
XX PD 22-AUG-2000.
XX
XX PF 26-APR-1999; 99US-0299843.
XX
XX PR 17-MAY-1994; 94US-0245242.
XX
XX PR 01-JUN-1998; 98US-0088337.
XX
XX PR 17-NOV-1992; 92US-0977452.
XX
XX PR 17-NOV-1993; 93US-0153848.
XX
XX PA (ICOS-) ICOS CORP.
XX
XX PI Schweickart VL, Gray PW, Godiska R;
XX
XX DR WPI; 2000-571335/53.
XX N-PSDB; A91707.
XX
XX PT Polynucleotide encoding seven transmembrane receptors, antibody
XX specific to the receptor, agonist and antagonist of the receptor useful
XX for treating inflammation in a mammal

```


CC agents. The mutant proteins are also useful in research settings for
 CC elucidating the roles of the receptors in normal and diseased conditions.
 CC Antagonists for a particular GPCR are useful for treating diseases and
 CC disorders associated with that receptor. Because the novel mutant GPCRs
 CC are constitutively active, they can be used directly for screening of
 CC compounds without the need for endogenous ligands. Sequences Y90643-
 CC Y90677 and Y90683-Y90687 the mutant human GPCRs of the invention.
 XX

SQ Sequence 378 AA;

Query Match 86.7%; Score 78; DB 21; Length 378;
 Best Local Similarity 77.8%; Pred. No. 1.8e-05;
 Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLFPWAVS 18
 Db 100 lavadilfltlfpways 117

RESULT 15

B50859
 ID B50859 standard; protein; 378 AA.

XX AC B50859;

DT 16-MAR-2001 (first entry)

DE Human CCR7.

XX Human; chemokine receptor 7; CCR7; chemokine beta-9; Ckbeta-9;
 KW allergy; autoimmune disease; ischaemia; atherosclerosis; cancer;
 KW chronic inflammatory disorder; organ transplant; tissue graft;
 KW chronic myelogenous leukaemia; infection.

XX OS Homo sapiens.

XX US6153441-A.

XX 28-NOV-2000.

PF 17-FEB-1999; 99US-0251545.

XX 17-FEB-1998; 98US-0074883.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX Appelbaum ER, White JR, Sarau HM;

XX WPI; 2001-049151/06.

XX Identifying agonists or antagonists of interaction between human
 PT protein, chemokine beta-9 and human CC chemokine receptor 7, by
 PT contacting cell expressing receptor with test compound -

PS Claim 1; Fig 1; 20pp; English.

XX The present sequence is human chemokine receptor 7 (CCR7), a cellular
 CC receptor for chemokine beta-9 (Ckbeta-9). The sequence may be
 CC used in a method for discovering agonists and antagonists of the
 CC interaction between Ckbeta-9 and CCR7. A cell expressing CCR7
 CC polypeptide on its surface, associated with a component capable of
 CC providing a detectable signal in response to binding of Ckbeta-9, is
 CC contacted with a compound in the presence of labelled or unlabelled
 CC Ckbeta-9. The compound is identified as an agonist/antagonist by
 CC determining whether it activates or inhibits the detectable signal.
 CC The method is useful for identifying agonists and antagonists of the
 CC interaction between Ckbeta-9 and CCR7 which are useful for treating
 CC diseases including allergic disorders, autoimmune diseases,
 CC ischaemia/reperfusion injury, development of atherosclerotic plaques,
 CC cancer, chronic inflammatory disorders, chronic rejection of
 CC transplanted organs or tissue grafts, chronic myelogenous leukaemia, and
 CC infection by HIV and other pathogens.

XX SQ Sequence 378 AA;
 Query Match 86.7%; Score 78; DB 22; Length 378;
 Best Local Similarity 77.8%; Pred. No. 1.8e-05;
 Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MAIADILFVLTLFPWAVS 18
 Db 100 lavadilfltlfpways 117

Search completed: May 23, 2001, 15:28:27
 Job time: 404 sec

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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:30:05 ; Search time 95.91 Seconds
(without alignments)
3.605 Million cell updates/sec

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	78	86.7	40	1 US-08-383-751A-3	Sequence 3, Appli
2	78	86.7	358	1 US-08-153-848-19	Sequence 19, Appl
3	78	86.7	358	3 US-09-299-843A-19	Sequence 19, Appl
4	78	86.7	358	5 PCT-US93-11153-19	Sequence 19, Appl
5	78	86.7	361	2 US-08-902-234-2	Sequence 2, Appli
6	78	86.7	361	3 US-08-178-637-2	Sequence 2, Appli
7	78	86.7	378	1 US-08-383-750-2	Sequence 2, Appli
8	78	86.7	378	1 US-08-383-751A-2	Sequence 2, Appli
9	78	86.7	378	1 US-08-153-848-15	Sequence 15, Appl
10	78	86.7	378	3 US-08-352-678-2	Sequence 2, Appli
11	78	86.7	378	3 US-09-299-843A-15	Sequence 15, Appl
12	78	86.7	378	4 US-09-251-545-1	Sequence 1, Appli
13	78	86.7	378	5 PCT-US93-09636-2	Sequence 2, Appli
14	78	86.7	378	5 PCT-US93-11153-15	Sequence 15, Appl
15	78	86.7	410	1 US-08-153-848-7	Sequence 7, Appli
16	78	86.7	410	3 US-09-299-843A-7	Sequence 7, Appli
17	78	86.7	410	5 PCT-US93-11153-7	Sequence 7, Appli
18	75	83.3	337	1 US-08-153-848-46	Sequence 46, Appl
19	75	83.3	337	3 US-09-299-843A-46	Sequence 46, Appl
20	75	83.3	337	5 PCT-US93-11153-46	Sequence 46, Appl
21	75	83.3	352	1 US-08-202-056-3	Sequence 3, Appli
22	75	83.3	352	1 US-08-076-093A-4	Sequence 4, Appli
23	75	83.3	352	1 US-08-450-393A-6	Sequence 6, Appli
24	75	83.3	352	1 US-08-701-265-4	Sequence 4, Appli
25	75	83.3	352	2 US-08-284-586-4	Sequence 4, Appli
26	75	83.3	352	2 US-08-805-478-4	Sequence 4, Appli
27	75	83.3	352	2 US-08-802-627A-4	Sequence 4, Appli

28	75	83.3	352	2	US-08-801-238-4	Sequence 4, Appli
29	75	83.3	352	2	US-08-801-228-4	Sequence 4, Appli
30	75	83.3	352	3	US-09-104-296-4	Sequence 4, Appli
31	75	83.3	352	4	US-08-446-669-6	Sequence 6, Appli
32	75	83.3	352	5	PCT-US95-00476-6	Sequence 6, Appli
33	72	80.0	359	1	US-08-153-848-24	Sequence 24, Appl
34	72	80.0	359	3	US-09-299-843A-24	Sequence 24, Appl
35	72	80.0	359	5	PCT-US93-11153-24	Sequence 24, Appl
36	72	80.0	378	3	US-09-299-843A-66	Sequence 66, Appl
37	70	77.8	312	1	US-08-118-270-38	Sequence 38, Appl
38	70	77.8	312	5	PCT-US93-08528-38	Sequence 38, Appl
39	69	76.7	350	1	US-08-202-056-1	Sequence 1, Appli
40	69	76.7	350	1	US-08-076-093A-2	Sequence 2, Appli
41	69	76.7	350	1	US-08-450-393A-7	Sequence 7, Appli
42	69	76.7	350	1	US-08-410-453A-1	Sequence 1, Appli
43	69	76.7	350	1	US-08-701-265-2	Sequence 2, Appli
44	69	76.7	350	1	US-08-410-454A-1	Sequence 1, Appli
45	69	76.7	350	2	US-08-284-586-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-383-751A-3
; Sequence 3, Application US/08383751A
; Patent No. 5753516
; GENERAL INFORMATION:
; APPLICANT: Heagy, Wyrta E.
; APPLICANT: Finberg, Robert W.
; TITLE OF INVENTION: Identification and Uses of Opioid
; TITLE OF INVENTION: Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: US
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/383,751A
; FILING DATE: 03-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: DFCI:001/WIM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-383-751A-3

Query Match 86.7%; Score 78; DB 1; Length 40;
Best Local Similarity 77.8%; Pred. No. 5.3e-06;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 MAIADILFVLTPFWAVS 18
DB 20 LAVADILFLTLTPFWAVS 37

```

RESULT 2
US-08-153-848-19
; Sequence 19, Application US/08153848
; Patent No. 5759804
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153,848
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5759804and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-153-848-19

Query Match 86.7%; Score 78; DB 1; Length 358;
Best Local Similarity 77.8%; Pred. No. 4.9e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLFPWAVS 18
; :|||||:|||||
DB 80 LAVADILFLLTLPFWAYS 97

RESULT 3
US-09-299-843A-19
; Sequence 19, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
```

```

; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,843A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/088,337
; FILING DATE: 01-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jill E. Uhl
; REGISTRATION NUMBER: 43,213
; REFERENCE/DOCKET NUMBER: 27866/32059B
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-299-843A-19

Query Match 86.7%; Score 78; DB 3; Length 358;
Best Local Similarity 77.8%; Pred. No. 4.9e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLFPWAVS 18
; :|||||:|||||
DB 80 LAVADILFLLTLPFWAYS 97

RESULT 4
PCT-US93-11153-19
; Sequence 19, Application PC/TUS93111153
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: Novel Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11153
; FILING DATE:
; CLASSIFICATION:
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;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/977,452
;; FILING DATE: 17-NOV-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Noland, Greta E.
;; REGISTRATION NUMBER: 35,302
;; REFERENCE/DOCKET NUMBER: 31794
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312) 474-6300
;; TELEFAX: (312) 474-0448
;; TELEX: 25-3856
;; INFORMATION FOR SEQ ID NO: 19:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 358 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
PCT-US93-11153-19

Query Match 86.7%; Score 78; DB 5; Length 358;
Best Local Similarity 77.8%; Pred. No. 4.9e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLFPWAVS 18
:|:||||:||||| I
Db 80 LAVADILFLLTLPWAVS 97

RESULT 5
US-08-902-294-2
; Sequence 2, Application US/08902294
; Patent No. 5874252
; GENERAL INFORMATION:
; APPLICANT: ZHU, YUAN
; TITLE OF INVENTION: A NOVEL SPLICING VARIANT OF
; TITLE OF INVENTION: THE EPSTEIN-BARR VIRUS-INDUCED G-PROTEIN COUPLED
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,294
; FILING DATE: 29-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-70177
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-902-294-2

Query Match 86.7%; Score 78; DB 2; Length 361;
Best Local Similarity 77.8%; Pred. No. 5e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLFPWAVS 18
:|:||||:||||| I
Db 100 LAVADILFLLTLPWAVS 117

RESULT 6
US-09-178-637-2
; Sequence 2, Application US/09178637
; Patent No. 6001972
; GENERAL INFORMATION:
; APPLICANT: ZHU, YUAN
; TITLE OF INVENTION: A No. 6001972el Splicing Variant of
; TITLE OF INVENTION: the Epstein-Barr Virus-Induced G-Protein Coupled Receptor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/178,637
; FILING DATE: 26-OCT-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/902,294
; FILING DATE: 29-JUL-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-70177-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-09-178-637-2

Query Match 86.7%; Score 78; DB 3; Length 361;
Best Local Similarity 77.8%; Pred. No. 5e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLFPWAVS 18
:|:||||:||||| I
Db 100 LAVADILFLLTLPWAVS 117

RESULT 7
US-08-383-750-2
; Sequence 2, Application US/08383750
; Patent No. 5744301
; GENERAL INFORMATION:
; APPLICANT: Birkenbach, Mark

```
;
; APPLICANT: Kieff, Elliot
; TITLE OF INVENTION: Epstein Barr Virus Induced Genes
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W.,
; STREET: Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/383,750
; FILING DATE: Herewith
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Fox, Samuel, L.
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 0627.3300001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-383-750-2

Query Match 86.7%; Score 78; DB 1; Length 378;
Best Local Similarity 77.8%; Pred. No. 5.2e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPFWAYS 18
Db 100 LAVADILFLLTLPFWAYS 117

RESULT 8
US-08-383-751A-2
; Sequence 2, Application US/08383751A
; Patent No. 5753516
; GENERAL INFORMATION:
; APPLICANT: Heagy, Wyrita E.
; APPLICANT: Finberg, Robert W.
; TITLE OF INVENTION: Identification and Uses of Opioid
; TITLE OF INVENTION: Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: US
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/383,751A
; FILING DATE: 03-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: DFCI:001/WIM
```

```
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-383-751A-2

Query Match 86.7%; Score 78; DB 1; Length 378;
Best Local Similarity 77.8%; Pred. No. 5.2e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPFWAYS 18
Db 100 LAVADILFLLTLPFWAYS 117

RESULT 9
US-08-153-848-15
; Sequence 15, Application US/08153848
; Patent No. 5759804
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: NO. 5759804el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153,848
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: NO. 5759804and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-153-848-15

Query Match 86.7%; Score 78; DB 1; Length 378;
Best Local Similarity 77.8%; Pred. No. 5.2e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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QY 1 MAIADILFVLTLFPWAVS 18
:|:||||:|||||
Db 100 LAVADILFLTLFPWAVS 117

RESULT 10
US-08-352-678-2
; Sequence 2, Application US/08352678
; Patent No. 6043351
; GENERAL INFORMATION:
; APPLICANT: Birkenbach, Mark
; APPLICANT: Kieff, Elliott
; TITLE OF INVENTION: EPSTEIN BARR VIRUS INDUCED GENES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/352,678
; FILING DATE: 30-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/980,518
; FILING DATE: 25-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gates, Edward R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: B0801/7044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-352-678-2

Query Match 86.7%; Score 78; DB 3; Length 378;
Best Local Similarity 77.8%; Pred. No. 5.2e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLFPWAVS 18
:|:||||:|||||
Db 100 LAVADILFLTLFPWAVS 117

RESULT 11
US-09-299-843A-15
; Sequence 15, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6107475e1 Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago

; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,843A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/088,337
; FILING DATE: 01-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jill E. Uhl
; REGISTRATION NUMBER: 43,213
; REFERENCE/DOCKET NUMBER: 27866/32059B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-299-843A-15

Query Match 86.7%; Score 78; DB 3; Length 378;
Best Local Similarity 77.8%; Pred. No. 5.2e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLFPWAVS 18
:|:||||:|||||
Db 100 LAVADILFLTLFPWAVS 117

RESULT 12
US-09-251-545-1
; Sequence 1, Application US/09251545
; Patent No. 6153441
; GENERAL INFORMATION:
; APPLICANT: Edward R. Appelbaum
; APPLICANT: Henry M. Sarau
; APPLICANT: John R. White
; TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND
; TITLE OF INVENTION: ANTAGONISTS OF THE INTERACTION BETWEEN HUMAN CCR7 RECEPTOR
; FILE REFERENCE: P50753
; CURRENT APPLICATION NUMBER: US/09/251,545
; CURRENT FILING DATE: 1999-02-17
; EARLIER APPLICATION NUMBER: 60/074,883
; EARLIER FILING DATE: 1998-02-17
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Human
US-09-251-545-1

Query Match 86.7%; Score 78; DB 4; Length 378;

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;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;

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, ZIP: 00000
, COMPUTER READABLE FORM:
, MEDIUM TYPE: Floppy disk
, COMPUTER: IBM PC compatible
, OPERATING SYSTEM: PC-DOS/MS-DOS
, SOFTWARE: PatentIn Release #1.0, Version #1.25
, CURRENT APPLICATION DATA:
, APPLICATION NUMBER: US/08/153,848
, FILING DATE:
, CLASSIFICATION: 514
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US 07/977,452
, FILING DATE: 17-NOV-1992
, ATTORNEY/AGENT INFORMATION:
, NAME: No. 5759804and, Greta E.
, REGISTRATION NUMBER: 35,302
, REFERENCE/DOCKET NUMBER: 31794
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: (312) 474-6300
, TELEFAX: (312) 474-0448
, TELEX: 25-3856
, INFORMATION FOR SEQ ID NO: 7:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 410 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-153-848-7

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Query Match      86.7%; Score 78; DB 1; Length 410;
Best Local Similarity 77.8%; Pred. No. 5.7e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 MAIADILFVLTLPFWAYS 18
   :|:||||:|||||||
Db 132 LAVADILFLLTLPFWAYS 149

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Search completed: May 23, 2001, 15:30:05
Job time: 412 sec

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GenCore version 4.5
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OM protein - protein search, using sw model.

Run on: May 23, 2001, 15:31:59 ; Search time 110.15 Seconds
(without alignments)
11.230 Million cell updates/sec

Title: US-08-887-977-10_COPY_79_96
Perfect score: 90
Sequence: 1 MAIADILFVLTLPFWAVS 18
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_67:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	90	100.0	369	JC5068	G protein-coupled
2	78	86.7	378	A45680	G protein-coupled
3	78	86.7	378	B5735	lymphocyte-specific
4	77	85.6	353	S28787	neuropeptide Y/pep
5	75	83.3	352	A45747	neuropeptide Y/pep
6	72	80.0	352	G00048	fusin (LESTRA) - C
7	72	80.0	378	A55735	G protein-coupled
8	70	77.8	355	J01231	interleukin-8 rece
9	69	76.7	350	A39445	interleukin-8 rece
10	69	76.7	360	A53611	interleukin-8 rece
11	69	76.7	367	J00349	interferon-inducib
12	67	74.4	383	S55594	G protein-coupled
13	66	73.3	356	S42096	interleukin-8 rece
14	66	73.3	358	A53752	interleukin-8 rece
15	66	73.3	359	A48921	interleukin-8 rece
16	66	73.3	360	JC4587	chemokine (C-C) re
17	65	72.2	359	JC1104	angiotensin II rec
18	65	72.2	359	S44425	angiotensin II rec
19	65	72.2	359	JC1194	angiotensin II rec
20	65	72.2	359	A48857	angiotensin II rec
21	65	72.2	359	A42656	angiotensin II rec
22	65	72.2	359	S15403	angiotensin II rec
23	65	72.2	359	J39418	angiotensin II rec
24	65	72.2	359	JH0621	angiotensin II rec
25	65	72.2	359	JC2134	angiotensin II rec
26	64	71.1	350	JN0621	G protein-coupled
27	64	71.1	352	A43113	chemokine (C-C) re
28	64	71.1	355	G02436	chemokine (C-C) re
29	64	71.1	360	JC2443	chemokine (C-C) re

30	64	71.1	374	2	I38450	chemokine (C-C) re
31	63	70.0	354	2	I58186	probable G protein
32	63	70.0	355	2	JC4304	orphan G protein-c
33	63	70.0	355	2	A45177	chemokine (C-C) re
34	62	68.9	359	2	J01516	angiotensin II rec
35	62	68.9	360	2	A57160	chemokine (C-C) re
36	62	68.9	380	2	I38435	angiotensin recept
37	61	67.8	177	2	PH1372	angiotensin II rec
38	60	66.7	341	2	S43252	platelet-activatin
39	60	66.7	342	2	S13638	platelet-activatin
40	60	66.7	344	2	JC5942	chemokine receptor
41	60	66.7	359	2	I49341	MIP-1 alpha recept
42	59	65.6	334	2	JC4681	bradykinin BI rece
43	59	65.6	352	2	S60024	bradykinin BI rece
44	59	65.6	353	2	A53858	bradykinin recepto
45	59	65.6	355	2	I49339	macrophage inflamm

ALIGNMENTS

RESULT 1
JC5068
G protein-coupled receptor CKR-L3 - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
C:Accession: JC5068
R:Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
Biochem. Biophys. Res. Commun. 227, 846-853, 1996
A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-lik
A:Reference number: JC5067; MUID:97040707
A:Accession: JC5068
A:Molecule type: DNA
A:Residues: 1-369 <ZAB>
A:Cross-references: EMBL:279784; NID:gl68737; PIDN:CAB02144.1; PID:gl68738
C:Comment: This protein belongs to the family of alpha chemokine receptors.
C:Genetics:
A:Gene: GDB:CKRB6; STR122; GPR29; CCR6; CKR-L3; GPR-CY4
A:Cross-references: GDB:5370639; OMIM:601835
A:Map position: 6q27-6q27
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein
F:42-68/Domain: transmembrane #status predicted <TM1>
F:79-99/Domain: transmembrane #status predicted <TM2>
F:115-136/Domain: transmembrane #status predicted <TM3>
F:160-180/Domain: transmembrane #status predicted <TM4>
F:212-233/Domain: transmembrane #status predicted <TM5>
F:250-271/Domain: transmembrane #status predicted <TM6>
F:292-315/Domain: transmembrane #status predicted <TM7>

Query Match 100.0%; Score 90; DB 2; Length 369;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPFWAVS 18
Db 83 MAIADILFVLTLPFWAVS 100
|||||

RESULT 2
A45680
G protein-coupled peptide receptor EBI 1 - human
C:Species: Homo sapiens (man)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C:Accession: A45680
R: Birkenbach, M.; Josefsen, K.; Yalamanchili, R.; Lenoir, G.; Kieff, E.
J. Virol. 67, 2209-2220, 1993
A:Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-couple
A:Reference number: A45680; MUID:93188173
A:Accession: A45680
A>Status: preliminary
A:Molecule type: nucleic acid

A:Residues: 1-378 <BIR>

A:Cross-references: GB:L08176; NID:gl83484; PID:g183485

A:Experimental source: B-lymphocytes

A:Note: sequence extracted from NCBI backbone (NCBIN:127094, NCBI:127095)

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 86.7%; Score 78; DB 2; Length 378;

Best Local Similarity 77.8%; Pred. No. 2.2e-05;

Matches 14; Conservative 3; Mismatches 1; Indels 0;

QY 1 MAIADILFVLTPFWAYS 18

:|:||||:|||||||

Db 100 LAVADILFLLTPFWAYS 117

RESULT 3

B5735

Lymphocyte-specific G protein-coupled receptor EB11 - human

N:Alternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1

C:Species: Homo sapiens (man)

C>Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 19-May-2000

C:Accession: B5735; S52443

R:Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.

Genomics 23, 643-650, 1994

A:Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor

A:Reference number: A55735; MUID:95154835

A:Accession: B5735

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-378 <SCH>

A:Cross-references: GB:L31581; NID:q468319; PIDN:AAA74231.1; PID:g468320

R:Burgstahler, R.; Kempkes, B.; Staube, K.; Lipp, M.

submitted to the EMBL Data Library, February 1995

A:Description: The expression of the chemokine receptor BLR2/EB11 is specifically trans

A:Reference number: S52443

A:Accession: S52443

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 21-378 <BUR>

A:Cross-references: EMBL:X84702

C:Genetics:

A:Gene: GDB:CMKBR7; EB11; BLR2; CCR7

A:Cross-references: GDB:342065; OMIM:600242

A:Map position: 17q12-17q21.2

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor

Query Match 86.7%; Score 78; DB 2; Length 378;

Best Local Similarity 77.8%; Pred. No. 2.2e-05;

Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTPFWAYS 18

:|:||||:|||||||

Db 100 LAVADILFLLTPFWAYS 117

RESULT 4

S2878

neuropeptide Y/peptide YY receptor Y3 - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 26-Aug-1999

C:Accession: S28787

R:Rimland, J.; Xin, W.; Sweetnam, P.; Saijoh, K.; Nestler, E.J.; Duman, R.S.

Mol. Pharmacol., 40, 869-875, 1991

A:Title: Sequence and expression of a neuropeptide Y receptor cDNA.

A:Reference number: S28787; MUID:92100053

A:Accession: S28787

A:Molecule type: mRNA

A:Residues: 1-353 <RIM>

A:Cross-references: EMBL:M86739

C:Superfamily: vertebrate rhodopsin

C:Keywords: appetite; G protein-coupled receptor; transmembrane protein

Query Match 85.6%; Score 77; DB 2; Length 353;

Best Local Similarity 76.5%; Pred. No. 3e-05;

Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTPFWAV 17

:|:||||:|||||||

Db 81 LSVADLLFVLTPFWAV 97

RESULT 5

A45747

neuropeptide Y/peptide YY receptor Y3 - human

N:Alternate names: fusin; HM89; leukocyte-derived seven-transmembrane receptor LESTR;

C:Species: Homo sapiens (man)

C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 05-Nov-1999

C:Accession: A45747; A53103; I53006; I59444; I69203; S32761

R:Federapfel, B.; Melhado, I.G.; Duncan, A.M.V.; Delaney, A.; Schappert, K.; Clark-L

Genomics 16, 707-712, 1993

A:Title: Molecular cloning of the cDNA and chromosomal localization of the gene for a

A:Reference number: A45747; MUID:93315164

A:Accession: A45747

A:Molecule type: mRNA

A:Residues: 1-352 <FED>

A:Cross-references: GB:M9293; NID:q292516; PIDN:AAA16617.1; PID:g292517

R:Loetscher, M.; Geiser, T.; O'Reilly, T.; Zwaalen, R.; Baggiolini, M.; Moser, B.

J. Biol. Chem. 269, 232-237, 1994

A:Title: Cloning of a human seven-transmembrane domain receptor, LESTR, that is highl

A:Reference number: A53103; MUID:94103215

A:Accession: A53103

A:Molecule type: mRNA

A:Residues: 1-352 <LOE>

A:Cross-references: EMBL:X71635; NID:q297099; PIDN:CAA50641.1; PID:g297100

R:Herzog, H.; Hort, Y.J.; Shine, J.; Selbie, L.A.

DNA Cell Biol. 12, 465-471, 1993

A:Title: Molecular cloning, characterization, and localization of the human homolog t

A:Reference number: I53006; MUID:93319629

A:Accession: I53006

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-352 <HER>

A:Cross-references: GB:L06797; NID:q414929; PIDN:AAA03209.1; PID:g414928

R:Jazin, E.E.; Yoo, H.; Blomqvist, A.G.; Yee, F.; Weng, G.; Walker, M.W.; Salon, J.;

Regul. Pept. 47, 247-258, 1993

A:Title: A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its human hom

A:Reference number: I59444; MUID:94052833

A:Accession: I59444

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-352 <REJ>

A:Cross-references: GB:L01639; NID:gl89313; PIDN:AAA16594.1; PID:g189314

R:Nomura, H.; Nielsen, B.W.; Matsushima, K.

Int. Immunol. 5, 1239-1249, 1993

A:Title: Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte c

A:Reference number: I54751; MUID:94092629

A:Accession: I69203

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-352 <RES>

A:Cross-references: GB:D10924; NID:g219868; PIDN:BAA01722.1; PID:g219869

C:Genetics:

A:Gene: GDB:NPY3R; NPY3

A:Cross-references: GDB:230002; OMIM:162643

A:Map position: 2q21-2q21

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 83.3%; Score 75; DB 2; Length 352;

Best Local Similarity 70.6%; Pred. No. 6.3e-05;

Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLFPWAV 17

:::|:|:|:|:|:|

Db 80 LSVADLLFVTLFPWAV 96

RESULT 6

G00048

fusin (LESTRA) - crab-eating macaque

C:Species: Macaca fascicularis (crab-eating macaque)

C:Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 26-Aug-1999

C:Accession: G00048

R:Tatsumi, M.

submitted to GenBank, July 1996

A:Reference number: H00048

A:Accession: G00048

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-352 <TAT>

A:Cross-references: GB:D86579; NID:g1468948; PID:g1468949

C:Superfamily: vertebrate rhodopsin

Query Match 80.0%; Score 72; DB 2; Length 352;

Best Local Similarity 64.7%; Pred. No. 0.0002;

Matches 11; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLFPWAV 17

:::|:|:|:|:|:|

Db 80 LSVADLLFVTLFPWAV 96

RESULT 7

A55735

G protein-coupled receptor EB11 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 24-Nov-1999

C:Accession: A55735

R:Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.

Genomics 23, 643-650, 1994

A:Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor

A:Reference number: A55735; MUID:95154835

A:Accession: A55735

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-378 <SCH>

A:Cross-references: GB:L31580; NID:g468340; PIDN:AAA74232.1; PID:g468341

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor

Query Match 80.0%; Score 72; DB 2; Length 378;

Best Local Similarity 72.2%; Pred. No. 0.00021;

Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLFPWAVS 18

:::|:|:|:|:|:|

Db 100 LAVADILFLILFPWAVS 117

RESULT 8

JQ1231

interleukin-8 receptor - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Nov-1999

C:Accession: JQ1231; A46483

R:Beckmann, M.P.; Munger, W.E.; Kozlosky, C.; VandenBos, T.; Price, V.; Lyman, S.; Gerard

Biochem. Biophys. Res. Commun. 179, 784-789, 1991

A:Title: Molecular characterization of the interleukin-8 receptor.

A:Reference number: JQ1231; MUID:91378994

A:Accession: JQ1231

A:Molecule type: DNA

A:Residues: 1-355 <BEC>

A:Cross-references: GB:M74240; NID:g165438; PIDN:AAA31375.1; PID:g165439

R:Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.

J. Immunol. 148, 1261-1264, 1992

A:Title: Characterization of complementary DNA clones encoding the rabbit IL-8 receptor

A:Reference number: A46483; MUID:92148149

A:Accession: A46483

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-355 <LEE>

A:Cross-references: GB:M82873; NID:g165440; PIDN:AAA31376.1; PID:g165441

A:Experimental source: neutrophils

A:Note: sequence extracted from NCBI backbone (NCBIN:81526, NCBIIP:81530)

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 77.8%; Score 70; DB 2; Length 355;

Best Local Similarity 66.7%; Pred. No. 0.00043;

Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLFPWAVS 18

:::|:|:|:|:|:|

Db 86 LAMADLLFALTPIWAVS 103

RESULT 9

A39445

N:Interleukin-8 receptor type A - human

C:Species: Homo sapiens (man)

C:Date: 22-Jan-1993 #sequence_revision 12-Apr-1996 #text_change 05-Nov-1999

C:Accession: I37449; I38710; I38711; A39445

R:Mollereau, C.; Muscatelli, F.; Mattei, M.G.; Vassart, G.; Parmentier, M.

Genomics 16, 248-251, 1993

A:Title: The high-affinity interleukin 8 receptor gene (IL8RA) maps to the 2q33-q36 r

A:Reference number: I37449; MUID:93252387

A:Accession: I37449

A:Molecule type: DNA

A:Residues: 1-350 <RES>

A:Cross-references: EMBL:X65858; NID:g312046; PIDN:CAA46688.1; PID:g312047

R:Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.

J. Biol. Chem. 269, 26381-26389, 1994

A:Title: Comparison of the genomic organization and promoter function for human inter

A:Reference number: I37898; MUID:95014476

A:Accession: I38710

A:Molecule type: DNA

A:Residues: 1-350 <RE2>

A:Cross-references: EMBL:U11870; NID:g511804; PIDN:AAA64378.1; PID:g511805

A:Accession: I38711

A:Molecule type: mRNA

A:Residues: 1-16 <RE3>

A:Cross-references: EMBL:U11871; NID:g511806; PIDN:AAA64379.1; PID:g733002

R:Holmes, W.E.; Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.

Science 253, 1278-1280, 1991

A:Title: Structure and functional expression of a human interleukin-8 receptor.

A:Reference number: A39445; MUID:91368199

A:Accession: A39445

A:Molecule type: mRNA

A:Residues: 1-275, 'T', 277-350 <HOL>

A:Cross-references: GB:M68932; NID:g186369; PIDN:AAA59159.1; PID:g186370

C:Genetics:

A:Gene: GDB:IL8RA

A:Cross-references: GDB:I35039; OMIM:146929

A:Map position: 2q35-2q35

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein

Query Match 76.7%; Score 69; DB 2; Length 350;

Best Local Similarity 66.7%; Pred. No. 0.00062;

Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPEWAVS 18
:|:|:|:| | | | | | | | | |

Db 81 LALADLLFALTLPWAAS 98

RESULT 10

A53611
Interleukin-8 receptor type B - human
C:Species: Homo sapiens (man)
C:Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 05-Nov-1999
C:Accession: I37898; I37812; A53611; A39446
R:Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
J. Biol. Chem. 269, 26381-26389, 1994
A:Title: Comparison of the genomic organization and promoter function for human interleukin-8 receptor type B and human interleukin-8 receptor type A
A:Reference number: I37898; MUID:95014476
A:Accession: I37898
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-360 <RES>
A:Cross-references: EMBL:U11869; NID:g511801; PIDN:AA60656.1; PID:g511803
A:Accession: I37812
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-15 <RE2>
A:Cross-references: EMBL:U11872; NID:g511808; PIDN:AAA64380.1; PID:g511809; EMBL:U11873; I1876; NID:g511816; PID:g511817; EMBL:U11877; NID:g511818; PID:g511819; EMBL:U11878; NID:R:Sprengr, H.; Lloyd, A.R.; Lautens, L.L.; Bonner, T.I.; Kelvin, D.J.
J. Biol. Chem. 269, 11065-11072, 1994
A:Title: Structure, genomic organization, and expression of the human interleukin-8 receptor type B
A:Reference number: A53611; MUID:94209273
A:Accession: A53611
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 6-360 <SPR>
A:Cross-references: GB:M99412; GB:L19593
R:Murphy, P.M.; Tiffany, H.L.
Science 253, 1280-1283, 1991
A:Title: Cloning of complementary DNA encoding a functional human interleukin-8 receptor
A:Reference number: A39446; MUID:91368200
A:Accession: A39446
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 6-360 <MUR>
A:Cross-references: GB:M73969
C:Comment: This receptor, unlike IL8RA, binds several peptides besides interleukin-8, in addition to interleukin-8
C:Genetics:
A:Gene: GDB:IL8RB; IL8RA
A:Cross-references: GDB:127868; OMIM:146928
A:Map position: 2q35-2q35
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 76.7%; Score 69; DB 2; Length 360;
Best Local Similarity 66.7%; Pred. No. 0.00063;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPEWAVS 18
:|:|:|:| | | | | | | | | |

Db 90 LALADLLFALTLPWAAS 107

RESULT 11

JE0349
Interferon-inducible protein 10 (IP-10) receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000
C:Accession: JE0349
R:Tamaru, M.; Tominaga, Y.; Yatsunami, K.; Narumi, S.
Biochem. Biophys. Res. Commun. 251, 41-48, 1998
A:Title: Cloning of the murine interferon-inducible protein 10 (IP-10) receptor and its expression
A:Reference number: JE0349; MUID:99009219
A:Accession: JE0349

A:Molecule type: mRNA

A:Residues: 1-367 <TAM>
A:Cross-references: DDBJ:AB003174; NID:g3798731; PIDN:BAA34045.1; PID:g3798732
C:Comment: This protein is important for lymphocyte trafficking to lymphoid organs.
C:Superfamily: vertebrate rhodopsin

Query Match 76.7%; Score 69; DB 2; Length 367;
Best Local Similarity 70.6%; Pred. No. 0.00064;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPEWAV 17
:|:|:|:| | | | | | | | | |

Db 94 LAVADVLLVLTPLWAV 110

RESULT 12

S55594
G protein-coupled receptor E1 - equine herpesvirus 2
C:Species: equine herpesvirus 2
C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 13-Aug-1999
C:Accession: S55594
R:Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A:Title: The DNA sequence of equine herpesvirus 2.
A:Reference number: S55594; MUID:95302501
A:Accession: S55594
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-383 <TEL>
A:Cross-references: GB:U20824; NID:g695172; PIDN:AAC13788.1; PID:g695173
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

Query Match 74.4%; Score 67; DB 2; Length 383;
Best Local Similarity 73.3%; Pred. No. 0.0014;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPEW 15
:|:|:|:| | | | | | | | | |

Db 114 LAISDLLLTLTLPEW 128

RESULT 13

S42096
Interleukin-8 receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-Aug-1999
C:Accession: S42096
R:Gobl, A.E.; Wang, S.; Zhou, Y.; Oeberg, K.
submitted to the EMBL Data Library, February 1994
A:Description: Molecular cloning of the rat IL8 receptor.
A:Reference number: S42096
A:Accession: S42096
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-356 <GOB>
A:Cross-references: EMBL:X7797
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 73.3%; Score 66; DB 2; Length 356;
Best Local Similarity 66.7%; Pred. No. 0.002;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPEWAVS 18
:|:|:|:| | | | | | | | | |

Db 89 LAIADLFFALTLPWAAAS 106

RESULT 14

A53752
 Interleukin-8 receptor (clone 5B1a) - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
 C:Accession: A53752
 R:Prado, G.N.; Thomas, K.M.; Suzuki, H.; LaRosa, G.J.; Wilkinson, N.; Folco, E.; Navarro, J. Biol. Chem. 269, 12391-12394, 1994
 A:Title: Molecular characterization of a novel rabbit interleukin-8 receptor isotype.
 A:Reference number: A53752; MUID:94230294
 A:Accession: A53752
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-358 <PRA>
 A:Cross-references: GB:L24445; NID:g437661; PIDN:AAA31378.1; PID:g437662
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 73.3%; Score 66; DB 2; Length 358;
 Best Local Similarity 66.7%; Pred. No. 0.002;
 Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MATADILFVLTLPTWAVS 18
 :||||:| | | | | | | |
 DB 88 LAIADLFFALTLPYWAAS 105

RESULT 15
 A48921
 Interleukin-8 receptor type B - mouse
 N:Alternate names: G-protein coupled receptor Gpcr16
 C:Species: Mus musculus (house mouse)
 C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999
 C:Accession: A48921; A53677; I49348; I55421; H48909; I53774
 R:Gerrett, D.P.; Nelson, N.; Kozlosky, C.J.; Morrissey, P.J.; Copeland, N.G.; Gilbert, Genomics 18, 410-413, 1993
 A:Title: The murine homologue of the human interleukin-8 receptor type B maps near the 180 kb IL-8 gene
 A:Reference number: A48921; MUID:94117014
 A:Accession: A48921
 A:Molecule type: DNA
 A:Residues: 1-359 <CER>
 A:Cross-references: GB:L23637; NID:g435093; PIDN:AAA39305.1; PID:g435094
 R:Suzuki, H.; Prado, G.N.; Wilkinson, N.; Navarro, J. J. Biol. Chem. 269, 18263-18266, 1994
 A:Title: The N terminus of interleukin-8 (IL-8) receptor confers high affinity binding to the IL-8 ligand
 A:Reference number: A53677; MUID:94308043
 A:Accession: A53677
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-359 <SUZ>
 A:Cross-references: GB:L26549
 A>Note: sequence extracted from NCBI backbone (NCBIP:149812)
 R:Lee, J.; Cacalano, G.; Camerato, T.; Toy, K.; Moore, M.W.; Wood, W.I. J. Immunol. 155, 2158-2164, 1995
 A:Title: Chemokine binding and activities mediated by the mouse IL-8 receptor.
 A:Reference number: I49348; MUID:95363183
 A:Accession: I49348
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-359 <RES>
 A:Cross-references: EMBL:U31207; NID:g950174; PIDN:AAC52239.1; PID:g950175
 R:Bozic, C.R.; Gerard, N.P.; von Döbeln, C.; Kolakowski, L.F. J. Biol. Chem. 269, 29355-29358, 1994
 A:Title: The murine interleukin 8 type B receptor homologue and its ligands. Expression of the murine interleukin 8 type B receptor homologue and its ligands. Expression
 A:Reference number: I55421; MUID:95050766
 A:Accession: I55421
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-359 <RE2>
 A:Cross-references: GB:L13239; NID:g293665; PIDN:AAA62109.1; PID:g293666
 R:Wilkie, T.M.; Chen, Y.; Gilbert, D.J.; Moore, K.J.; Yu, L.; Simon, M.I.; Copeland, N.G. Genomics 18, 175-184, 1993
 A:Title: Identification, chromosomal location, and genome organization of mammalian G-protein-coupled receptor type B

A:Reference number: A48909; MUID:94116980
 A:Accession: H48909
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 145-258 <WIL>
 A:Cross-references: GB:L20337; NID:g438800; PIDN:AAA16853.1; PID:g438801
 R:Harada, A.; Kuno, K.; Nomura, H.; Mukaida, N.; Murakami, S.; Matsushima, K. Gene 142, 297-300, 1994
 A:Title: Cloning of a cDNA encoding a mouse homolog of the interleukin-8 receptor.
 A:Reference number: I53774; MUID:94252584
 A:Accession: I53774
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-359 <RE3>
 A:Cross-references: GB:DI7630; NID:g493671; PIDN:BAA04536.1; PID:g493672
 C:Genetics:
 A:Gene: IL8rb
 A:Introns: #status absent
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
 F:49-74/Domain: transmembrane #status predicted <TM1>
 F:84-106/Domain: transmembrane #status predicted <TM2>
 F:120-141/Domain: transmembrane #status predicted <TM3>
 F:163-182/Domain: transmembrane #status predicted <TM4>
 F:213-234/Domain: transmembrane #status predicted <TM5>
 F:251-271/Domain: transmembrane #status predicted <TM6>
 F:308-328/Domain: transmembrane #status predicted <TM7>

Query Match 73.3%; Score 66; DB 2; Length 359;
 Best Local Similarity 66.7%; Pred. No. 0.002;
 Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MATADILFVLTLPTWAVS 18
 :||||:| | | | | | | |
 DB 89 LAIADLFFALTLPYWAAS 106

Search completed: May 23, 2001, 15:31:59
 Job time: 506 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:36:17 ; Search time 62.39 Seconds
(without alignments)
9.883 Million cell updates/sec

Title: US-08-887-977-10_COPY_79_96

Perfect score: 90

Sequence: 1 MATADILFVTLTLPFWAVS 18

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	90	100.0	374	1	CKR6_HUMAN
2	83	92.2	367	1	CKR6_MOUSE
3	78	86.7	378	1	CKR7_HUMAN
4	77	85.6	192	1	CCR4_SHEEP
5	77	85.6	353	1	CCR4_BOVIN
6	77	85.6	353	1	CCR4_FELCA
7	75	83.3	349	1	CCR4_RAT
8	75	83.3	352	1	CCR4_CERTO
9	75	83.3	352	1	CCR4_HUMAN
10	75	83.3	352	1	CCR4_MACMU
11	75	83.3	352	1	CCR4_PAPAN
12	75	83.3	356	1	IL8B_CANFA
13	75	83.3	357	1	CKR9_HUMAN
14	75	83.3	359	1	CCR4_MOUSE
15	73	81.1	369	1	CKR9_MOUSE
16	72	80.0	352	1	CCR4_MACFA
17	72	80.0	378	1	CKR7_MOUSE
18	71	78.9	354	1	CKR5_MOUSE
19	71	78.9	354	1	CKR5_RAT
20	71	78.9	373	1	CKR2_MOUSE
21	71	78.9	373	1	CKR2_RAT
22	70	77.8	355	1	IL8A_RABIT
23	69	76.7	350	1	IL8A_GORGO
24	69	76.7	350	1	IL8A_HUMAN
25	69	76.7	350	1	IL8A_PANTR
26	69	76.7	353	1	IL8B_GORGO
27	69	76.7	353	1	IL8B_MACMU
28	69	76.7	353	1	IL8B_PANTR
29	69	76.7	360	1	IL8B_HUMAN
30	69	76.7	367	1	CCR3_MOUSE
31	68	75.6	352	1	CKR5_CERAE
32	68	75.6	352	1	CKR5_CERTO
33	68	75.6	352	1	CKR5_MACMU
					P51684 homo sapien
					O54689 mus musculus
					P32248 homo sapien
					Q28553 ovis aries
					P25930 bos taurus
					P58498 felis silve
					O08565 rattus norv
					O62747 cercocobus
					P30991 homo sapien
					P79394 macaca mula
					P58491 papio anubi
					O97571 canis fami
					P51686 homo sapien
					P70658 mus musculus
					O9wt7 mus musculus
					Q28474 macaca fasc
					P47774 mus musculus
					P51682 mus musculus
					O08556 rattus norv
					P51683 mus musculus
					O55193 rattus norv
					P21109 oryctolagus
					P55919 gorilla gor
					P25024 homo sapien
					P55920 pan troglod
					Q28422 gorilla gor
					Q28519 macaca mula
					Q28807 pan troglod
					P25025 homo sapien
					O88410 mus musculus
					P56493 cercopithec
					O62743 cercocobus
					P79436 macaca mula

RESULT 1

ID	CKR6_HUMAN	STANDARD;	PRT;	374 AA.
AC	P51684: Q92846; P78553;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DE	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CC-CKR-6) (CCR-6) (LARC RECEPTOR) (GPR-CY4) (GPCY4) (CHEMOKINE RECEPTOR-LIKE 3) (CKR-L3) (DRY6).			
GN	CKR6 OR CMKR6 OR STRL22 OR GPR29 OR CKRL3.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND FUNCTION.			
RX	MEDLINE:97313465; PubMed:9169459;			
RA	Baba M., Imai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K.,			
RA	Nomiyama H., Yoshie O.;			
RT	"Identification of CCR6, the specific receptor for a novel			
RT	lymphocyte-directed CC chemokine LARC.;"			
RL	J. Biol. Chem. 272:14893-14898(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Lautens L.L., Modi W., Bonner T.I.;			
RL	Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE:97040707; PubMed:8886020;			
RA	Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G.;			
RT	"Molecular cloning and RNA expression of two new human chemokine			
RT	receptor-like genes.;"			
RL	Biochem. Biophys. Res. Commun. 227:846-853(1996).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	McCoy R., Perlmuter D.H.;			
RL	Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE:97224503; PubMed:9070937;			
RA	Liao F., Lee H.-H., Farber J.M.;			
RT	"Cloning of STRL22, a new human gene encoding a G-protein-coupled			
RT	receptor related to chemokine receptors and located on chromosome			
RT	6q27.;"			
RL	Genomics 40:175-180(1997).			
CC	-!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-			
CC	ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE			
CC	INTRACELLULAR CALCIUM IONS LEVEL.			
CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	-!- TISSUE SPECIFICITY: SPLEEN, LYMPH NODES, APPENDIX, AND FETAL			
CC	LIVER. EXPRESSED IN LYMPHOCYTES, T CELLS AND B CELLS BUT NOT IN			
CC	NATURAL KILLER CELLS, MONOCYTES, OR GRANULOCYTES.			
CC	-!- INDUCTION: INTERLEUKIN-2.			
CC	-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-6 IS THE INITIATOR.			

P56441 papio hamad
Q9wv26 cavia porce
P70612 rattus norv
P35344 oryctolagus
P35343 mus musculus
P35407 rattus norv
P51680 mus musculus
P25104 bos taurus
P43240 canis fami
P30556 homo sapien
P29794 mus musculus
P30555 sus scrofa

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 CC EMBL; U45984; AAB62714.1; -;
 DR EMBL; 279784; CAB02144.1; ALT_INIT.
 DR EMBL; U60000; AAB06949.1; -;
 DR EMBL; U68030; AAC51124.1; -;
 DR EMBL; U68032; AAC51125.1; -;
 DR HSSP; P34996; 1DDD.
 DR GCRdb; GCR1037; -;
 DR GCRdb; GCR1075; -;
 DR GCRdb; GCR1906; -;
 DR GCRdb; GCR1919; -;
 DR GCRdb; GCR1941; -;
 DR GCRdb; GCR2110; -;
 DR MIM; 601835; -;
 DR InterPro: IPR000276; -;
 DR Pfam; PF00001; 7tm.1; 1;
 DR PRINTS; PR00237; GPCRHOOPS.
 DR PROSITE; PS00237; G-PROTEIN_RECF_F1_1; 1;
 DR PROSITE; PS0262; G-PROTEIN_RECF_F1_2; 1;
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 47
 FT TRANSMEM 48 74
 FT DOMAIN 75 83
 FT TRANSMEM 84 104
 FT DOMAIN 105 119
 FT TRANSMEM 120 141
 FT DOMAIN 142 159
 FT TRANSMEM 160 180
 FT DOMAIN 181 211
 FT TRANSMEM 212 238
 FT DOMAIN 239 254
 FT TRANSMEM 255 279
 FT DOMAIN 280 303
 FT TRANSMEM 304 321
 FT DOMAIN 322 338
 FT TRANSMEM 339 374
 FT DISULFID 118 197
 FT CARBOHYD 7 7
 FT CARBOHYD 23 23
 FT CONFLICT 60 60
 FT CONFLICT 74 74
 FT CONFLICT 86 86
 FT CONFLICT 164 164
 FT CONFLICT 182 182
 FT CONFLICT 192 192
 FT CONFLICT 206 206
 FT CONFLICT 225 225
 FT CONFLICT 370 374
 SQ SEQUENCE 374 AA; 42494 MW; D7F963534E990BC4 CRC64;

 Query Match 100.0%; Score 90; DB 1; Length 374;
 Best Local Similarity 100.0%; Pred. No. 4.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAIADILFVLTLPPFWVS 18
 |||||
 Db 88 MAIADILFVLTLPPFWVS 105

 RESULT 2
 ID CKR6_MOUSE STANDARD; PRT; 367 AA.
 AC O54689;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)
 GN C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CCR-6) (KY411).
 GN CCR6 OR CKR6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yanagihara S., Komura E., Yamaguchi Y.;
 RT "Mouse G-protein-coupled receptor KY411.";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99077268; PubMed=9862452;
 RA Varona R., Zaballós A., Gutierrez J., Martin P., Roncal F.,
 RA Albar J.P., Ardavin C., Marquez G.;
 RT "Molecular cloning, functional characterization and mRNA expression
 analysis of the murine chemokine receptor CCR6 and its specific ligand
 MIP-3alpha.";
 RL MIP-3alpha.";
 RL FEBS Lett. 440:188-194(1998).
 CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-
 ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE
 INTRACELLULAR CALCIUM IONS LEVEL.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 CC EMBL; AB009369; BAA23776.1; -;
 DR EMBL; AJ222714; CAA10956.1; -;
 DR MGD; MGI:1333797; Cmkbr6.
 DR InterPro: IPR000276; -;
 DR Pfam; PF00001; 7tm.1; 1;
 DR PRINTS; PR00237; GPCRHOOPS.
 DR PROSITE; PS00237; G-PROTEIN_RECF_F1_1; 1;
 DR PROSITE; PS0262; G-PROTEIN_RECF_F1_2; 1;
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 39
 FT TRANSMEM 40 66
 FT DOMAIN 67 75
 FT TRANSMEM 76 96
 FT DOMAIN 97 111
 FT TRANSMEM 112 133
 FT DOMAIN 134 151
 FT TRANSMEM 152 172
 FT DOMAIN 173 203
 FT TRANSMEM 204 230
 FT DOMAIN 231 246
 FT TRANSMEM 247 271
 FT DOMAIN 272 295
 FT TRANSMEM 296 313
 FT DOMAIN 314 367
 FT DISULFID 110 189
 FT CARBOHYD 2 2
 FT CARBOHYD 35 35
 SQ SEQUENCE 367 AA; 42102 MW; 6A309AF833B1117E CRC64;

 Query Match 92.2%; Score 83; DB 1; Length 367;
 Best Local Similarity 88.9%; Pred. No. 6e-06;
 Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MAIADILFVLTLPPFWVS 18
 |||||
 Db 80 MAITDILFVLTLPPFWAVT 97

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RESULT 3
CKR7_HUMAN STANDARD; PRT; 378 AA.
ID CKR7_HUMAN STANDARD; PRT; 378 AA.
AC P32248;
DT 01-OCT-1993 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 7 PRECURSOR (C-C KKR-7) (CCR-7)
DE (MIP-3 BETA RECEPTOR) (EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 1)
DE (EBI1) (BLR2).
DE CCR7 OR CMKBR7 OR EBI1 OR EVI1.
GN CCR7 OR CMKBR7 OR EBI1 OR EVI1.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93188173; PubMed=8383238;
RA Birkenbach M.P., Josefsen K., Yalamanchili R.R., Lenoir G.M.,
RA Elliott K.;
RT "Epstein-Barr virus-induced genes: first lymphocyte-specific G
RT protein-coupled peptide receptors.";
RL J. Virol. 67:2209-2220(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=95154835; PubMed=7851893;
RA Schweickart V.L., Raport C.J., Godiska R., Byers M.G., Eddy R.L. Jr.,
RA Shows T.B., Gray P.W.;
RT "Cloning of human and mouse EB1, a lymphoid-specific
RT G-protein-coupled receptor encoded on human chromosome 17q12-q21.2.";
RL Genomics 23:643-650(1994).
CC -!- FUNCTION: RECEPTOR FOR THE MIP-3-BETA CHEMOKINE. PROBABLE MEDIATOR
CC OF EBV EFFECTS ON B LYMPHOCYTES OR OF NORMAL LYMPHOCYTE FUNCTIONS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN VARIOUS LYMPHOID TISSUES AND
CC ACTIVATED B AND T LYMPHOCYTES, STRONGLY UPREGULATED IN B CELLS
CC INFECTED WITH EPSTEIN-BARR VIRUS AND T CELLS INFECTED WITH
CC HERPESVIRUS 6 OR 7.
CC -!- INDUCTION: BY EBV.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL; L08176; AAA58615.1; -
CC EMBL; L31584; AAA74230.1; -
CC EMBL; L31582; AAA74230.1; JOINED.
CC EMBL; L31583; AAA74230.1; JOINED.
CC EMBL; L31581; AAA74231.1; -
CC PIR; A45680; A45680.
CC HSP; P34996; IDDD.
CC GCRDB; GCR_0492; -
CC GCRDB; GCR_0958; -
CC MIM; 600242; -
CC InterPro; IPR001718; -
CC InterPro; IPR000276; -
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODOPS.
CC PRINTS; PR00641; CHEMOKINER7.
CC PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
CC PROSITE; PS00262; G_PROTEIN_RECEPTOR_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
KW SIGNAL
FT CHAIN 1 24 POTENTIAL.
FT CHAIN 25 378 C-C CHEMOKINE RECEPTOR TYPE 7.
FT DOMAIN 25 59 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 60 86 1 (POTENTIAL).

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FT DOMAIN 87 95 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 96 116 2 (POTENTIAL).
FT DOMAIN 117 130 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 131 152 3 (POTENTIAL).
FT DOMAIN 153 170 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 171 191 4 (POTENTIAL).
FT DOMAIN 192 219 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 220 247 5 (POTENTIAL).
FT DOMAIN 248 263 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 264 289 6 (POTENTIAL).
FT DOMAIN 290 313 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 314 331 7 (POTENTIAL).
FT DOMAIN 332 378 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 36 36 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 129 210 BY SIMILARITY.
FT CONFLICT 182 183 IW -> SA (IN REF. 1).
FT CONFLICT 337 337 L -> I (IN REF. 1).
SQ SEQUENCE 378 AA; 42874 MW; D4CB4213841A1BD4 CRC64;

Query Match 86.7%; Score 78; DB 1; Length 378;
Best Local Similarity 77.8%; Pred. No. 3.7e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPEFAVS 18
Db 100 LAVADIILFLLTLPFAVS 117
:|:|:|:|:|:|:|:|:|

RESULT 4
CCR4_SHEEP STANDARD; PRT; 192 AA.
AC O28553;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (CXCR-4) (SDF-1 RECEPTOR)
DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LEUKOCYTE-DERIVED
DE SEVEN TRANSMEMBRANE DOMAIN RECEPTOR) (LESTR) (FRAGMENT).
GN CXCR4 OR LESTR.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hypothalamus;
RA Dyer C.J., Matteri R.L., Keisler D.H.;
RT "Development of an ovine Y3 cDNA and expression of the Y3 receptor
RT mRNA in the ovine hypothalamus and pituitary.";
RL Abstr. - Soc. Neurosci. 21:1890-1890(1995).
CC -!- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -!- CAUTION: WAS ORIGINALLY THOUGHT TO BE A RECEPTOR FOR NEUROPEPTIDE
CC Y, TYPE 3 (NPY3-R).
CC
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CC
CC EMBL; U38942; AAA81347.1; -
CC GCRDB; GCR_1581; -
CC InterPro; IPR000276; -
CC Pfam; PF00001; 7tm_1; 1.
CC PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
CC PROSITE; PS00262; G_PROTEIN_RECEPTOR_F1_2; 1.

```

KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT NON_TER 1
 FT DOMAIN <1 29
 FT TRANSMEM 30 53
 FT DOMAIN 54 69
 FT TRANSMEM 70 89
 FT DOMAIN 90 100
 FT TRANSMEM 101 122
 FT DOMAIN 123 144
 FT TRANSMEM 145 165
 FT DOMAIN 166 190
 FT TRANSMEM 191 >192
 FT DISULFID 99 176
 FT NON_TER 192 192
 SQ SEQUENCE 192 AA; 22178 MW; A8BCFE303C52BD98 CRC64;

Query Match 85.6%; Score 77; DB 1; Length 192;
 Best Local Similarity 76.5%; Pred. No. 2.9e-05;
 Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPFWAV 17
 ::::|||||
 DB 70 LSVADLLFVLTLPFWAV 86

RESULT 5
 CCR4_BOVIN STANDARD; PRT; 353 AA.
 AC P25930;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (SDF-1 RECEPTOR)
 DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LEUKOCYTE-DERIVED
 SEVEN TRANSMEMBRANE DOMAIN RECEPTOR) (LESTR) (LCRI).
 GN CXCR4.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Locus coeruleus;
 RX MEDLINE=92100053; PubMed=1661837;
 RA Rinland J., Xin W., Sweetnam P., Saijoh K., Nestler E.J., Duman R.S.;
 RT "Sequence and expression of a neuropeptide Y receptor cDNA";
 RL Mol. Pharmacol. 40:869-875(1991).
 RN [2]
 RP SHOWS THAT IT IS NOT A NPY3-R.
 RX MEDLINE=94052833; PubMed=8234509;
 RA Jazin E.E., Yoo H., Blomqvist G., Yee F., Weng G., Walker M.W.,
 RA Salon J., Larhammar D., Wahlestedt C.R.;
 RT "A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its
 human homologue, confers neither NPY binding sites nor NPY
 responsiveness on transfected cells";
 RL Regul. Pept. 47:247-258(1993).
 CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
 SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: BRAIN, HEART, KIDNEY, LUNG AND LIVER.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -1- CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO BE A RECEPTOR FOR
 NEUROPEPTIDE Y, TYPE 3 (NPY3-R).
 CC
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CC EMBL; M86739; -, NOT_ANNOTATED_CDS.
 DR PIR; S28787; S28787.
 DR GCRDB; GCR_0180; -.
 DR InterPro; IPR000276; -.
 DR Pfam; PF0001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00645; LCR1ORPHAN.
 DR PROSITE; PS00237; G_PROTEIN_RECIP_F1_1; 1.
 DR PROSITE; PSS0262; G_PROTEIN_RECIP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 40
 FT TRANSMEM 41 64
 FT DOMAIN 65 80
 FT TRANSMEM 81 100
 FT DOMAIN 101 111
 FT TRANSMEM 112 133
 FT DOMAIN 134 155
 FT TRANSMEM 156 176
 FT DOMAIN 177 201
 FT TRANSMEM 202 221
 FT DOMAIN 222 241
 FT TRANSMEM 242 262
 FT DOMAIN 263 286
 FT TRANSMEM 287 306
 FT DOMAIN 307 353
 FT CARBOHYD 11 11
 FT DISULFID 110 187
 SQ SEQUENCE 353 AA; 39938 MW; 42FFE5BC7545505E CRC64;

Query Match 85.6%; Score 77; DB 1; Length 353;
 Best Local Similarity 76.5%; Pred. No. 5e-05;
 Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPFWAV 17
 ::::|||||
 DB 81 LSVADLLFVLTLPFWAV 97

RESULT 6
 CCR4_FELCA STANDARD; PRT; 353 AA.
 ID P56498; P79172; O02700;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (SDF-1 RECEPTOR)
 DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LESTR).
 GN CXCR4.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97404646; PubMed=9261358;
 RA Willett B.J., Picard L., Hosie M.J., Turner J.D., Adema K.,
 RA Clapham P.R.;
 RT "Shared usage of the chemokine receptor CXCR4 by the feline and human
 immunodeficiency viruses";
 RL J. Virol. 71:6407-6415(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Willett B.J.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Lerner D.L., Elder J.H.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
 SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC
 DR EMBL; U63558; AAC48852.1; -;
 DR EMBL; U92795; AAB51765.1; -;
 DR GCRDb; GCR_1113; -;
 DR GCRDb; GCR_1114; -;
 DR InterPro; IPR000276; -;
 DR InterPro; IPR001277; -;
 DR Pfam; PF00001; 7tm_1; 1;
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00645; LCR1ORPHANR.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1;
 DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1;
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 40
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 41 64
 FT DOMAIN 65 80
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 81 100
 FT DOMAIN 101 111
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 112 133
 FT DOMAIN 134 155
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 156 176
 FT DOMAIN 177 201
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 202 221
 FT DOMAIN 222 241
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 242 262
 FT DOMAIN 263 286
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 287 306
 FT DOMAIN 307 353
 FT CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 11 11
 FT DISULFID 110 187
 FT BY SIMILARITY.
 FT CONFLICT 67 67 Q -> H (IN REF. 3).
 FT CONFLICT 263 263 D -> E (IN REF. 3).
 SQ SEQUENCE 353 AA; 39935 MW; EA2BD4608A6C05B CRC64;

Query Match 85.68; Score 77; DB 1; Length 353;
 Best Local Similarity 76.5%; Pred. No. 5e-05;
 Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTPFWAV 17
 DB 81 LSVADLLFVLTPFWAV 97

RESULT 7
 CCR4_RAT
 ID CCR4_RAT STANDARD; PRT; 349 AA.
 AC O08565;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (CXCR-4) (SDF-1 RECEPTOR)
 DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LEUKOCYTE-DERIVED
 DE SEVEN TRANSMEMBRANE DOMAIN RECEPTOR) (LESTR).
 GN CXCR4 OR CMKAR4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WISTAR; TISSUE=Spleen;
 RA Harrison J.K., Salafranca M.N.;

RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
 CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC
 DR EMBL; U90610; AAB50408.1; -;
 DR GCRDb; GCR_1401; -;
 DR InterPro; IPR000276; -;
 DR InterPro; IPR001277; -;
 DR Pfam; PF00001; 7tm_1; 1;
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00645; LCR1ORPHANR.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1;
 DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1;
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 36
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 37 60
 FT DOMAIN 61 76
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 77 96
 FT DOMAIN 97 107
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 108 129
 FT DOMAIN 130 151
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 152 172
 FT DOMAIN 173 197
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 198 217
 FT DOMAIN 218 237
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 238 258
 FT DOMAIN 259 282
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 283 302
 FT DOMAIN 303 349
 FT CYTOPLASMIC (POTENTIAL).
 FT DISULFID 106 183
 FT CARBOHYD 8 8
 FT BY SIMILARITY.
 FT CONFLICT 8 8 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 349 AA; 39334 MW; 7E0789A605C60C09 CRC64;

Query Match 83.38; Score 75; DB 1; Length 349;
 Best Local Similarity 70.6%; Pred. No. 0.0001;
 Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTPFWAV 17
 DB 77 LSVADLLFVLTPFWAV 93

RESULT 8
 CCR4_CERTO
 ID CCR4_CERTO STANDARD; PRT; 352 AA.
 AC O62747;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (CXCR-4) (SDF-1 RECEPTOR)
 DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LESTR).
 GN CXCR4.
 OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Cercopithecus.
 OX NCBI_TaxID=9531;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=98321155; PubMed=9656999;
 RA Chen Z., Gettler A., Ho D.D., Marx P.A.;
 RT "Primary SIVsm isolates use the CCR5 coreceptor from sooty mangabey

naturally infected in west Africa: a comparison of coreceptor usage of primary HIV-1, HIV-2, and SIVmac.",
 RT Virology 246:113-124(1998).
 RL
 CC -!- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
 CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
 CC
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC
 CC EMBL; AF051906; AAC39834.1; -
 CC InterPro; IPR000276; -
 CC InterPro; IPR001277; -
 CC Pfam; PF00001; 7tm_1; 1.
 CC PRINTS; PR00237; GPCRHHODPSN.
 CC PRINTS; PR00645; LCRIPRPHNR.
 CC PROSITE; PS00237; G-PROTEIN RECF_1.1; 1.
 CC PROSITE; PS00262; G-PROTEIN RECF_2.1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein.
 KW DOMAIN 1 39
 FT TRANSMEM 40 63
 FT DOMAIN 64 79
 FT TRANSMEM 80 99
 FT DOMAIN 100 110
 FT TRANSMEM 111 132
 FT DOMAIN 133 154
 FT TRANSMEM 155 175
 FT DOMAIN 176 200
 FT TRANSMEM 201 220
 FT DOMAIN 221 240
 FT TRANSMEM 241 261
 FT DOMAIN 262 285
 FT TRANSMEM 286 305
 FT DOMAIN 306 352
 FT CARBOHYD 11 11
 FT DISULFID 109 186
 SQ SEQUENCE 352 AA; 39648 MW; 4027432B8032F87E CRC64;

Query Match 83.3%; Score 75; DB 1; Length 352;
 Best Local Similarity 70.6%; Pred No. 0.0001;
 Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTPFWAV 17
 :::::|||||
 Db 80 LSVADLLFVLTPFWAV 96

RESULT 9
 CCR4_HUMAN STANDARD; PRT; 352 AA.
 ID CCR4_HUMAN
 AC P30991; P56438;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (SDF-1 RECEPTOR)
 DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LEUKOCYTE-DERIVED
 DE SEVEN TRANSMEMBRANE DOMAIN RECEPTOR) (LESTR) (LCR1) (FB22) (NPYRL)
 DE (HM89).
 GN CXCR4.
 OS Homo sapiens (Human), and Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606; 9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human; TISSUE=Lung;

RX MEDLINE-93319629; PubMed-8329116;
 RA Herzog H., Hort Y.J., Shine J., Selbie L.A.;
 RT "Molecular cloning, characterization, and localization of the human
 RT homolog to the reported bovine NPY Y3 receptor: lack of NPY binding
 RT and activation.";
 RL DNA Cell Biol. 12:465-471(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human; TISSUE=Brain;
 RX MEDLINE-94052833; PubMed-8234909;
 RA Jazin E.E., Yoo H., Blomqvist G., Yee F., Weng G., Walker M.W.,
 RA Salom J., Larhammar D., Wahlstedt C.R.;
 RT "A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its
 RT human homologue, confers neither NPY binding sites nor NPY
 RT responsiveness on transfected cells.";
 RL Regul. Pept. 47:247-258(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human; TISSUE=Spleen;
 RX MEDLINE-93315164; PubMed-8325644;
 RA Federspiel B., Delaney A.D., Clark-Lewis I., Jirik F., Duncan A.M.,
 RA Schappert K.T., Melhado I.;
 RT "Molecular cloning of the cDNA and chromosomal localization of the
 RT gene for a putative seven-transmembrane segment (7-TMS) receptor
 RT isolated from human spleen.";
 RL Genomics 16:707-712(1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human; TISSUE=Leukocyte;
 RX MEDLINE-94103215; PubMed-8276799;
 RA Loetscher M., Geisler T., O'Reilly T., Zwahlen R., Baggiolini M.,
 RA Moser B.;
 RT "Cloning of a human seven-transmembrane domain receptor, LESTR, that
 RT is highly expressed in leukocytes.";
 RL J. Biol. Chem. 269:232-237(1994).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human; TISSUE=Monocytes;
 RX MEDLINE-94092629; PubMed-7505609;
 RA Nomura H., Nielsen B.W., Matsushima K.;
 RT "Molecular cloning of cDNAs encoding a LD78 receptor and putative
 RT leukocyte chemotactic peptide receptors.";
 RL Int. Immunol. 5:1239-1249(1993).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human;
 RA Wegner S.A., Ehrenberg P.K., Chang G., Dayhoff D.E., Michael N.L.;
 RT Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human;
 RX MEDLINE-98258970; PubMed-9599023;
 RA Caruz A., Samsom M., Alonso J.M., Alcamí J., Balleux F.,
 RA Virelizier J.L., Parmentier M., Arenzana-Seisdedos F.;
 RT "Genomic organization and promoter characterization of human CXCR4
 RT gene.";
 RL FEBS Lett. 426:271-278(1998).
 RN [8]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human;
 RA Xiao L., Weiss S., Qari S., Rudolph D., Hodge T., Lal R.;
 RT "Partial resistance to infection by syncytium-inducing primary HIV-1
 RT in exposed uninfected individuals homozygous for CCR5 32bp
 RT deletion.";
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human; TISSUE=Blood;
 RA Frodl R., Moepfs B., Gierschik P.;
 RT "Genomic organization and expression pattern of the human chemokine
 RT receptor CXCR4.";
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RN [10]

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BEAGLE;
 RA Chang Y.F., Novosel V., Chang C.F.;
 RT "The isolation and sequence of canine interleukin-8 receptor
 homolog.";
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
 CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
 CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
 CC G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER SYSTEM. THE AFFINITY OF THIS RECEPTOR IS IL-8 >> NAP-2 >
 CC MGS (GRO).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC
 CC EMBL: AF047047; AAC98968.1; -
 CC InterPro: IPR000057; -
 CC InterPro: IPR000174; -
 CC InterPro: IPR000276; -
 CC InterPro: IPR000355; -
 CC InterPro: IPR001277; -
 CC Pfam: PF000001; 7tm_1; 1.
 CC PRINTS: PR00237; GPCRHHODOPSIN.
 CC PRINTS: PR00427; INTRLEUKIN8R.
 CC PRINTS: PR00573; INTRLEUKIN8R.
 CC PRINTS: PR00645; LCR1ORPHANR.
 CC PRINTS: PR00657; CCHEMOKINR.
 CC PROSITE: PS00237; G-PROTEIN RECEPTOR FL1; 1.
 CC PROSITE: PS0262; G-PROTEIN RECEPTOR FL2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Chemotaxis.
 FT DOMAIN 1 46 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 47 73 1 (POTENTIAL).
 FT DOMAIN 74 82 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 83 103 2 (POTENTIAL).
 FT DOMAIN 104 118 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 119 140 3 (POTENTIAL).
 FT DOMAIN 141 161 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 162 181 4 (POTENTIAL).
 FT DOMAIN 182 206 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 207 229 5 (POTENTIAL).
 FT DOMAIN 230 249 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 250 269 6 (POTENTIAL).
 FT DOMAIN 270 290 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 291 311 7 (POTENTIAL).
 FT DOMAIN 312 356 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 117 194 BY SIMILARITY.
 SQ SEQUENCE 356 AA; 40505 MW; 2B67DD4E8DD39B15 CRC64;

Query Match 83.3%; Score 75; DB 1; Length 356;
 Best Local Similarity 77.8%; Pred. No. 0.0001;
 Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 MAIADILVLTLPFWAS 18
 :|||||:|||||
 Db 88 LAIADLLFALTPIWAS 105

RESULT 13

CKR9_HUMAN
 ID CKR9_HUMAN STANDARD; PRT; 357 AA.
 AC P51686;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 9 (C-C CKR-9) (CCR-9) (GPR-9-
 DE 6).
 GN CCR9 OR CMKBR9.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lautens L.L., Tiffany H.L., Gao J.-L., Modi W., Murphy P.M.,
 RA Bonner T.I.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 RL [2]
 CC CHARACTERIZATION.
 CC MEDLINE=99248139; PubMed=10229797;
 CC Zaballos A., Gutierrez J., Varona R., Ardavin C., Marquez G.;
 CC "Cutting edge: identification of the orphan chemokine receptor GPR-9-6
 CC as CCR9, the receptor for the chemokine TECK.";
 CC J. Immunol. 162:5671-5675(1999).
 CC -!- FUNCTION: RECEPTOR FOR CHEMOKINE SCYA25/TECK. SUBSEQUENTLY
 CC TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS
 CC LEVEL.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE THYMUS AND LOW IN
 CC LYMPH NODES AND SPLEEN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC
 CC EMBL: U45982; AAA93319.1; -
 CC MIM: 604738; -
 CC GCRDb: GCR_1943; -
 CC InterPro: IPR000276; -
 CC Pfam: PF000001; 7tm_1; 1.
 CC PRINTS: PR00237; GPCRHHODOPSIN.
 CC PROSITE: PS00237; G-PROTEIN RECEPTOR FL1; 1.
 CC PROSITE: PS0262; G-PROTEIN RECEPTOR FL2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein.
 KW DOMAIN 1 37 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 38 64 1 (POTENTIAL).
 FT DOMAIN 65 73 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 74 94 2 (POTENTIAL).
 FT DOMAIN 95 108 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 109 130 3 (POTENTIAL).
 FT DOMAIN 131 148 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 149 169 4 (POTENTIAL).
 FT DOMAIN 170 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 226 5 (POTENTIAL).
 FT DOMAIN 227 242 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 243 268 6 (POTENTIAL).
 FT DOMAIN 269 292 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 293 310 7 (POTENTIAL).
 FT DOMAIN 311 357 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 107 186 BY SIMILARITY.
 SQ SEQUENCE 357 AA; 40713 MW; 96982E0B922F6B31 CRC64;

Query Match 83.3%; Score 75; DB 1; Length 357;
 Best Local Similarity 66.7%; Pred. No. 0.0001;
 Matches 12; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLFPWAVS 18
 DB 78 LAIADLLFLVTLFPWAIA 95

RESULT 14
 CCR4_MOUSE STANDARD; PRT; 359 AA.
 AC P70658; P70346; O09062; O09059; P70233;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (SDF-1 RECEPTOR)
 DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LEUKOCYTE-DERIVED
 SEVEN TRANSMEMBRANE DOMAIN RECEPTOR) (LESTR).
 GN CXCR4 OR LESTR OR CMKAR4 OR SDF1R.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
 RA Moepps B., Frodl R., Kessler H., Gierschik P.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV;
 RA Heesen M., Berman M.A., Gerard C., Dorf M.E.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RA Heesen M., Berman M.A., Benson J.D., Gerard C., Dorf M.E.;
 RL "Cloning of the mouse fusin gene, homologue to a human HIV-1
 co-factor.";
 RT J. Immunol. 157:5455-5460(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bone marrow;
 RA Nagasawa T., Nakajima T., Tachibana K., Iizasa H., Bleul C.C.,
 RA Yoshie O., Matsushima K., Yoshida N., Springer T.A., Kishimoto T.;
 RT "Molecular cloning and characterization of a murine pre-B-cell
 growth-stimulating factor/stromal cell-derived factor 1 receptor, a
 murine homolog of the human immunodeficiency virus 1 entry coreceptor
 fusin.";
 RT Proc. Natl. Acad. Sci. U.S.A. 93:14726-14729(1996).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Thymus;
 RA Suzuki G., Nakata Y., Uzawa A., Shirasawa T., Saito T., Mita K.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV; TISSUE=Thymus;
 RA Schubel A., Burgstahler R., Lipp M.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
 SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC

DR EMBL; X99581; CAA67893.1; -
 DR EMBL; X99582; CAA67894.1; -
 DR EMBL; U59760; AAB07725.1; -
 DR EMBL; U65580; AAC52953.1; -
 DR EMBL; D87747; BAA13451.1; -
 DR EMBL; AB00803; BAA19187.1; -
 DR EMBL; Z80111; CAB02201.1; -
 DR EMBL; Z80112; CAB02202.1; -
 DR GCRDB; GCR_1138; -
 DR GCRDB; GCR_1387; -
 DR GCRDB; GCR_1646; -
 DR GCRDB; GCR_1730; -
 DR GCRDB; GCR_2592; -
 DR MGD; MGI:109563; Cmkar4.
 DR InterPro: IPR000276; -
 DR InterPro: IPR001277; -
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODOPS.
 DR PRINTS; PR00645; LCR10RPHAN.
 DR PROSITE; PS00237; G_PROTEIN_REC_F1.1; 1.
 DR PROSITE; PS0262; G_PROTEIN_REC_F1.2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 41
 FT TRANSMEM 42 65
 FT DOMAIN 66 81
 FT TRANSMEM 82 101
 FT DOMAIN 102 112
 FT TRANSMEM 113 134
 FT DOMAIN 135 156
 FT TRANSMEM 157 177
 FT DOMAIN 178 207
 FT TRANSMEM 208 227
 FT DOMAIN 228 247
 FT TRANSMEM 248 268
 FT DOMAIN 269 292
 FT TRANSMEM 293 312
 FT DOMAIN 313 359
 FT DISULFID 111 193
 FT CARBOHYD 13 13
 FT CONFLICT 6 7
 FT CONFLICT 216 216 I -> V (IN REF. 1 AND 5).
 SQ SEQUENCE 359 AA; 40426 MW; 33D1B5552A31595B CRC64;
 Query Match 83.3%; Score 75; DB 1; Length 359;
 Best Local Similarity 70.6%; Pred. No. 0.00011;
 Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAIADILFVLTLFPWAV 17
 DB 82 LSVADLLFVTLFPWAV 98
 RESULT 15
 CCR9_MOUSE STANDARD; PRT; 369 AA.
 AC O9WU7;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 9 (C-C CKR-9) (CCR-9)
 DE (CHEMOKINE C-C RECEPTOR 10).
 GN CCR9 OR CMKBR10.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thymus;
 RX MEDLINE=99248139; PubMed=10229797;
 RA Zaballos A., Gutierrez J., Varona R., Ardavin C., Marquez G.;
 RT "Cutting edge: identification of the orphan chemokine receptor GPR-9-6

RT as CCR9, the receptor for the chemokine TECK.";
RL J. Immunol. 162:5671-5675(1999).
CC -1- FUNCTION: RECEPTOR FOR CHEMOKINE SCYA25/TECK. SUBSEQUENTLY
CC TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS
CC LEVEL.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE THYMUS AND LOW IN
CC LYMPH NODES AND SPLEEN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; AJ132336; CAB43480.1; -;
DR MGD; MGI:1341902; Cmkbr10.
DR InterPro; IPR000174; -;
DR InterPro; IPR000248; -;
DR InterPro; IPR000276; -;
DR InterPro; IPR000355; -;
DR InterPro; IPR000496; -;
DR InterPro; IPR001277; -;
DR InterPro; IPR001718; -;
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PRINTS; PR00241; ANGIOTENSINR.
DR PRINTS; PR00425; BRADYKININR.
DR PRINTS; PR00427; INTRLEUKIN8R.
DR PRINTS; PR00641; CHEMOKINER7.
DR PRINTS; PR00645; LCR1ORPHANR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 49 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 50 76 1 (POTENTIAL).
FT DOMAIN 77 85 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 86 106 2 (POTENTIAL).
FT DOMAIN 107 120 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 121 142 3 (POTENTIAL).
FT DOMAIN 143 160 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 161 181 4 (POTENTIAL).
FT DOMAIN 182 210 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 211 238 5 (POTENTIAL).
FT DOMAIN 239 254 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 255 280 6 (POTENTIAL).
FT DOMAIN 281 304 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 305 322 7 (POTENTIAL).
FT DOMAIN 323 369 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 32 32 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 119 198 BY SIMILARITY.
SQ SEQUENCE 369 AA; 41913 MW; 6971F76F0A24B4AE CRC64;

Query Match 81.1%; Score 73; DB 1; Length 369;
Best Local Similarity 66.7%; Pred. No. 0.00022;
Matches 12; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTPFWAS 18
:|||||:|||||:
Db 90 LAIADLLFLATLPFWAIA 107

Search completed: May 23, 2001, 15:36:17
Job time: 648 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:35:12 ; Search time 189.03 Seconds
(without alignments)
11.161 Million cell updates/sec

Title: US-08-887-977-10_COPY_79_96
Perfect score: 90
Sequence: 1 MAIADILFVLTLPFWAVS 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues
Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL15:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phase:
10: sp_plant:
11: sp_rodent:
12: sp_unclassified:
13: sp_vertebrate:
14: sp_virus:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	83	92.2	367	11	Q9R1V0	Q9R1V0 mus musculus
2	78	86.7	353	13	Q93247	Q93247 cyprinus ca
3	78	86.7	353	13	Q9PTF7	Q9PTF7 brachydanio
4	77	85.6	357	13	Q42445	Q42445 oncorhynchus
5	75	83.3	334	6	Q9N1P4	Q9N1P4 cercopithec
6	75	83.3	334	6	Q9N1P3	Q9N1P3 hylobates l
7	75	83.3	334	6	Q9N1P2	Q9N1P2 saquinus oe
8	75	83.3	334	6	Q9N130	Q9N130 saimiri bol
9	75	83.3	346	6	Q9WZM4	Q9WZM4 nycticebus
10	75	83.3	346	6	Q9WZM3	Q9WZM3 nycticebus
11	75	83.3	346	6	Q9WZM2	Q9WZM2 nycticebus
12	75	83.3	347	6	Q9WZQ3	Q9WZQ3 pygathrix a
13	75	83.3	347	6	Q9WZQ2	Q9WZQ2 rhinopithec
14	75	83.3	347	6	Q9WZQ1	Q9WZQ1 pygathrix b
15	75	83.3	347	6	Q9WZQ0	Q9WZQ0 pygathrix n
16	75	83.3	347	6	Q9WZP9	Q9WZP9 nasalis lar
17	75	83.3	347	6	Q9WZP8	Q9WZP8 colobus pol
18	75	83.3	347	6	Q9WZP7	Q9WZP7 presbytis s
19	75	83.3	347	6	Q9WZP6	Q9WZP6 presbytis j

20	75	83.3	347	6	Q9MZP5	Q9MZP5 presbytis p
21	75	83.3	347	6	Q9MZP4	Q9MZP4 presbytis f
22	75	83.3	347	6	Q9MZP3	Q9MZP3 presbytis e
23	75	83.3	347	6	Q9MZP2	Q9MZP2 mandrillus
24	75	83.3	347	6	Q9MZP1	Q9MZP1 mandrillus
25	75	83.3	347	6	Q9MZP0	Q9MZP0 macaca assa
26	75	83.3	347	6	Q9MZN9	Q9MZN9 macaca thib
27	75	83.3	347	6	Q9MZN8	Q9MZN8 macaca arc
28	75	83.3	347	6	Q9MZN7	Q9MZN7 macaca neme
29	75	83.3	347	6	Q9MZN6	Q9MZN6 hylobates c
30	75	83.3	347	6	Q9MZN5	Q9MZN5 hylobates h
31	75	83.3	347	6	Q9MZN4	Q9MZN4 hylobates l
32	75	83.3	347	6	Q9MZN3	Q9MZN3 hylobates s
33	75	83.3	347	6	Q9MZN2	Q9MZN2 pongo pygma
34	75	83.3	347	6	Q9MZN1	Q9MZN1 gorilla gor
35	75	83.3	347	6	Q9MZN0	Q9MZN0 alouatta se
36	75	83.3	347	6	Q9MZN9	Q9MZN9 ateles pani
37	75	83.3	347	6	Q9MZN8	Q9MZN8 callithrix
38	75	83.3	347	6	Q9MZN6	Q9MZN6 callicebus
39	75	83.3	347	6	Q9MZN5	Q9MZN5 pithecia pi
40	75	83.3	347	6	Q9MZN1	Q9MZN1 eulemur mac
41	75	83.3	347	6	Q9MZN0	Q9MZN0 perodicticu
42	75	83.3	352	6	O77488	O77488 cercopithec
43	75	83.3	352	6	Q9TSQ8	Q9TSQ8 cercopithec
44	75	83.3	356	4	Q9UKN2	Q9UKN2 homo sapien
45	75	83.3	360	4	O60835	O60835 homo sapien

ALIGNMENTS

RESULT 1
Q9R1V0 PRELIMINARY; PRT; 367 AA.
ID Q9R1V0
AC Q9R1V0
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE CC-CHEMOKINE LARC SPECIFIC RECEPTOR.
GN MCCR6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Tanaka Y.;
RT "Molecular Cloning of Murine Homologue of CCR6, the Specific Receptor
for CC Chemokine LARC.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB016031; BAA82443.1;
DR INTERPRO: IPR000190;
DR INTERPRO: IPR000276;
DR INTERPRO: IPR000355;
DR PFAM: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCRHOPOPSN.
DR PRINTS: PR00635; ANGIOTENSINR.
DR PRINTS: PR00635; ANGIOTENSINR.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 367 AA; 42082 MW; 207FD98B2F7A6DD3 CRC64;

Query Match 92.2%; Score 83; DB 11; Length 367;
Best Local Similarity 88.9%; Pred. No. 2.2e-05;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPFWAVS 18
DB 80 MAITDILFVLTLPFWAVT 97

RESULT 2

O93247
ID O93247 PRELIMINARY; PRT; 353 AA.
AC O93247;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE CXCR4.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RA Fujiki K., Nakao M., Shin D., Yano T.;
RT "cDNA cloning of a carp homologue of mammalian CXCR4.";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AB012310; BAA32797.1; -;
DR INTERPRO; IPR000276; -;
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
SQ SEQUENCE 353 AA; 39633 MW; 84924BE413FB3B3F CRC64;

Query Match 86.7%; Score 78; DB 13; Length 353;
Best Local Similarity 82.4%; Pred. No. 0.00013;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAIADILFVLTLPFWAV 17
Db 78 LSIADLLFVLTLPFWAV 94

Query Match 86.7%; Score 78; DB 13; Length 353;
Best Local Similarity 82.4%; Pred. No. 0.00013;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MAIADILFVLTLPFWAV 17
Db 78 LSIADLLFVLTLPFWAV 94

RESULT 4
ID O42445 PRELIMINARY; PRT; 357 AA.
AC O42445;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE CXC CHEMOKINE RECEPTOR.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Daniels G.D., Charlemagne J., Secombes C.J.;
RT "Cloning and sequencing of a rainbow trout, Oncorhynchus mykiss, chemokine receptor homolog.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AJ001039; CAA04493.1; -;
DR INTERPRO; IPR000276; -;
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
SQ SEQUENCE 357 AA; 39817 MW; 14EC2F0DA1222C4 CRC64;

Query Match 85.6%; Score 77; DB 13; Length 357;
Best Local Similarity 76.5%; Pred. No. 0.00019;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MAIADILFVLTLPFWAV 17
Db 82 LSVADLLFVLTLPFWAV 98

RESULT 5
ID Q9N1P4 PRELIMINARY; PRT; 334 AA.
AC Q9N1P4;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CXC CHEMOKINE RECEPTOR 4 (FRAGMENT).
GN CXCR4.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RA Zubair S., Metzberg S.;
RT "CXCR4 homologs of Gibbon ape, African green monkey, and Cotton-top marmoset.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF178082; AAF42990.1; -;
KW Receptor.
FT NON_TER 1 1
FT NON_TER 334 334
SQ SEQUENCE 334 AA; 37752 MW; 8C91CED8AB54D131 CRC64;

Query Match 83.3%; Score 75; DB 6; Length 334;
Best Local Similarity 70.6%; Pred. No. 0.00037;

Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLFPWAV 17
:::|||||
Db 67 LSVADLLFVITLFPWAV 83

RESULT 6

Q9NIP3 ID Q9NIP3 PRELIMINARY; PRT; 334 AA.
AC Q9NIP3; 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DE CXCR4 RECEPTOR (FRAGMENT).
GN CXCR4.
OS Hylobates lar (Common gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=9580;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPHOSARCOMA;
RA Zubair S., Metzberg S.;
RT "CXCR4 homologs of Gibbon ape, African green monkey, and Cotton-top marmoset."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF178083; AAF42991.1; -
KW Receptor.
FT NON_TER 1 1
FT NON_TER 334 334
SQ SEQUENCE 334 AA; 37725 MW; C8813B0CB3CF9A61 CRC64;

Query Match 83.3%; Score 75; DB 6; Length 334;

Best Local Similarity 70.6%; Pred. No. 0.00037;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLFPWAV 17
:::|||||
Db 67 LSVADLLFVITLFPWAV 83

RESULT 7

Q9NIP2 ID Q9NIP2 PRELIMINARY; PRT; 334 AA.
AC Q9NIP2; 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DE CXCR4 RECEPTOR (FRAGMENT).
GN CXCR4.
OS Saguinus oedipus (Cotton-top tamarin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
OX NCBI_TaxID=9490;
RN [1]
RP SEQUENCE FROM N.A.
RA Zubair S., Metzberg S.;
RT "CXCR4 homologs of Gibbon ape, African green monkey, and Cotton-top marmoset."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF178084; AAF42992.1; -
KW Receptor.
FT NON_TER 1 1
FT NON_TER 334 334
SQ SEQUENCE 334 AA; 37877 MW; EB2362E88D0957C5 CRC64;

Query Match 83.3%; Score 75; DB 6; Length 334;

Best Local Similarity 70.6%; Pred. No. 0.00037;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLFPWAV 17
:::|||||
Db 67 LSVADLLFVITLFPWAV 83

RESULT 8

Q9N130 ID Q9N130 PRELIMINARY; PRT; 334 AA.
AC Q9N130; 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DE CXCR4 RECEPTOR (FRAGMENT).
GN CXCR4.
OS Saimiri boliviensis (Bolivian squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.
OX NCBI_TaxID=27679;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RA Zubair S., Metzberg S.;
RT "CXCR4 homologs of Gibbon ape, African green monkey, Cotton-top marmoset, and Bolivian squirrel monkey."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF229128; AAF37288.1; -
KW Receptor.
FT NON_TER 1 1
FT NON_TER 334 334
SQ SEQUENCE 334 AA; 37943 MW; 277227E898098DB5 CRC64;

Query Match 83.3%; Score 75; DB 6; Length 334;

Best Local Similarity 70.6%; Pred. No. 0.00037;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLFPWAV 17
:::|||||
Db 67 LSVADLLFVITLFPWAV 83

RESULT 9

Q9M2M4 ID Q9M2M4 PRELIMINARY; PRT; 346 AA.
AC Q9M2M4; 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DE CHEMOKINE RECEPTOR CXCR4 (FRAGMENT).
GN CXCR4.
OS Nycticebus coucang (Slow loris).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Loridae; Nycticebus.
OX NCBI_TaxID=9470;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
RT "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in Primates."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF172239; AAF89359.1; -
KW Receptor.
FT NON_TER 1 1
SQ SEQUENCE 346 AA; 39235 MW; BC1766D2E634CCEE CRC64;

Query Match 83.3%; Score 75; DB 6; Length 346;

Best Local Similarity 70.6%; Pred. No. 0.00038;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLFPWAV 17
:::|||||
Db 75 LSVADLLFVITLFPWAV 91

```
RESULT 10
Q9MZM3
ID Q9MZM3 PRELIMINARY; PRT; 346 AA.
AC Q9MZM3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE CHEMOKINE RECEPTOR CXCR4 (FRAGMENT).
GN CXCR4.
OS Nycticebus intermedius.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Loridae; Nycticebus.
OX NCBI_TaxID=101277;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
RT "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in
RT Primates.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF172240; AAF89360.1;
KW Receptor.
FT NON_TER
SQ SEQUENCE 346 AA; 39235 MW; BC1766D2E634CCEE CRC64;

Query Match 83.3%; Score 75; DB 6; Length 346;
Best Local Similarity 70.6%; Pred. No. 0.00038;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPFWAV 17
Db 75 LSVADLLFVITLPFWAV 91
:::|:|:|:|:|:|:|

RESULT 11
Q9MZM2
ID Q9MZM2 PRELIMINARY; PRT; 346 AA.
AC Q9MZM2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE CHEMOKINE RECEPTOR CXCR4 (FRAGMENT).
GN CXCR4.
OS Nycticebus pygmaeus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Loridae; Nycticebus.
OX NCBI_TaxID=101278;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
RT "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in
RT Primates.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF172241; AAF89361.1;
KW Receptor.
FT NON_TER
SQ SEQUENCE 346 AA; 39235 MW; BC1766D2E634CCEE CRC64;

Query Match 83.3%; Score 75; DB 6; Length 346;
Best Local Similarity 70.6%; Pred. No. 0.00038;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPFWAV 17
Db 75 LSVADLLFVITLPFWAV 91
:::|:|:|:|:|:|:|

RESULT 12
Q9MZQ3
ID Q9MZQ3 PRELIMINARY; PRT; 347 AA.
AC Q9MZQ3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE CHEMOKINE RECEPTOR CXCR4 (FRAGMENT).
GN CXCR4.
OS Pygathrix avunculus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=66062;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
RT "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in
RT Primates.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF172210; AAF89330.1;
KW Receptor.
FT NON_TER
SQ SEQUENCE 347 AA; 39205 MW; E96B66136541515C CRC64;

Query Match 83.3%; Score 75; DB 6; Length 347;
Best Local Similarity 70.6%; Pred. No. 0.00038;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPFWAV 17
Db 75 LSVADLLFVITLPFWAV 91
:::|:|:|:|:|:|:|

RESULT 13
Q9MZQ2
ID Q9MZQ2 PRELIMINARY; PRT; 347 AA.
AC Q9MZQ2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE CHEMOKINE RECEPTOR CXCR4 (FRAGMENT).
GN CXCR4.
OS Rhinopithecus roxellanae.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=101279;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
RT "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in
RT Primates.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF172211; AAF89331.1;
KW Receptor.
FT NON_TER
SQ SEQUENCE 347 AA; 39205 MW; E96B66136541515C CRC64;

Query Match 83.3%; Score 75; DB 6; Length 347;
Best Local Similarity 70.6%; Pred. No. 0.00038;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPFWAV 17
Db 75 LSVADLLFVITLPFWAV 91
:::|:~|:~|:~|:~|:~|

RESULT 14
Q9MZQ1
ID Q9MZQ1 PRELIMINARY; PRT; 347 AA.
AC Q9MZQ1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE CHEMOKINE RECEPTOR CXCR4 (FRAGMENT).
GN CXCR4.
OS Pygathrix avunculus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=66062;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
RT "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in
RT Primates.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF172211; AAF89331.1;
KW Receptor.
FT NON_TER
SQ SEQUENCE 347 AA; 39205 MW; E96B66136541515C CRC64;

Query Match 83.3%; Score 75; DB 6; Length 347;
Best Local Similarity 70.6%; Pred. No. 0.00038;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPFWAV 17
Db 75 LSVADLLFVITLPFWAV 91
:::~|:~|:~|:~|:~|
```

```
DE CHEMOKINE RECEPTOR CXCR4 (FRAGMENT).
GN CXCR4.
OS Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=61621;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
RT "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in
RT Primates.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF172212; AAF89332.1; -
KW Receptor.
FT NON_TER
SQ SEQUENCE 347 AA; 39205 MW; E96B66136541515C CRC64;

Query Match 83.3%; Score 75; DB 6; Length 347;
Best Local Similarity 70.6%; Pred. No. 0.00038;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAIADILFVLTLPFWAV 17
   :::::|||||
Db 75 LSVADLLFVLTLPFWAV 91

RESULT 15
Q9MZQ0 PRELIMINARY; PRT; 347 AA.
AC Q9MZQ0;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE CHEMOKINE RECEPTOR CXCR4 (FRAGMENT).
GN CXCR4.
OS Pygathrix nemaeus (Dove langur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=54133;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
RT "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in
RT Primates.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF172213; AAF89333.1; -
KW Receptor.
FT NON_TER
SQ SEQUENCE 347 AA; 39205 MW; E96B66136541515C CRC64;

Query Match 83.3%; Score 75; DB 6; Length 347;
Best Local Similarity 70.6%; Pred. No. 0.00038;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAIADILFVLTLPFWAV 17
   :::::|||||
Db 75 LSVADLLFVLTLPFWAV 91

Search completed: May 23, 2001, 15:35:12
Job time: 618 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:28:27 ; Search time 184.73 Seconds
(without alignments)
4.332 Million cell updates/sec

Title: US-08-887-977-10_COPY_97_110

Perfect score: 81

Sequence: 1 HATGAWVFSNATCK 14

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_0401.*
1: /SID56/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID56/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID56/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SID56/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SID56/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SID56/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SID56/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SID56/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SID56/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SID56/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SID56/gcgdata/geneseq/geneseq/AA1990.DAT.*
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13: /SID56/gcgdata/geneseq/geneseq/AA1992.DAT.*
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22: /SID56/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	81	100.0	365	19	Human dendritic ce
2	81	100.0	365	21	Primate (human) ch
3	49	60.5	1455	19	Fanconi anaemia of
4	47	58.0	360	16	Human monocyte che
5	47	58.0	360	18	Human monocyte che
6	47	58.0	374	16	Human monocyte che
7	45	55.6	415	21	Human G protein-co
8	45	55.6	415	21	Human mutant G pro
9	44.5	54.9	428	21	Human B5 receptor
10	44.5	54.9	430	21	Novel human G-prot
11	44.5	54.9	430	21	Human neuropeptide

12	44.5	54.9	432	21	Y93146	Novel rat G-protei
13	44.5	54.9	432	21	Y79373	Rat neurotrophin F
14	44.5	54.9	432	21	Y56886	Rat B5 receptor po
15	43	53.1	321	21	G31332	Arabidopsis thalia
16	43	53.1	342	21	G31331	Arabidopsis thalia
17	43	53.1	349	21	G31330	Arabidopsis thalia
18	43	53.1	354	19	W54037	Mouse CC-CRR5 prot
19	42	51.9	131	21	B24020	Arachidonic acid m
20	42	51.9	213	21	Y68859	A kappa3-related o
21	42	51.9	341	21	Y68861	A kappa3-related o
22	42	51.9	343	21	Y68856	A kappa3-related o
23	42	51.9	343	21	Y68860	A kappa3-related o
24	42	51.9	365	21	Y68862	A kappa3-related o
25	42	51.9	367	16	R74298	Mouse kappa-3 opio
26	42	51.9	367	16	R71968	Rat opioid recep
27	42	51.9	367	16	R67671	Mouse opioid recep
28	42	51.9	367	16	R76638	Rat opioid recep
29	42	51.9	367	21	B07868	A rat mu opioid re
30	42	51.9	370	21	Y55988	Variant orphan noc
31	42	51.9	663	21	B24019	Arachidonic acid m
32	41	50.6	310	21	G21034	Arabidopsis thalia
33	41	50.6	310	21	G50071	Arabidopsis thalia
34	41	50.6	324	21	G21033	Arabidopsis thalia
35	41	50.6	324	21	G50070	Arabidopsis thalia
36	41	50.6	368	21	G21032	Arabidopsis thalia
37	41	50.6	368	21	G50069	Arabidopsis thalia
38	41	50.6	2150	21	Y53898	Amino acid sequenc
39	40	49.4	66	21	B33299	Pinus radiata tran
40	40	49.4	263	17	W11236	G-protein conjugat
41	40	49.4	263	17	R91233	Rabbit G-protein c
42	40	49.4	362	20	Y06324	Mouse G-protein co
43	40	49.4	362	20	W92976	Rat mACHR-6 protei
44	40	49.4	369	17	W06125	Neurotrophin recep
45	40	49.4	370	20	W92977	Rat mACHR-6 protei

ALIGNMENTS

RESULT	1
W48086	W48086 standard; Protein; 365 AA.
ID	W48086
XX	
AC	W48086;
XX	
DT	11-JUN-1998 (first entry)
XX	
DE	Human dendritic cell chemokine receptor.
XX	
DE	Human; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta;
KW	receptor; dendritic cell; macrophage; inflammation; asthma.
XX	
OS	Homo sapiens.
XX	
EH	Key
FT	Misc-difference 193
FT	/note= "encoded by CAN"
XX	
PN	WO9801557-A2.
XX	
PD	15-JAN-1998.
XX	
PF	02-JUL-1997; 97WO-US10819.
XX	
PR	04-JUN-1997; 97US-0048593.
PR	05-JUL-1996; 96US-0675814.
PR	11-OCT-1996; 96US-0028329.
XX	
PA	(SCHE) SCHERING CORP.
XX	
PI	Gish KC, Schall TJ, Vicari A, Wang W, Zlotnik A;
XX	
DR	WPI; 1998-101054/09.

DR N-PSDB; V15418.
 XX Novel chemokines, e.g. thymus expressed chemokine - used for
 PT treating inflammatory conditions including asthma.
 XX
 XX Claim 3; Page 94-95; 202pp; English.
 XX
 CC The present sequence represents human dendritic cell chemokine receptor.
 CC Antibodies which bind to the protein can be used in detecting or
 CC diagnosing various immunological conditions related to expression
 CC of the protein. The nucleic acid can be used for screening and
 CC isolating DNA clones for the chemokines, especially from other
 CC species. The chemokine can be used in the treatment of conditions
 CC associated with abnormal physiology or development, including
 CC inflammatory conditions such as asthma.
 XX
 XX Sequence 365 AA;
 SQ

Query Match 100.0%; Score 81; DB 19; Length 365;
 Best Local Similarity 100.0%; Pred. No. 1.8e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HATGAWFSNATCK 14
 |||||
 Db 97 hatgawfsnatck 110

RESULT 2
 Y97077
 ID Y97077 standard; Protein; 365 AA.
 XX
 XX Y97077;
 AC
 XX
 XX
 DT 04-DEC-2000 (first entry)
 XX
 DE Primate (human) chemokine receptor CCR6.
 XX
 KW MIP-3-alpha; chemokine; CCR6 receptor; ligand; cytostatic; agonist;
 KW antagonist; anti-psoriatic; dermatological; immunosuppressive;
 KW anti-inflammatory.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 193 /note= "Encoded by CAN#"
 FT
 XX
 XX WO200046248-A1.
 XX
 XX 10-AUG-2000.
 PD
 XX
 XX 02-FEB-2000; 2000WO-US00511.
 PF
 XX
 XX 03-FEB-1999; 99US-0244281.
 PR
 XX
 XX (SCHE) SCHERING CORP.
 PA
 XX
 XX Oldham ER, Homey B, Dieu-Nosjean M, Caux C, Zlotnik A;
 PI
 XX
 XX WPI; 2000-543477/49.
 DR
 DR N-PSDB; A51971.
 XX
 PT Novel methods for modulating the migration of cells within or to the
 PT skin using MIP-3-alpha or CCR6 agonists or antagonists, useful for
 PT treating skin disorders, e.g. cancer
 XX
 XX Disclosure; Page 53-54; 61pp; English.
 PS
 XX
 XX The MIP-3-alpha chemokine is expressed in inflamed skin cells. This
 CC chemokine is the ligand for the CCR6 receptor. MIP-3-alpha or CCR6
 CC agonists or antagonists can be used to modulate the migration of a cell
 CC within or to the skin of a mammal. MIP-3-alpha can be used to purify a

CC population of cells expressing a MIP-3-alpha receptor. The methods are
 CC useful for treating a mammalian subject with a skin disease or condition,
 CC e.g. cancer, metastasis, psoriasis, atopic or contact dermatitis,
 CC systemic lupus erythematosus and lichen ruber planus, or for treating
 CC skin transplants or grafts.
 XX
 XX Sequence 365 AA;
 SQ

Query Match 100.0%; Score 81; DB 21; Length 365;
 Best Local Similarity 100.0%; Pred. No. 1.8e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HATGAWFSNATCK 14
 |||||
 Db 97 hatgawfsnatck 110

RESULT 3
 W48663
 ID W48663 standard; Protein; 1455 AA.
 XX
 XX W48663;
 AC
 XX
 XX 28-AUG-1998 (first entry)
 DT
 XX
 DE Fanconi anaemia of complementation group A protein.
 XX
 KW Fanconi anaemia of complementation group A; FA-A; genetic defect;
 KW prenatal FA-A; FA-A carrier detection; disease diagnosis.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO9814462-A1.
 PN
 XX
 XX 09-APR-1998.
 PD
 XX
 XX 03-OCT-1997; 97WO-US18010.
 PF
 XX
 XX 04-OCT-1996; 96US-0726012.
 PR
 XX
 XX (FANC-) FANCONI ANEMIA RES FUND INC.
 PA
 XX
 XX Joenje H, Lo Ten Foe JR;
 PI
 XX
 XX WPI; 1998-240012/21.
 DR
 DR N-PSDB; V18187.
 XX
 XX DNA for Fanconi Anaemia complementation group A - useful for, e.g.
 PT developing products for diagnosis and screening of disease and gene
 PT therapy
 PT
 XX
 XX Claim 1; Fig 3; 63pp; English.
 PS
 XX
 CC This sequence is the Fanconi anaemia of complementation group A
 CC (FA-A) protein of the invention. The DNA's may be used to complement a
 CC genetic defect in a cell (especially the FA-A gene). The products can be
 CC used for screening (especially prenatal FA-A), detection of FA-A carriers
 CC and FA-A disease diagnosis.
 CC
 XX
 XX Sequence 1455 AA;
 SQ

Query Match 60.5%; Score 49; DB 19; Length 1455;
 Best Local Similarity 53.8%; Pred. No. 12;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 HATGAWFSNATC 13
 |||
 Db 204 havgswifnrlcc 216

RESULT 4

R79166
ID -R79166 standard; Protein: 360 AA.
XX AC R79166;
XX
XX 29-DEC-1995 (first entry)
XX DT Human monocyte chemoattractant protein-1 receptor MCP-1RB.
XX DE Human monocyte chemoattractant protein-1 receptor; MCP-1R; chemokine.
XX KW Monocyte chemoattractant protein-1 receptor; MCP-1R; chemokine.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT 49..70
XX FT /label= transmembrane
XX FT 80..700
XX FT /label= transmembrane
XX FT 115..136
XX FT /label= transmembrane
XX FT 154..178
XX FT /label= transmembrane
XX FT 204..231
XX FT /label= transmembrane
XX FT 244..268
XX FT /label= transmembrane
XX FT 295..313
XX FT /label= transmembrane
XX FT 314..360
XX FT /label= carboxyl tail
XX FT 1..48
XX FT /label= extracellular
XX W09519436-A.
XX
XX 20-JUL-1995.
XX
XX 11-JAN-1995; 95WO-US00476.
XX
XX 13-JAN-1994; 94US-0182962.
XX
XX (REGC) UNIV CALIFORNIA.
XX Charo I., Coughlin S;
XX WPI: 1995-263866/34.
XX N-PSDB; Q96298.
XX
XX DNA encoding monocyte chemoattractant protein-1 receptor - used partic.
XX PT for identifying antagonists and for treating diseases characterised by
XX PT monocyte infiltrates
XX
XX Claim 2; Fig 2; 84pp; English.
XX
XX To identify and clone new members of the chemokine receptor gene
XX family, degenerate oligo primers were designed corresp. to the
XX conserved sequences R79167 in the second and R79168 in the third
XX transmembrane domains of the MIP-1alpha/RANTES receptor, the IL-8
XX receptors and the HUMSTRS orphan receptor (GenBank Accession #M99293.
XX The degenerate oligo incorporating EcoRI and XhoI sites at their 5'
XX ends are Q96299 and Q96300. Amplification of cDNA derived from MM6
XX cells with the primers yielded a number of PCR products. One cDNA
XX appeared to encode a novel protein. To obtain a full-length version
XX of this clone, a MM6 cDNA library was constructed in pFROG and probed
XX with the PCR product. A 2.1 kb cDNA clone was obt'd. Analysis of
XX additional clones in the MM6 cDNA library revealed a second
XX sequence that was identical to the 2.1 kb cDNA sequence first obt'd.
XX from the 5' UTR through the putative seventh transmembrane domain
XX but contained a different cytoplasmic tail. The second sequence
XX appears to represent alternative splicing of the carboxyl-terminal
XX tail of the MCP-1R protein. The two sequences are denoted MCP-1RA
XX and MCP-1RB (see Q96297/R79165 & Q96298/R79166). Active mature
XX MCP-1RA has a predicted mol. wt. of about 42,000 daltons. MCP-1RB

CC has a mol. wt. of about 41,000 daltons.
XX
XX Sequence 360 AA;
SQ
Query Match 58.0%; Score 47; DB 16; Length 360;
Best Local Similarity 61.5%; Pred. No. 5.9;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 ATGAWVFSNATCK 14
DB 102 aaewwvfgnamck 114
RESULT 5
W35833
ID W35833 standard; Protein: 360 AA.
XX
XX W35833;
XX
XX 27-FEB-1998 (first entry)
XX Human monocyte chemoattractant protein 1 receptor.
XX
XX Human; MCP-1; monocyte chemoattractant protein; receptor; tumour;
XX inflammatory disease; viral; allergy; diabetes.
XX
XX Homo sapiens.
XX
XX JP09238688-A.
XX
XX 16-SEP-1997.
XX
XX 11-MAR-1996; 96JP-0053574.
XX
XX 11-MAR-1996; 96JP-0053574.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX
XX WPI: 1997-506557/47.
XX N-PSDB; T96976.
XX
XX DNA encoding human monocyte chemoattractant protein 1 receptor -
XX used to treat tumours and inflammatory, viral, infectious, allergic,
XX diabetic and central nervous system diseases
XX
XX Disclosure; Page 12-14; 15pp; Japanese.
XX
XX The present sequence represents human monocyte chemoattractant protein 1
XX (MCP-1) receptor protein. The MCP-1 receptor protein and encoding DNA
XX are used for the prevention and treatment of tumours and inflammatory,
XX viral, infectious, allergic, diabetic and central nervous system
XX diseases.
XX
XX Sequence 360 AA;
SQ
Query Match 58.0%; Score 47; DB 18; Length 360;
Best Local Similarity 61.5%; Pred. No. 5.9;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 ATGAWVFSNATCK 14
DB 102 aaewwvfgnamck 114
RESULT 6
R79165
ID R79165 standard; Protein: 374 AA.
XX
XX R79165;
XX
XX 29-DEC-1995 (first entry)
DT

XX DE Human monocyte chemoattractant protein-1 receptor MCP-1RA.
 XX KW Monocyte chemoattractant protein-1 receptor; MCP-1R; chemokine.
 XX OS Homo sapiens.
 XX

Key Location/Qualifiers
 FH Domain 49..70
 FT /label= transmembrane
 FT Domain 80..700
 FT /label= transmembrane
 FT Domain 115..136
 FT /label= transmembrane
 FT Domain 154..178
 FT /label= transmembrane
 FT Domain 204..231
 FT /label= transmembrane
 FT Domain 244..268
 FT /label= transmembrane
 FT Domain 295..313
 FT /label= transmembrane
 FT Region 314..375
 FT /label= carboxyl tail
 FT Domain 1..48
 FT /label= extracellular

XX WO9519436-A.
 PN
 XX 20-JUL-1995.
 PD
 XX 11-JAN-1995; 95WO-US00476.
 XX
 PR 13-JAN-1994; 94US-0182962.
 XX

XX (REGC) UNIV CALIFORNIA.
 PA

XX Charo I, Coughlin S;
 XX

DR WPI: 1995-263866/34.
 DR N-PSDB; Q96297.
 XX

PT DNA encoding monocyte chemo-attractant protein-1 receptor - used partic.
 PT for identifying antagonists and for treating diseases characterised by
 PT monocytic infiltrates

PS Claim 2; Fig 1; 84pp; English.

XX To identify and clone new members of the chemokine receptor gene
 CC family, degenerate oligo primers were designed corresp. to the
 CC conserved sequences R79167 in the second and R79168 in the third
 CC transmembrane domains of the MIP-1alpha/RANTES receptor, the IL-8
 CC receptors and the HUMSTRS orphan receptor (GenBank Accession #M99293).
 CC The degenerate oligo incorporating EcoRI and XhoI sites at their 5',
 CC ends are Q96299 and Q96300. Amplification of cDNA derived from MM6
 CC cells with the primers yielded a number of PCR products. One cDNA
 CC appeared to encode a novel protein. To obtain a full-length version
 CC of this clone, a MM6 cDNA library was constructed in pPROG and probed
 CC with the PCR product. A 2.1 kb cDNA clone was obt'd. Analysis of
 CC additional clones in the MM6 cDNA library revealed a second
 CC sequence that was identical to the 2.1 kb cDNA sequence first obt'd.
 CC from the 5' UTR through the putative seventh transmembrane domain
 CC but contained a different cytoplasmic tail. The second sequence
 CC appears to represent alternative splicing of the carboxyl-terminal
 CC tail of the MCP-1R protein. The two sequences are denoted MCP-1RA
 CC and MCP-1RB (see Q96297/R79165 & Q96298/R79166). Active mature
 CC MCP-1RA has a predicted mol. wt. of about 42,000 daltons. MCP-1RB
 CC has a mol. wt. of about 41,000 daltons.

XX Sequence 374 AA;
 SQ

Query Match 58.0%; Score 47; DB 16; Length 374;

Best Local Similarity 61.5%; Pred. No. 6.1;
 Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ATGAWVFSNATCK 14
 | | | | | | | |
 Db 102 aanewfngnamck 114

RESULT 7

Y90634
 ID Y90634 standard; Protein; 415 AA.

XX AC Y90634;

XX DT 21-AUG-2000 (first entry)

XX DE Human G protein-coupled receptor GPR-NGA.

XX KW G protein-coupled receptor; GPCR; constitutively active;
 intracellular loop 3; transmembrane domain 6; drug screening;
 agonist; antagonist.

XX OS Homo sapiens.

XX PN WO200022129-A1.

XX PD 20-APR-2000.

XX PF 12-OCT-1999; 99WO-US23938.

XX PR 13-OCT-1998; 98US-0170496.

XX PA (AREN-) ARENA PHARM INC.

XX PI Behan DP, Chalmers DT, Liaw CW;

XX DR WPI: 2000-329165/28.

XX DR N-PSDB; A30649.

XX Non-endogenous constitutively activated human G protein-coupled
 PT receptors, useful for identifying agonists for use as pharmaceutical
 PT agents -

PS Example 1; Page 175-176; 341pp; English.

XX The invention relates to constitutively active, non-endogenous versions
 CC of endogenous human orphan G protein-coupled receptors (GPCRs, Y90643-
 CC Y90677 and Y90683-Y90687), and to DNA encoding them (A30709-A30743 and
 CC A30775-A30779). The mutant proteins of the invention contain a
 CC mutation in a portion of the protein comprising intracellular loop 3
 CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
 CC is substituted for an endogenous residue in IC3 at a position 16 amino
 CC acids N-terminal of an endogenous proline in TM6 to form a sequence
 CC X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or
 CC Ala, and is preferably Lys. When the endogenous residue at this position
 CC is Lys, this residue is replaced by His, Arg or preferably Ala. The 15
 CC amino acid stretch between the substituted amino acid and the Pro may be
 CC endogenous, non-endogenous, or a mixture of endogenous and non-endogenous
 CC residues. The constitutively active GPCRs are useful for identifying
 CC antagonists, agonists and partial agonists for use as pharmaceutical
 CC agents. The mutant proteins are also useful in research settings for
 CC elucidating the roles of the receptors in normal and diseased conditions.
 CC Antagonists for a particular GPCR are useful for treating diseases and
 CC disorders associated with that receptor. Because the novel mutant GPCRs
 CC are constitutively active, they can be used directly for screening of
 CC compounds without the need for endogenous ligands. The present
 CC sequence represents a human wild-type GPCR referred to in an
 CC exemplification of the invention.

XX Sequence 415 AA;
 SQ

Query Match 55.6%; Score 45; DB 21; Length 415;

Best Local Similarity 58.3%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 TGAWVFSNATCK 14
||| :||||
Db 128 tgrwtlgsatck 139

RESULT 8
Y90668
ID Y90668 standard; Protein; 415 AA.
XX
AC Y90668;
XX
XX 21-AUG-2000 (first entry)
XX
XX Human mutant G protein-coupled receptor GPR-NGA (I275K).
DE
XX G protein-coupled receptor; GPCR; constitutively active;
KW intracellular loop 3; transmembrane domain 6; drug screening;
KW agonist; antagonist; mutant; mutain.
XX
XX Homo sapiens.
OS Synthetic.
OS
XX WO200022129-A1.
XX
XX 20-APR-2000.
XX
XX 12-OCT-1999; 99WO-US23938.
XX
XX 13-OCT-1998; 98US-0170496.
XX
XX (AREN-) ARENA PHARM INC.
XX
XX Behan DP, Chalmers DT, Liaw CW;
PI
XX WPI; 2000-329165/28.
DR N-PSDB; A30734.
XX
XX Non-endogenous constitutively activated human G protein-coupled
PT receptors, useful for identifying agonists for use as pharmaceutical
PT agents
PT
XX
XX Example 2; Page 273-274; 34lpp; English.
XX
XX The invention relates to constitutively active, non-endogenous versions
CC of endogenous human orphan G protein-coupled receptors (GPCRs, Y90643-
CC Y90677 and Y90683-Y90687), and to DNA encoding them (A30709-A30743 and
CC A30775-A30779). The mutant proteins of the invention contain a
CC mutation in a portion of the protein comprising intracellular loop 3
CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
CC is substituted for an endogenous residue in IC3 at a position 16 amino
CC acids N-terminal of an endogenous proline in TM6 to form a sequence
CC X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or
CC Ala, and is preferably Lys. When the endogenous residue at this position
CC is Lys, this residue is replaced by His, Arg or preferably Ala. The 15
CC amino acid stretch between the substituted amino acid and the Pro may be
CC endogenous, non-endogenous, or a mixture of endogenous and non-endogenous
CC residues. The constitutively active GPCRs are useful for identifying
CC antagonists, agonists and partial agonists for use as pharmaceutical
CC agents. The mutant proteins are also useful in research settings for
CC elucidating the roles of the receptors in normal and diseased conditions.
CC Antagonists for a particular GPCR are useful for treating diseases and
CC disorders associated with that receptor. Because the novel mutant GPCRs
CC are constitutively active, they can be used directly for screening of
CC compounds without the need for endogenous ligands. Sequences Y90643-
CC Y90677 and Y90683-Y90687 the mutant human GPCRs of the invention.
XX
XX Sequence 415 AA;

Query Match 55.6%; Score 45; DB 21; Length 415;

Best Local Similarity 58.3%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 TGAWVFSNATCK 14
||| :||||
Db 128 tgrwtlgsatck 139

RESULT 9
Y56887
ID Y56887 standard; Protein; 428 AA.
XX
XX Y56887;
XX
XX 14-APR-2000 (first entry)
XX
XX Human B5 receptor polypeptide.
DE
XX G protein coupled receptor; B5 receptor; intracellular cell signaling;
KW human.
KW
XX Homo sapiens.
OS
XX CA2269192-A1.
PN
XX 16-OCT-1999.
PD
XX 16-APR-1999; 99CA-2269192.
PF
XX 16-APR-1998; 98US-0081995.
PR
XX (ALLX) ALLELIX BIOPHARMACEUTICALS INC.
PA
XX Zastawny RL, McWhinnie EA;
PI
XX WPI; 2000-127208/12.
DR N-PSDB; Z46951.
XX
XX New nucleic acids encoding rat and human G protein coupled receptors,
PT useful in drug screening assays -
PT
XX Claim 3; Fig 2; 60pp; English.
PS
XX The invention provides nucleic acids encoding rat and human G protein
CC coupled receptors, defined as the B5 receptors. The G protein coupled
CC receptors are involved in the intracellular cell signaling mechanism.
CC The B5 receptors are useful for screening candidate ligands which include
CC candidate drug compounds. Expression of the B5 receptor encoding DNA can
CC be used to produce fragments of the receptor in soluble form for
CC structure investigation and for raising antibodies for experimental uses.
CC The present sequence represents the human B5 receptor.
XX
XX Sequence 428 AA;

Query Match 54.9%; Score 44.5; DB 21; Length 428;
Best Local Similarity 75.0%; Pred. No. 18;
Matches 9; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 3 TGAWVFSNATCK 14
||| :||||
Db 105 tg-wpfdnatck 115

RESULT 10
Y93151
ID Y93151 standard; Protein; 430 AA.
XX
XX Y93151;
AC
XX 06-DEC-2000 (first entry)
DT
XX Novel human G-protein coupled receptor h07T022.

XX KW G-protein coupled receptor; human; bovine; nervous system disorder;
 XX rat; mouse; somatostatin excretion.
 XX OS Homo sapiens.
 XX PN WO200029441-A1.
 XX PD 25-MAY-2000.
 XX PF 11-NOV-1999; 99WO-JP06283.
 XX PR 13-NOV-1998; 98JP-0323759.
 XX PR 08-MAR-1999; 99JP-0060030.
 XX PR 14-APR-1999; 99JP-0106812.
 XX PR 14-JUN-1999; 99JP-0166672.
 XX PR 04-AUG-1999; 99JP-0221640.
 XX PR 14-SEP-1999; 99JP-0259818.
 XX PA (TAKE) TAKEDA CHEM IND LTD.
 XX PI Watanabe T, Kikuchi K, Terao Y, Shintani Y, Hinuma S, Fukusumi S;
 XX PI Fujii R, Hosoya M, Kitada C;
 XX PI WPI; 2000-387747/33.
 XX DR N-PSDB; A70507, A70508.
 XX PT G protein coupled receptor protein and antibodies to it for treatment
 XX and diagnosis of nerve diseases
 XX PS Disclosure; Page 178-180; 184pp; Japanese.
 XX CC The invention relates to the isolation of novel G-protein coupled
 CC receptor (GPCR) genes and their encoded proteins. This sequence
 CC represents the protein sequence of a human cPCR encoded by the clone
 CC h017702 which has 2 alleles (A70507 and A70508). The DNAs and proteins
 CC are used for the treatment, prevention and diagnosis of disorders of
 CC the nervous system. The proteins and its fragments are also promoters
 CC of somatostatin excretion.
 XX SQ Sequence 430 AA;

Query Match 54.9%; Score 44.5; DB 21; Length 430;
 Best Local Similarity 75.0%; Pred. No. 18;
 Matches 9; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 3 TCANVFSNATCK 14
 || | | |||||
 Db 107 tg-wpfdnatck 117

RESULT 11
 Y79376
 ID Y79376 standard; Protein: 430 AA.
 XX AC Y79376;
 XX DT 01-AUG-2000 (first entry)
 XX DE Human neuropeptide FF (NPFF1) receptor.
 XX KW Neuropeptide FF receptor; NPFF1 receptor; human; antiinflammatory;
 KW antidiabetic; antidiabetic; immunostimulant; immunosuppressive;
 KW nootropic; neuroprotective; analgesic; anorectic; antipsychotic;
 KW antidiabetic; antidiabetic; hypertensive; hypotensive; cardiant;
 KW antidiabetic; therapy; G protein coupled receptor.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Domain 42..68
 FT /note= "transmembrane domain I"

FT Domain 78..102
 FT /note= "transmembrane domain II"
 FT Domain 121..139
 FT /note= "transmembrane domain III"
 FT Domain 158..178
 FT /note= "transmembrane domain IV"
 FT Domain 217..240
 FT /note= "transmembrane domain V"
 FT Domain 268..293
 FT /note= "transmembrane domain VI"
 FT Domain 313..336
 FT /note= "transmembrane domain VII"
 XX WO200018438-A1.
 XX PN 06-APR-2000.
 XX PD 24-SEP-1999; 99WO-US22384.
 XX PF 25-SEP-1998; 98US-0161113.
 XX PR 22-FEB-1999; 99US-0255368.
 XX PA (SYNA-) SYNAPTIC PHARM CORP.
 XX PI Gerald CPG, Jones KA, Bonini JA, Borowsky B;
 XX PI WPI; 2000-293017/25.
 XX DR N-PSDB; 294668.
 XX PT Nucleic acid encoding a mammalian neuropeptide FF (NPFF) receptor,
 XX useful for treatment of e.g pain, obesity, diabetes, hypertension,
 XX hypotension, hypoglycemia, respiratory disorders
 XX Claim 17; Fig 13; 253pp; English.
 XX CC The present sequence is that of a human neuropeptide FF (NPFF1)
 CC receptor full-length polypeptide, as deduced from isolated
 CC cosmid cDNA (see 294668). Expression patterns suggest a modulatory
 CC role for NPFF1 in multiple systems within the central nervous system,
 CC and a role in sensory transmission, modulation of the limbic system,
 CC modulation of feeding/circadian rhythms, and modulation of
 CC extrapyramidal motor systems. High levels in the spinal cord and
 CC thalamus imply a role in sensory transmission or modulation
 CC (including nociception). Expression in the hippocampus and amygdala
 CC suggest involvement in modulation of learning and memory and a role
 CC in regulation of fear and mood. NPFF1 may provide a target for
 CC treatment of depression, anxiety, phobias, mood and movement
 CC disorders. The invention provides rat and human NPFF polypeptides
 CC and polynucleotides, vectors, host cells, antibodies, nucleic acid
 CC probes, antisense oligonucleotides, transgenic animals, methods
 CC of isolating mammalian NPFF receptors, methods of treating an
 CC abnormality associated with NPFF receptors, methods of determining
 CC determining binding of compounds to NPFF receptors, methods of
 CC identifying agonists and antagonists of NPFF receptors, and the
 CC agonists and antagonists obtained. Claimed methods of treating
 CC an abnormality that is alleviated by increasing/decreasing NPFF
 CC activity involve administering an NPFF receptor agonist/antagonist.
 CC The abnormality is a lower urinary tract disorder, an epinephrine
 CC release disorder, a gastrointestinal disorder, irritable bowel
 CC syndrome, a cardiovascular disorder, an electrolyte balance
 CC disorder, diuresis, hypertension, hypotension, diabetes,
 CC hypoglycemia, a respiratory disorder, asthma, a reproductive
 CC function disorder, an immune disorder, an endocrine disorder, a
 CC musculoskeletal disorder, a neuroendocrine disorder, a cognitive
 CC disorder, a memory disorder, a sensory modulation and
 CC transmission disorder, a motor coordination disorder, a sensory
 CC integration disorder, obesity, pain, psychotic behaviour,
 CC morphine tolerance, nicotine addiction, opiate addiction,
 CC affective disorder or migraine (all claimed).
 XX SQ Sequence 430 AA;

Query Match 54.9%; Score 44.5; DB 21; Length 430;
 Best Local Similarity 75.0%; Pred. No. 18;
 Matches 9; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 3 TGAWVFSNATCK 14
 II | | | | |
 Db 107 tg-wpfdnack 117

RESULT 12
 Y93146
 ID Y93146 standard; Protein; 432 AA.
 XX
 AC Y93146;
 XX
 XX 06-DEC-2000 (first entry)
 DT
 XX
 DE Novel rat G-protein coupled receptor #3.
 XX
 KW G-protein coupled receptor; human; bovine; nervous system disorder;
 KW rat; mouse; somatostatin excretion.
 XX
 XX Rattus sp.
 OS
 XX WO200029441-A1.
 PN
 XX
 XX 25-MAY-2000.
 PD
 XX
 PF 11-NOV-1999; 99WO-JP06283.
 XX
 PR 13-NOV-1998; 98JP-0323759.
 PR 08-MAR-1999; 99JP-0060030.
 PR 14-APR-1999; 99JP-0106812.
 PR 14-JUN-1999; 99JP-0166672.
 PR 04-AUG-1999; 99JP-0221640.
 PR 14-SEP-1999; 99JP-0259818.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Watanabe T, Kikuchi K, Terao Y, Shintani Y, Hinuma S, Fukusumi S;
 PI Fujii R, Hosoya M, Kitada C;
 XX
 XX WPI; 2000-387747/33.
 DR N-PSDB; A70506.
 XX
 XX G protein coupled receptor protein and antibodies to it for treatment
 PT and diagnosis of nerve diseases -
 XX
 XX Claim 23; Page 169-170; 184pp; Japanese.
 PS
 CC The invention relates to the isolation of novel G-protein coupled
 CC receptor (GPCR) genes and their encoded proteins. This sequence
 CC represents the protein sequence of a rat GPCR. The DNAs and proteins
 CC are used for the treatment, prevention and diagnosis of disorders of
 CC the nervous system. The proteins and its fragments are also promoters
 CC of somatostatin excretion.
 XX
 XX Sequence 432 AA;
 SQ

Query Match 54.9%; Score 44.5; DB 21; Length 432;
 Best Local Similarity 75.0%; Pred. No. 18;
 Matches 9; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 3 TGAWVFSNATCK 14
 II | | | | |
 Db 107 tg-wpfdnack 117

RESULT 13
 Y79373
 ID Y79373 standard; Protein; 432 AA.
 XX

AC Y79373;
 XX 01-AUG-2000 (first entry)
 DT
 XX Rat neurotrophin-4 (NPFFL) receptor.
 DE
 XX Neurotrophin-4 receptor; NPFFL receptor; rat; antiinflammatory;
 KW antiasthmatic; antidiabetic; immunostimulant; immunosuppressive;
 KW neurotrophic; neuroprotective; analgesic; anorectic; antipsychotic;
 KW antiaddictive; antimigraine; hypertensive; hypotensive; cardiatic;
 KW antiasthmatic; therapy; G protein coupled receptor.
 XX
 OS Rattus norvegicus.
 XX
 XX Key Location/Qualifiers
 PH Domain 42..69 /note= "transmembrane domain I"
 FT Domain 78..102 /note= "transmembrane domain II"
 FT Domain 121..139 /note= "transmembrane domain III"
 FT Domain 158..178 /note= "transmembrane domain IV"
 FT Domain 217..240 /note= "transmembrane domain V"
 FT Domain 270..295 /note= "transmembrane domain VI"
 FT Domain 313..338 /note= "transmembrane domain VII"
 FT Modified-site 10 /note= "N-glycosylated"
 FT Modified-site 18 /note= "N-glycosylated"
 FT Modified-site 113 /note= "N-glycosylated"
 FT Modified-site 195 /note= "N-glycosylated"
 FT Modified-site 154 /note= "O-phosphorylated"
 FT Modified-site 263 /note= "O-phosphorylated"
 FT Modified-site 264 /note= "O-phosphorylated"
 XX
 PN WO200018438-A1.
 XX
 XX 06-APR-2000.
 PD
 XX 24-SEP-1999; 99WO-US22384.
 PF
 XX 25-SEP-1998; 98US-0161113.
 PR 22-FEB-1999; 99US-0255368.
 XX
 PA (SYNA-) SYNAPTIC PHARM CORP.
 XX
 XX Gerald CPG, Jones KA, Bonini JA, Borowsky B;
 PI WPI; 2000-293017/25.
 XX N-PSDB; Z94665.
 DR
 XX Nucleic acid encoding a mammalian neurotrophin-4 (NPFFL) receptor,
 PT useful for treatment of e.g pain, obesity, diabetes, hypertension,
 PT hypotension, hypoglycemia, respiratory disorders -
 XX
 XX Claim 13; Fig 2; 253pp; English.
 PS
 XX The present sequence is that of rat neurotrophin-4 (NPFFL)
 CC receptor, as deduced from a cDNA clone (see Z94665) isolated
 CC from a rat hypothalamus cDNA library. Expression patterns suggest
 CC roles for NPFFL in neuroendocrine regulation, and in regulation of
 CC circadian rhythm, regulation of appetite and other functions
 CC modulated by the hypothalamus. A possible role in modulation of
 CC mood, fear, phobia and anxiety is also suggested, and NPFFL may

CC provide a target for treatment of depression and other
 CC neuropsychiatric disorders. NPFF1 may also play a role in endocrine
 CC regulation and reproductive function. The invention provides rat
 CC and human NPFF polypeptides and polynucleotides, vectors, host
 CC cells, antibodies, nucleic acid probes, antisense oligonucleotides,
 CC transgenic animals, methods of isolating mammalian NPFF receptors,
 CC methods of treating an abnormality associated with NPFF receptor
 CC activity, methods of determining binding of compounds to NPFF
 CC receptors, methods of identifying agonists and antagonists of NPFF
 CC receptors, and the agonists and antagonists obtained. Claimed
 CC methods of treating an abnormality that is alleviated by
 CC increasing/decreasing NPFF activity involve administering an NPFF
 CC receptor agonist/antagonist. The abnormality is a lower urinary
 CC tract disorder, an epinephrine release disorder, a gastrointestinal
 CC disorder, irritable bowel syndrome, a cardiovascular disorder, an
 CC electrolyte balance disorder, diuresis, hypertension, hypotension,
 CC diabetes, hypoglycemia, a respiratory disorder, asthma, a
 CC reproductive function disorder, an immune disorder, an endocrine
 CC disorder, a musculoskeletal disorder, a neuroendocrine disorder, a
 CC cognitive disorder, a memory disorder, a sensory modulation and
 CC transmission disorder, a motor coordination disorder, a sensory
 CC integration disorder, obesity, pain, psychotic behaviour,
 CC morphine tolerance, nicotine addiction, opiate addiction,
 CC affective disorder or migraine (all claimed).

XX
 SQ Sequence 432 AA;

Query Match 54.9%; Score 44.5; DB 21; Length 432;
 Best Local Similarity 75.0%; Pred. No. 18;
 Matches 9; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 3 TGAWVFSNATCK 14
 || | | | | | | |
 Db 107 tg-wpfdnatck 117

RESULT 14

Y56886
 ID Y56886 standard; Protein; 432 AA.

XX
 AC Y56886;

XX 14-APR-2000 (first entry)

XX Rat B5 receptor polypeptide.

XX G protein coupled receptor; B5 receptor; intracellular cell signaling;
 KW rat.

XX Rattus sp.

XX CA2269192-A1.

XX 16-OCT-1999.

XX 16-APR-1999; 99CA-2269192.

XX 16-APR-1998; 98US-0081995.

XX (ALIX) ALLELIX BIOPHARMACEUTICALS INC.

XX Zastawny RL, McWhinnie EA;

XX WPI; 2000-127208/12.

XX N-PSDB; 246950.

XX New nucleic acids encoding rat and human G protein coupled receptors,
 PT useful in drug screening assays

XX Claim 1; Fig 1; 60pp; English.

XX The invention provides nucleic acids encoding rat and human G protein

CC coupled receptors, defined as the B5 receptors. The G protein coupled
 CC receptors are involved in the intracellular cell signaling mechanism.
 CC The B5 receptors are useful for screening candidate ligands which include
 CC candidate drug compounds. Expression of the B5 receptor encoding DNA can
 CC be used to produce fragments of the receptor in soluble form for
 CC structure investigation and for raising antibodies for experimental uses.
 CC The present sequence represents the rat B5 receptor.

XX
 SQ Sequence 432 AA;

Query Match 54.9%; Score 44.5; DB 21; Length 432;
 Best Local Similarity 75.0%; Pred. No. 18;
 Matches 9; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 3 TGAWVFSNATCK 14
 || | | | | | | |
 Db 107 tg-wpfdnatck 117

RESULT 15

G31332
 ID G31332 standard; Protein; 321 AA.

XX
 AC G31332;

XX 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 37610.

XX Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

XX 09-MAR-1999; 99US-0123548.

XX 23-MAR-1999; 99US-0125788.

XX 25-MAR-1999; 99US-0126284.

XX 29-MAR-1999; 99US-0126785.

XX 01-APR-1999; 99US-0127462.

XX 06-APR-1999; 99US-0128234.

XX 08-APR-1999; 99US-0128714.

XX 16-APR-1999; 99US-0129845.

XX 19-APR-1999; 99US-0130077.

XX 21-APR-1999; 99US-0130449.

XX 23-APR-1999; 99US-0130510.

XX 28-APR-1999; 99US-0130891.

XX 30-APR-1999; 99US-0131449.

XX 30-APR-1999; 99US-0132048.

XX 04-MAY-1999; 99US-0132407.

XX 05-MAY-1999; 99US-0132485.

XX 06-MAY-1999; 99US-0132486.

XX 07-MAY-1999; 99US-0132487.

XX 07-MAY-1999; 99US-0132863.

XX 11-MAY-1999; 99US-0134256.

XX 14-MAY-1999; 99US-0134218.

XX 14-MAY-1999; 99US-0134219.

XX 14-MAY-1999; 99US-0134221.

XX 14-MAY-1999; 99US-0134370.

XX 18-MAY-1999; 99US-0134768.

XX 19-MAY-1999; 99US-0134941.

XX 20-MAY-1999; 99US-0135124.

XX 21-MAY-1999; 99US-0135353.

PR	24-MAY-1999;	99US-0135629.	PR	02-AUG-1999;	99US-0146389.
PR	25-MAY-1999;	99US-0136021.	PR	03-AUG-1999;	99US-0147038.
PR	27-MAY-1999;	99US-0136392.	PR	04-AUG-1999;	99US-0147204.
PR	28-MAY-1999;	99US-0136782.	PR	04-AUG-1999;	99US-0147302.
PR	01-JUN-1999;	99US-0137222.	PR	05-AUG-1999;	99US-0147192.
PR	03-JUN-1999;	99US-0137528.	PR	05-AUG-1999;	99US-0147260.
PR	04-JUN-1999;	99US-0137502.	PR	06-AUG-1999;	99US-0147303.
PR	07-JUN-1999;	99US-0137724.	PR	06-AUG-1999;	99US-0147416.
PR	08-JUN-1999;	99US-0138094.	PR	09-AUG-1999;	99US-0147493.
PR	10-JUN-1999;	99US-0138540.	PR	09-AUG-1999;	99US-0147935.
PR	10-JUN-1999;	99US-0138847.	PR	10-AUG-1999;	99US-0148171.
PR	14-JUN-1999;	99US-0139119.	PR	11-AUG-1999;	99US-0148319.
PR	16-JUN-1999;	99US-0139452.	PR	12-AUG-1999;	99US-0148341.
PR	16-JUN-1999;	99US-0139453.	PR	13-AUG-1999;	99US-0148565.
PR	17-JUN-1999;	99US-0139492.	PR	13-AUG-1999;	99US-0148684.
PR	18-JUN-1999;	99US-0139454.	PR	16-AUG-1999;	99US-0149368.
PR	18-JUN-1999;	99US-0139455.	PR	17-AUG-1999;	99US-0149175.
PR	18-JUN-1999;	99US-0139456.	PR	18-AUG-1999;	99US-0149426.
PR	18-JUN-1999;	99US-0139457.	PR	20-AUG-1999;	99US-0149722.
PR	18-JUN-1999;	99US-0139463.	PR	20-AUG-1999;	99US-0149723.
PR	18-JUN-1999;	99US-0139458.	PR	20-AUG-1999;	99US-0149929.
PR	18-JUN-1999;	99US-0139459.	PR	23-AUG-1999;	99US-0149902.
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PR	18-JUN-1999;	99US-0139461.	PR	25-AUG-1999;	99US-0150566.
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PR	18-JUN-1999;	99US-0139763.	PR	27-AUG-1999;	99US-0151066.
PR	21-JUN-1999;	99US-0139817.	PR	27-AUG-1999;	99US-0151080.
PR	22-JUN-1999;	99US-0139899.	PR	30-AUG-1999;	99US-0151303.
PR	23-JUN-1999;	99US-0140353.	PR	31-AUG-1999;	99US-0151438.
PR	23-JUN-1999;	99US-0140354.	PR	01-SEP-1999;	99US-0151930.
PR	24-JUN-1999;	99US-0140695.	PR	07-SEP-1999;	99US-0152363.
PR	28-JUN-1999;	99US-0140823.	PR	10-SEP-1999;	99US-0153070.
PR	29-JUN-1999;	99US-0140981.	PR	13-SEP-1999;	99US-0153758.
PR	30-JUN-1999;	99US-0141287.	PR	15-SEP-1999;	99US-0154018.
PR	01-JUL-1999;	99US-0141842.	PR	16-SEP-1999;	99US-0154039.
PR	01-JUL-1999;	99US-0142154.	PR	20-SEP-1999;	99US-0154779.
PR	02-JUL-1999;	99US-0142055.	PR	22-SEP-1999;	99US-0155139.
PR	06-JUL-1999;	99US-0142390.	PR	23-SEP-1999;	99US-0155486.
PR	08-JUL-1999;	99US-0142803.	PR	24-SEP-1999;	99US-0155659.
PR	09-JUL-1999;	99US-0142920.	PR	28-SEP-1999;	99US-0156458.
PR	12-JUL-1999;	99US-0142977.	PR	29-SEP-1999;	99US-0156596.
PR	13-JUL-1999;	99US-0143542.	PR	04-OCT-1999;	99US-0157117.
PR	14-JUL-1999;	99US-0143624.	PR	05-OCT-1999;	99US-0157753.
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PR	19-JUL-1999;	99US-0144325.	PR	12-OCT-1999;	99US-0158369.
PR	19-JUL-1999;	99US-0144331.	PR	13-OCT-1999;	99US-0159293.
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PR	20-JUL-1999;	99US-0144632.	PR	14-OCT-1999;	99US-0159637.
PR	20-JUL-1999;	99US-0144884.	PR	14-OCT-1999;	99US-0159638.
PR	21-JUL-1999;	99US-0144814.	PR	18-OCT-1999;	99US-0159584.
PR	21-JUL-1999;	99US-0145086.	PR	21-OCT-1999;	99US-0160741.
PR	21-JUL-1999;	99US-0145088.	PR	21-OCT-1999;	99US-0160767.
PR	22-JUL-1999;	99US-0145085.	PR	21-OCT-1999;	99US-0160768.
PR	22-JUL-1999;	99US-0145087.	PR	21-OCT-1999;	99US-0160770.
PR	22-JUL-1999;	99US-0145089.	PR	21-OCT-1999;	99US-0160814.
PR	22-JUL-1999;	99US-0145192.	PR	21-OCT-1999;	99US-0160815.
PR	23-JUL-1999;	99US-0145145.	PR	22-OCT-1999;	99US-0160980.
PR	23-JUL-1999;	99US-0145218.	PR	22-OCT-1999;	99US-0160981.
PR	23-JUL-1999;	99US-0145224.	PR	22-OCT-1999;	99US-0160989.
PR	26-JUL-1999;	99US-0145276.	PR	25-OCT-1999;	99US-0161404.
PR	27-JUL-1999;	99US-0145913.	PR	25-OCT-1999;	99US-0161405.
PR	27-JUL-1999;	99US-0145918.	PR	25-OCT-1999;	99US-0161406.
PR	27-JUL-1999;	99US-0145919.	PR	26-OCT-1999;	99US-0161359.
PR	28-JUL-1999;	99US-0145951.	PR	26-OCT-1999;	99US-0161360.
PR	02-AUG-1999;	99US-0146386.	PR	26-OCT-1999;	99US-0161361.
PR	02-AUG-1999;	99US-0146388.	PR	28-OCT-1999;	99US-0161920.

PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 53.1%; Score 43; DB 21; Length 321;
 Best Local Similarity 46.2%; Pred. No. 23;
 Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 HATGAWVFSNATC 13
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 Db 205 hcidtwllsnstc 217

Search completed: May 23, 2001, 15:28:28
 Job time: 405 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:30:05 ; Search time 95.91 Seconds
(without alignments)
2.804 Million cell updates/sec

Title: US-08-887-977-10_COPY_97_l10
Perfect score: 81
Sequence: 1 HATGAWFVNATC 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	47	58.0	347	1	US-08-461-244-3
4	47	58.0	360	1	US-08-450-393A-4
5	47	58.0	360	4	US-08-446-669-4
6	47	58.0	360	5	PCT-US95-00476-4
7	47	58.0	374	1	US-08-450-393A-2
8	47	58.0	374	5	PCT-US95-00476-2
9	47	58.0	374	5	US-08-446-669-2
10	47	51.9	367	2	US-08-147-949A-2
11	42	51.9	367	2	US-08-454-549-2
12	42	51.9	367	3	US-08-454-552-2
13	42	51.9	367	3	US-08-676-351-2
14	42	51.9	367	3	US-08-147-592A-6
15	42	51.9	367	3	US-08-889-108-17
16	42	51.9	367	5	PCT-US94-10358-17
17	40	49.4	263	4	US-08-513-974B-54
18	40	49.4	263	4	US-08-513-974B-376
19	40	49.4	362	2	US-08-985-090-5
20	40	49.4	362	3	US-09-165-543-32
21	40	49.4	369	5	PCT-US95-05616-4
22	40	49.4	371	1	US-08-415-818-6
23	40	49.4	371	2	US-08-894-236-6
24	40	49.4	371	2	US-08-919-624-4
25	40	49.4	371	5	PCT-US96-01444-6
26	40	49.4	377	5	PCT-US95-05616-6
27	40	49.4	389	2	US-08-846-705-2

28	40	49.4	402	3	US-08-846-704-4	Sequence 4, Appli
29	40	49.4	402	5	PCT-US95-05616-2	Sequence 2, Appli
30	40	49.4	425	3	US-08-846-704-2	Sequence 2, Appli
31	40	49.4	445	2	US-08-985-090-2	Sequence 2, Appli
32	40	49.4	445	3	US-09-165-543-2	Sequence 2, Appli
33	40	49.4	445	3	US-09-165-543-5	Sequence 5, Appli
34	40	49.4	445	4	US-09-167-354-7	Sequence 7, Appli
35	39	48.1	257	1	US-07-828-790B-2	Sequence 2, Appli
36	39	48.1	355	1	US-08-012-988A-2	Sequence 2, Appli
37	39	48.1	355	1	US-08-450-393A-5	Sequence 5, Appli
38	39	48.1	355	4	US-08-446-669-5	Sequence 5, Appli
39	39	48.1	355	5	PCT-US95-00476-5	Sequence 5, Appli
40	38	46.9	269	1	US-08-307-499-30	Sequence 30, Appli
41	38	46.9	373	2	US-08-559-524A-4	Sequence 4, Appli
42	38	46.9	373	3	US-08-749-707-4	Sequence 4, Appli
43	38	46.9	383	3	US-09-045-186-2	Sequence 2, Appli
44	38	46.9	384	1	US-08-232-144-4	Sequence 4, Appli
45	38	46.9	384	2	US-08-555-268A-15	Sequence 15, Appli

ALIGNMENTS

RESULT 1
US-08-726-012B-2
; Sequence 2, Application US/08726012B
; Patent No. 5952190
; GENERAL INFORMATION:
; APPLICANT: Hans Joenje, et al.
; TITLE OF INVENTION: CDNA FOR FANCONI ANEMIA COMPLEMENTATION GROUP A
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh & Whinston, LLP
; STREET: One World Trade Center, Suite 1600, 121 S.W. Salmon Street
; CITY: Portland
; STATE: OR
; COUNTRY: USA
; ZIP: 97204-2988
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3.5-inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: WordPerfect 5.1+, ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726,012B
; FILING DATE: 10/04/96
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard J. Polley
; REGISTRATION NUMBER: 28,107
; REFERENCE/DOCKET NUMBER: 3812-45520/RJP/DJE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1455
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: Linear
US-08-726-012B-2

Query Match 60.5%; Score 49; DB 2; Length 1455;
Best Local Similarity 53.8%; Pred. No. 5.5;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Qy: 1 HATGAWFVNATC 13
Db 204 HAVGSWLFNLC 216

RESULT 2
US-08-466-343D-9
; Sequence 9, Application US/08466343D
; Patent No. 6025154
; GENERAL INFORMATION:
; APPLICANT: LI, YI
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,343D
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-466-343D-9

Query Match 58.0%; Score 47; DB 3; Length 344;
Best Local Similarity 61.5%; Pred. No. 2.6;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATGAWVFSNATCK 14
| | | | |
DB 85 AANEWVFGNAMCK 97

RESULT 3
US-08-461-244-3
; Sequence 3, Application US/08461244
; Patent No. 5776729
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R.
; APPLICANT: Yi, Li
; APPLICANT: Ruben, Steven M.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBR32
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; ADDRESSEE: STUART & OLSTEIN
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,244
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-445
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 347 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-461-244-3

Query Match 58.0%; Score 47; DB 1; Length 347;
Best Local Similarity 61.5%; Pred. No. 2.6;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATGAWVFSNATCK 14
| | | | |
DB 89 AANEWVFGNAMCK 101

RESULT 4
US-08-450-393A-4
; Sequence 4, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/020US
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816CooleyPA
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-450-393A-4

Query Match 58.0%; Score 47; DB 1; Length 360;
Best Local Similarity 61.5%; Pred. No. 2.7;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATGAWVFSNATCK 14
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Db 102 AANEWVFGNAMCK 114

RESULT 5

US-08-446-669-4
; Sequence 4, Application US/08446669
; Patent No. 6132987
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446.669
; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Neeley, Richard
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-237/0105
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; TELEX: 380816COOLEYPA
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-446-669-4

Query Match 58.0%; Score 47; DB 4; Length 360;
Best Local Similarity 61.5%; Pred. No. 2.7;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATGAWVFSNATCK 14
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Db 102 AANEWVFGNAMCK 114

RESULT 6

PCT-US95-00476-4
; Sequence 4, Application PC/TUS9500476
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 N. Figueroa Street, 5th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012-2628
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00476
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berliner, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-977-1001
; TELEFAX: 310-977-1003
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-00476-4

Query Match 58.0%; Score 47; DB 5; Length 360;
Best Local Similarity 61.5%; Pred. No. 2.7;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATGAWVFSNATCK 14
| ||| || ||
Db 102 AANEWVFGNAMCK 114

RESULT 7

US-08-450-393A-2
; Sequence 2, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cseiff, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/0205
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-843-5165
 TELEFAX: 415-8857-0663
 TELEX: 380816CoolleyPA
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 374 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-450-393A-2

Query Match 58.0%; Score 47; DB 1; Length 374;
 Best Local Similarity 61.5%; Pred. No. 2.8;
 Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATGAWFVSNAACK 14
 | ||| || ||
 Db 102 AANEWVFGNAMCK 114

RESULT 8

US-08-446-669-2

; Sequence 2, Application US/08446669
 ; Patent No. 6132987
 ; GENERAL INFORMATION:
 ; APPLICANT: Charo, Israel
 ; APPLICANT: Coughlin, Shaun
 ; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
 ; STREET: 5 Palo Alto Square
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94306-2155

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/446.669
 ; FILING DATE: May 25, 1995
 ; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:
 ; NAME: Neeley, Richard
 ; REGISTRATION NUMBER: 30,092
 ; REFERENCE/DOCKET NUMBER: UCAL-237/0105
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-843-5000
 ; TELEFAX: 415-857-0663
 ; TELEX: 380816CoolleyPA

; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 374 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-446-669-2

Query Match 58.0%; Score 47; DB 4; Length 374;
 Best Local Similarity 61.5%; Pred. No. 2.8;
 Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATGAWFVSNAACK 14
 | ||| || ||
 Db 102 AANEWVFGNAMCK 114

RESULT 9

PCT-US95-00476-2
 ; Sequence 2, Application PC/TUS9500476
 ; GENERAL INFORMATION:
 ; APPLICANT: The Regents of the University of California
 ; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Robbins, Berliner & Carson
 ; STREET: 201 N. Figueroa Street, 5th Floor
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 90012-2628

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/00476
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Berliner, Robert
 ; REGISTRATION NUMBER: 20,121
 ; REFERENCE/DOCKET NUMBER: 5555-291

; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 310-977-1001
 ; TELEFAX: 310-977-1003
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 374 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; PCT-US95-00476-2

Query Match 58.0%; Score 47; DB 5; Length 374;
 Best Local Similarity 61.5%; Pred. No. 2.8;
 Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATGAWFVSNAACK 14
 | ||| || ||
 Db 102 AANEWVFGNAMCK 114

RESULT 10

US-08-147-949A-2
 ; Sequence 2, Application US/08147949A
 ; Patent No. 5747279
 ; GENERAL INFORMATION:
 ; APPLICANT: Pasternak, Gavrill W.
 ; APPLICANT: Pan, Ying-Xian

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
 ; TITLE OF INVENTION: KAPPA3 OPIOID RECEPTORS, RECEPTORS
 ; TITLE OF INVENTION: ENCODED THEREBY, AND USES THEREOF
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper & Dunham
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.30

;; CURRENT APPLICATION DATA:
 ;; APPLICATION NUMBER: US/08/147,949A
 ;; FILING DATE: 05-NOV-1993
 ;; ATTORNEY/AGENT INFORMATION:
 ;; NAME: White, John P.
 ;; REGISTRATION NUMBER: 28,678
 ;; REFERENCE/DOCKET NUMBER: 44782/JPW/JKM
 ;; TELECOMMUNICATION INFORMATION:
 ;; TELEPHONE: (212) 278-0400
 ;; TELEFAX: (212) 391-0525
 ;; TELEX: 422523 COOP UI
 ;; INFORMATION FOR SEQ ID NO: 2:
 ;; SEQUENCE CHARACTERISTICS:
 ;; LENGTH: 367 amino acids
 ;; TYPE: amino acid
 ;; TOPOLOGY: linear
 ;; MOLECULE TYPE: protein
 ;; US-08-147-949A-2

Query Match 51.9%; Score 42; DB 1; Length 367;
 Best Local Similarity 63.6%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GAWVFSNATCK 14
 | | | | |
 Db 111 GFWPFGNALCK 121

RESULT 11
 US-08-454-549-2
 ; Sequence 2, Application US/08454549
 ; Patent No. 5866324
 ; GENERAL INFORMATION:
 ; APPLICANT: EPPLE, C. Mark
 ; APPLICANT: OZENBERGER, Bradley A.
 ; APPLICANT: HULMES, Jeffrey D.
 ; TITLE OF INVENTION: CDNA'S ENCODING PROTEINS CLOSELY RELATED
 ; TITLE OF INVENTION: TO OPIOID RECEPTORS
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Darby & Darby, P.C.
 ; STREET: 805 Third Avenue
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10022
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/454,549
 ; FILING DATE: 30-MAY-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Robinson, Joseph R.
 ; REGISTRATION NUMBER: 33,448
 ; REFERENCE/DOCKET NUMBER: 0646/1A818-US5
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 527-7700
 ; TELEFAX: (212) 753-6237
 ; TELEX: 236687
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 367 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: not relevant
 ; MOLECULE TYPE: protein
 ; ORIGINAL SOURCE:
 ; ORGANISM: Rat

US-08-454-549-2

Query Match 51.9%; Score 42; DB 2; Length 367;
 Best Local Similarity 63.6%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GAWVFSNATCK 14
 | | | | |
 Db 111 GFWPFGNALCK 121

RESULT 12
 US-08-454-552-2
 ; Sequence 2, Application US/08454552
 ; Patent No. 6005072
 ; GENERAL INFORMATION:
 ; APPLICANT: EPPLE, C. Mark
 ; APPLICANT: OZENBERGER, Bradley A.
 ; APPLICANT: HULMES, Jeffrey D.
 ; TITLE OF INVENTION: CDNA'S ENCODING PROTEINS CLOSELY RELATED
 ; TITLE OF INVENTION: TO OPIOID RECEPTORS
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Darby & Darby, P.C.
 ; STREET: 805 Third Avenue
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10022
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/454,552
 ; FILING DATE: 30-MAY-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Robinson, Joseph R.
 ; REGISTRATION NUMBER: 33,448
 ; REFERENCE/DOCKET NUMBER: 0646/1A818-US4
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 527-7700
 ; TELEFAX: (212) 753-6237
 ; TELEX: 236687
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 367 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: not relevant
 ; MOLECULE TYPE: protein
 ; ORIGINAL SOURCE:
 ; ORGANISM: Rat
 ; US-08-454-552-2

Query Match 51.9%; Score 42; DB 3; Length 367;
 Best Local Similarity 63.6%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GAWVFSNATCK 14
 | | | | |
 Db 111 GFWPFGNALCK 121

RESULT 13
 US-08-676-351-2
 ; Sequence 2, Application US/08676351C
 ; Patent No. 6046026
 ; GENERAL INFORMATION:

```
; APPLICANT: EPPLER, CECIL
; APPLICANT: OZENBERGER, BRADLEY
; APPLICANT: HULMES, JEFFREY
; TITLE OF INVENTION: CDNAS ENCODING PROTEINS CLOSELY RELATED
; TITLE OF INVENTION: TO OPIOID RECEPTORS
; FILE REFERENCE: 0646/1A818US1
; CURRENT APPLICATION NUMBER: US/08/676,351C
; CURRENT FILING DATE: 1996-09-12
; EARLIER APPLICATION NUMBER: PCT/US95/00939
; EARLIER FILING DATE: 1995-01-20
; EARLIER APPLICATION NUMBER: US 08/185,360
; EARLIER FILING DATE: 1994-01-21
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Rat
US-08-676-351-2

Query Match          51.9%; Score 42; DB 3; Length 367;
Best Local Similarity 63.6%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 4; Indels 4; Gaps 0;

QY      4 GAWVFSNATCK 14
      | | | | |
Db      111 GFWPFGNALCK 121

RESULT 14
US-08-147-592A-6
; Sequence 6, Application US/08147592A
; Patent No. 6096513
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I
; APPLICANT: Reisine, Terry
; APPLICANT: Yasuda, Kazuki
; TITLE OF INVENTION: Opioid Receptor Genes,
; TITLE OF INVENTION: Compositions and Methods
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,592A
; FILING DATE: 05-NOV-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/100,694
; FILING DATE: 30-JUL-1993
; CLASSIFICATION: 435
; APPLICATION NUMBER: 08/066,296
; FILING DATE: 20-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:105
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; N/A
; INFORMATION FOR SEQ ID NO: 6:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 367 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-147-592A-6

Query Match          51.9%; Score 42; DB 3; Length 367;
Best Local Similarity 63.6%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 4; Indels 4; Gaps 0;

QY      4 GAWVFSNATCK 14
      | | | | |
Db      111 GFWPFGNALCK 121

RESULT 15
US-08-889-108-17
; Sequence 17, Application US/08889108
; Patent No. 6103492
; GENERAL INFORMATION:
; APPLICANT: Yu, Lei
; TITLE OF INVENTION: Mu Opioid Receptors: Compositions and Methods
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/889,108
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/305,518
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: INDA005\WIM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 367 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-889-108-17

Query Match          51.9%; Score 42; DB 3; Length 367;
Best Local Similarity 63.6%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 4; Indels 4; Gaps 0;

QY      4 GAWVFSNATCK 14
      | | | | |
Db      111 GFWPFGNALCK 121

Search completed: May 23, 2001, 15:30:06
Job time: 413 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 23, 2001, 15:31:59 ; Search time 110.15 seconds
(without alignments)
8.735 Million cell updates/sec

Title: US-08-887-977-10_COPY_97_110

Perfect score: 81

Sequence: 1 HATGAWVFSNATCK 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_67:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	369	2 JC5068	G protein-coupled
2	49	60.5	660	2 T02755	fanconi anemia com
3	47	58.0	356	2 I49340	Mip-1 alpha recept
4	47	58.0	360	2 JC2443	chemokine (C-C) re
5	47	58.0	374	2 I38450	chemokine (C-C) re
6	45	55.6	415	2 S74237	probable G protein
7	45	55.6	452	1 S14332	rhodopsin - northe
8	44	54.3	319	2 S34806	hypothetical prote
9	44	54.3	526	2 T13484	frizzled protein h
10	44	54.3	1073	1 T08228	plasmid replicatio
11	43	53.1	349	2 T06680	hypothetical prote
12	43	53.1	5627	2 C83339	hypothetical prote
13	42	51.9	98	2 A83339	hypothetical prote
14	42	51.9	209	2 H83133	hypothetical prote
15	42	51.9	367	2 I49022	kappa opioid recep
16	42	51.9	367	2 JC2421	opioid receptor ho
17	42	51.9	367	2 I56520	G protein-coupled
18	42	51.9	370	2 S43087	orphan opioid rece
19	42	51.9	412	2 S37906	translation elonga
20	42	51.9	663	1 A38283	arachidonate 12-11
21	41	50.6	103	2 S69712	hypothetical prote
22	41	50.6	126	2 B82448	hypothetical prote
23	41	50.6	487	2 T49211	hypothetical prote
24	41	50.6	646	2 E82133	ATP-dependent heli
25	41	50.6	2165	2 T21371	hypothetical prote
26	40	49.4	297	2 T21898	hypothetical prote
27	40	49.4	346	2 T21398	hypothetical prote
28	40	49.4	352	1 S27357	complement C5a ana
29	40	49.4	407	1 EDBEQ3	immediate-early pr

30	40	49.4	426	2 T16340	hypothetical prote
31	40	49.4	721	2 JC4643	lanosterol synthas
32	39	48.1	190	2 S07000	modulation protein
33	39	48.1	257	1 S13642	thyroxine deiodina
34	39	48.1	276	2 A69437	dehydrase homolog
35	39	48.1	352	2 S74238	probable G protein
36	39	48.1	355	2 A45177	chemokine (C-C) re
37	39	48.1	365	2 T06693	hypothetical prote
38	39	48.1	398	2 A57510	mu opioid receptor
39	39	48.1	417	2 T04955	hypothetical prote
40	39	48.1	440	1 S60755	rhodopsin - Allote
41	39	48.1	480	2 T15839	hypothetical prote
42	39	48.1	488	2 T15941	hypothetical prote
43	39	48.1	495	2 B71360	hypothetical prote
44	39	48.1	507	1 XYOF5	site-specific DNA-
45	39	48.1	557	2 S21596	extracellular prot

ALIGNMENTS

RESULT 1

JC5068

G protein-coupled receptor CKR-L3 - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000

C:Accession: JC5068

R:Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.

Biochem. Biophys. Res. Commun. 227, 846-853, 1996

A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-lik

A:Reference number: JC5067; MUID:97040707

A:Accession: JC5068

A:Molecule type: DNA

A:Residues: 1-369 <ZAB>

A:Cross-references: EMBL:279784; NID:gl668737; PIDN:CAB02144.1; PID:gl668738

C:Comment: This protein belongs to the family of alpha chemokine receptors.

C:Genetics:

A:Gene: GDB:CMKBR6; STRL22; GPR29; CCR6; CKR-L3; GPR-CV4

A:Cross-references: GDB:5370639; OMIM:601835

A:Map position: 6q27-6q27

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

F:42-68/Domain: transmembrane #status predicted <TM1>

F:79-99/Domain: transmembrane #status predicted <TM2>

F:115-136/Domain: transmembrane #status predicted <TM3>

F:160-180/Domain: transmembrane #status predicted <TM4>

F:212-233/Domain: transmembrane #status predicted <TM5>

F:250-271/Domain: transmembrane #status predicted <TM6>

F:292-315/Domain: transmembrane #status predicted <TM7>

Query Match 100.0%; Score 81; DB 2; Length 369;

Best Local Similarity 100.0%; Pred. NO. 4.5e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HATGAWVFSNATCK 14

Db 101 HATGAWVFSNATCK 114

RESULT 2

T02755

fanconi anemia complementation group A protein - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999

C:Accession: T02755

R:Ricke, D.O.; Bruce, D.; Mundt, M.; Doggett, N.; Munk, C.; Saunders, E.; Robinson, D

re, J.; White, S.; Deng, S.; Fatum, O.; Campbell, C.; Fawcett, J.; Maltbie, M.; Deave

submitted to the EMBL Data Library, August 1998

A:Description: Sequencing of human fanconi anemia complementation group A gene genom

A:Reference number: Z14721

A:Accession: T02755

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-660 <RIC>
A:Cross-references: EMBL:AC005567; NID:g3493327; PID:g3493328
C:Genetics:
A:Gene: FAA
A:Map position: 16
A:Note: Intron positions not resolved (incomplete sequence)

Query Match 60.5%; Score 49; DB 2; Length 660;
Best Local Similarity 53.8%; Pred. No. 1.7;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 HATGAWVFSNATC 13
I I I I I I I
Db 30 HAVGSLFRNLCC 42

RESULT 3
I49340
MIP-1 alpha receptor like-1 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C:Accession: I49340
R:Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A:Title: Cloning and differential tissue-specific expression of three mouse beta chemokine
A:Reference number: I49339; MUID:95340546
A:Accession: I49340
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-356 <RES>
A:Cross-references: EMBL:U28405; NID:g881549; PIDN:AAA89154.1; PID:g881550
C:Superfamily: vertebrate rhodopsin

Query Match 58.0%; Score 47; DB 2; Length 356;
Best Local Similarity 63.6%; Pred. No. 2;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GAWVFSNATCK 14
I I I I I I I
Db 98 GDWIFGNAMCK 108

RESULT 4
JC2443
chemokine (C-C) receptor 2, splice form B - human
N:Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chem
C:Species: Homo sapiens (man)
C:Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Jun-2000
C:Accession: JC2443; I38463
R:Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.
Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994
A:Title: cDNA cloning and functional expression of a human monocyte chemoattractant prot
A:Reference number: JC2443; MUID:94324942
A:Accession: JC2443
A:Molecule type: mRNA
A:Residues: 1-360 <YAM>
A:Cross-references: DBJ:J29984; NID:g531246; PIDN:BAA06253.1; PID:g531247
R:Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A:Title: Molecular cloning and functional expression of two monocyte chemoattractant pr
A:Reference number: A53477; MUID:94195821
A:Accession: I38463
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-360 <RES>
A:Cross-references: EMBL:U03905; NID:g472557; PIDN:AAA19120.1; PID:g472558
C:Genetics:
A:Gene: GDB:CMKBR2
A:Cross-references: GDB:337364; OMIM:601267
A:Map position: 3p21-3p21

C:Superfamily: vertebrate rhodopsin
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembr
F:43-70/Domain: transmembrane #status predicted <TM1>
F:81-100/Domain: transmembrane #status predicted <TM2>
F:115-136/Domain: transmembrane #status predicted <TM3>
F:154-178/Domain: transmembrane #status predicted <TM4>
F:207-226/Domain: transmembrane #status predicted <TM5>
F:244-268/Domain: transmembrane #status predicted <TM6>
F:287-309/Domain: transmembrane #status predicted <TM7>
F:14/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:113-190/Disulfide bonds: #status predicted

Query Match 58.0%; Score 47; DB 2; Length 360;
Best Local Similarity 61.5%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ATGAWVFSNATCK 14
I I I I I I I
Db 102 AANWVFGNAMCK 114

RESULT 5
I38450
chemokine (C-C) receptor 2, splice form A - human
N:Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte c
C:Species: Homo sapiens (man)
C:Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 13-Aug-1999
C:Accession: I38450
R:Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A:Title: Molecular cloning and functional expression of two monocyte chemoattractant
A:Reference number: A53477; MUID:94195821
A:Accession: I38450
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <RES>
A:Cross-references: EMBL:U03882; NID:g472555; PIDN:AAA19119.1; PID:g472556
C:Genetics:
A:Gene: GDB:CMKBR2
A:Cross-references: GDB:337364; OMIM:601267
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembr
F:44-68/Domain: transmembrane #status predicted <TM1>
F:115-136/Domain: transmembrane #status predicted <TM2>
F:154-178/Domain: transmembrane #status predicted <TM3>
F:208-226/Domain: transmembrane #status predicted <TM4>
F:244-265/Domain: transmembrane #status predicted <TM5>
F:292-309/Domain: transmembrane #status predicted <TM6>
F:14/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:32-277,113-190/Disulfide bonds: #status predicted

Query Match 58.0%; Score 47; DB 2; Length 374;
Best Local Similarity 61.5%; Pred. No. 2.1;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ATGAWVFSNATCK 14
I I I I I I I
Db 102 AANWVFGNAMCK 114

RESULT 6
S74237
probable G protein-coupled receptor - human
N:Alternate names: GPR-NGA
C:Species: Homo sapiens (man)
C:Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 20-Apr-2000
C:Accession: S74237; G02628
R:O'Dowd, B.F.; Nguyen, T.; Lynch, K.R.; Kolakowski, L.F.; Thompson, M.; Cheng, R.; M
FEBS Lett. 394, 325-329, 1996

A:Title: A novel gene codes for a putative G protein-coupled receptor with an abundant
A:Reference number: S74237; MUID:96427280
A:Accession: S74237
A>Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-415 <ODD>
A:Cross-references: EMBL:U64871; NID:gl1575512
R:Bonner, T.
submitted to the EMBL Data Library, April 1996
A:Reference number: H01502
A:Accession: G02628
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-305, 'K', 307-415 <BON>
A:Cross-references: EMBL:U55312; NID:gl1323695; PIDN:AAB00316.1; PID:gl1323696
C:Genetics:

A:Gene: GDB:GPR19
A:Cross-references: GDB:3770734
A:Map position: 12pter-12qter
A:Introns: #status absent
C:Superfamily: neurokinin 1 receptor
C:Keywords: G protein-coupled receptor; transmembrane protein
F:45-87/Domain: transmembrane #status predicted <TM1>
F:102-124/Domain: transmembrane #status predicted <TM2>
F:140-161/Domain: transmembrane #status predicted <TM3>
F:183-204/Domain: transmembrane #status predicted <TM4>
F:223-243/Domain: transmembrane #status predicted <TM5>
F:277-298/Domain: transmembrane #status predicted <TM6>
F:310-329/Domain: transmembrane #status predicted <TM7>

Query Match 55.6%; Score 45; DB 2; Length 415;
Best Local Similarity 58.3%; Pred. No. 5;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TGAWFNSATCK 14
||| :|||
Db 128 TGRWTLGSATCK 139

RESULT 7

SI4332
rhodopsin - northern European squid
C:Species: Loligo forbesi (northern European squid)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 22-Jun-1999
C:Accession: SI4332
R:Hall, M.D.; Hoon, M.A.; Ryba, N.J.P.; Pottinger, J.D.D.; Keen, J.N.; Saibil, H.R.; Finn
Biochem. J. 274, 35-40, 1991
A:Title: Molecular cloning and primary structure of squid (Loligo forbesi) rhodopsin, a
A:Reference number: SI4332; MUID:91158727
A:Accession: SI4332
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-452 <HAL>
A:Cross-references: EMBL:X56788; NID:g9513; PIDN:CAA40108.1; PID:g603851
C:Superfamily: Octopus rhodopsin
C:Keywords: chromoprotein; color vision; G protein-coupled receptor; glycoprotein; lipop
F:36-60/Domain: transmembrane #status predicted <TM1>
F:73-97/Domain: transmembrane #status predicted <TM2>
F:106-130/Domain: transmembrane #status predicted <TM3>
F:152-176/Domain: transmembrane #status predicted <TM4>
F:200-223/Domain: transmembrane #status predicted <TM5>
F:262-285/Domain: transmembrane #status predicted <TM6>
F:301-322/Domain: transmembrane #status predicted <TM7>
F:8/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:305/Binding site: retinal (Lys) (covalent) #status predicted
F:336, 337/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 55.6%; Score 45; DB 1; Length 452;
Best Local Similarity 77.8%; Pred. No. 5.4;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 WFFSNATCK 14
||| |||
Db 101 WFGNAACK 109

RESULT 8

SI34806
hypothetical protein 2 [imported] - Halobacterium salinarum plasmid pHH1
C:Species: Halobacterium salinarum
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 03-Nov-2000
C:Accession: S34806
R:Preifer, F.; Ghahraman, P.
Mol. Gen. Genet. 238, 193-200, 1993
A:Title: Plasmid pHH1 of Halobacterium salinarum: characterization of the replicon r
A:Reference number: S34806; MUID:93241154
A:Accession: S34806
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-319 <PPE>
A:Cross-references: EMBL:X67101; NID:g297409; PID:g297410
A:Note: the source is designated as Halobacterium salinarium
C:Comment: this ORF is considered not to be required for plasmid replication [validat
PNRC100.
C:Genetics:
A:Genome: plasmid pHH1

Query Match 54.3%; Score 44; DB 2; Length 319;
Best Local Similarity 58.3%; Pred. No. 5.7;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 HATGAWVFSNAT 12
||| :||| :|
Db 59 HLTASWVFSGST 70

RESULT 9

TI13484
frizzled protein homolog - fruit fly (Drosophila melanogaster)
N:Alternate names: hypothetical protein EG:34F3.6
C:Species: Drosophila melanogaster
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C:Accession: TI13484
R:Valenti, P.; Salles, C.; Campbell, L.; Glover, D.
submitted to the EMBL Data Library, April 1999
A:Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A:Reference number: ZI7685
A:Accession: TI13484
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-526 <PHI>
A:Cross-references: EMBL:AL031583; PIDN:CAA20896.1
C:Genetics:
A:Cross-references: FlyBase:FBgn0025623
A:Introns: 18/3
A:Note: EG:34F3.6

Query Match 54.3%; Score 44; DB 2; Length 526;
Best Local Similarity 58.3%; Pred. No. 9.3;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 TGAWFNSATCK 14
||| ||| :|
Db 449 TGLWWSRKTC 460

RESULT 10

T08228
plasmid replication protein repH [validated] - Halobacterium sp. (strain NRC-1) plasm
N:Alternate names: hypothetical protein H0136
C:Species: Halobacterium sp.
A:Variety: strain NRC-1

C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
C;Accession: T08228; A40600
R;Ng, W.V.; Clufo, S.A.; Smith, T.M.; Bumgarner, R.E.; Baskin, D.; Faust, J.; Hall, B.;
Genome Res. 8, 1131-1141, 1998
A;Title: Snapshot of a large dynamic replicon in a halophilic Archaeon: megaplasmid or
A;Reference number: Z16408; MUID:99063795
A;Accession: T08228
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1073 <NGW>
A;Cross-references: EMBL:AF016485; NID:g2822278; PID:g2822289; HALOSP:H0136
A;Experimental source: strain NRC-1
R;Ng, W.L.; DasSarma, S.
J. Bacteriol. 175, 4584-4596, 1993
A;Title: Minimal replication origin of the 200-kilobase Halobacterium plasmid pNRC100.
A;Reference number: A40600; MUID:93328662
A;Accession: A40600
A;Molecule type: DNA
A;Residues: 65-806; 'PFGRGD', 807-1073 <NGA>
A;Cross-references: GB:LI9296
A;Note: the source is designated as Halobacterium halobium
C;Genetics:
A;Gene: repH; H0136
A;Genome: plasmid pNRC100
C;Function:
C;Superfamily: Halobacterium plasmid pNRC100 replication protein repH
C;Keywords: plasmid replication

Query Match 54.3%; Score 44; DB 1; Length 1073;
Best Local Similarity 58.3%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 HATGAWFVSNTAT 12
||| :|||| :|
Db 722 HLTASWVFGST 733

RESULT 11
T06680
hypothetical protein T17F15.100 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 02-Sep-2000
C;Accession: T06680
R;Quetier, F.; Choisme, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artig
Submitted to the Protein Sequence Database, April 1999
A;Reference number: Z15793
A;Accession: T06680
A;Molecule type: DNA
A;Residues: 1-349 <QUE>
A;Cross-references: EMBL:AL049658; GSPDB:GN00061; ATSP:T17F15.100
A;Experimental source: cultivar Columbia; BAC clone T17F15
C;Genetics:
A;Gene: ATSP:T17F15.100
A;Map position: 3
A;Introns: 26/1; 81/2
C;Superfamily: RING finger homology
F;203-254/Domain: RING finger homology <RRN>

Query Match 53.1%; Score 43; DB 2; Length 349;
Best Local Similarity 46.2%; Pred. No. 9.2;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 HATGAWFVSNTATC 13
| :| :||| :|
Db 233 HCIDTWLLSNSTC 245

RESULT 12
C83339
hypothetical protein PA2462 [imported] - Pseudomonas aeruginosa (strain PA01)

C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: C83339
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A;Reference number: A82950; MUID:20437337
A;Accession: C83339
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-5627 <STO>
A;Cross-references: GB:AE004673; GB:AE004091; NID:g9948501; PIDN:AAG05850.1; GSPDB:GN
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA2462

Query Match 53.1%; Score 43; DB 2; Length 5627;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGAWFVSNTAT 12
||||| |||
Db 5313 TGAWVAGNAT 5322

RESULT 13
A83339
hypothetical protein PA2460 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: A83339
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A;Reference number: A82950; MUID:20437337
A;Accession: A83339
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <STO>
A;Cross-references: GB:AE004673; GB:AE004091; NID:g9948501; PIDN:AAG05848.1; GSPDB:GN
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA2460

Query Match 51.9%; Score 42; DB 2; Length 98;
Best Local Similarity 80.0%; Pred. No. 4;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGAWFVSNTAT 12
||||| |||
Db 35 TGAWVARNAT 44

RESULT 14
H83133
hypothetical protein PA4103 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: H83133
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A;Reference number: A82950; MUID:20437337
A;Accession: H83133
A;Status: preliminary

A:Molecule type: DNA
A:Residues: 1-209 <STO>
A:Cross-references: GB:AE004826; GB:AE004091; NID:g9950296; PIDN:AAG07490.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA4103

Query Match 51.9%; Score 42; DB 2; Length 209;
Best Local Similarity 46.2%; Pred. No. 8.2;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 HATGAWVFSNATC 13
|:|:|:|:|:
Db 153 HSTGTWVLGIFC 165

RESULT 15.
I49022
kappa opioid receptor 3 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 19-May-2000
C:Accession: I49022
R;Pan, Y.X.; Cheng, J.; Xu, J.; Rossi, G.; Jacobson, E.; Ryan-Moro, J.; Brooks, A.I.; De
Mol. Pharmacol. 47, 1180-1188, 1995
A:Title: Cloning and functional characterization through antisense mapping of a kappa 3-
A:Reference number: I49022; MUID:95327076
A:Accession: I49022
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-367 <RES>
A:Cross-references: EMBL:U09421; NID:g551484; PIDN:AAA81333.1; PID:g551485
C:Superfamily: vertebrate rhodopsin

Query Match 51.9%; Score 42; DB 2; Length 367;
Best Local Similarity 63.6%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 GAWVFSNATCK 14
|:|:|:|:|:
Db 111 GFWPFGNALCK 121

Search completed: May 23, 2001, 15:32:00
Job time: 507 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:36:17 ; Search time 62.39 Seconds
(without alignments)

7.687 Million cell updates/sec

Title: US-08-887-977-10_COPY_97_110

Perfect score: 81

Sequence: 1 HATGANVFSNATCK 14

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	374	1	CKR6_HUMAN
2	60	74.1	367	1	CKR6_MOUSE
3	49	60.5	1455	1	FACA_HUMAN
4	47	58.0	356	1	CKRV_MOUSE
5	47	58.0	374	1	CKR2_HUMAN
6	45	55.6	415	1	GPRJ_HUMAN
7	45	55.6	452	1	OPSD_LOLFO
8	44	54.3	354	1	CKR5_RAT
9	44	54.3	373	1	CKR2_MOUSE
10	44	54.3	373	1	CKR2_RAT
11	43	53.1	354	1	CKR5_MOUSE
12	42	51.9	367	1	OPRX_MOUSE
13	42	51.9	367	1	OPRX_RAT
14	42	51.9	370	1	OPRX_HUMAN
15	42	51.9	370	1	OPRX_PIG
16	42	51.9	412	1	ERH_YEAST
17	42	51.9	662	1	LOXP_HUMAN
18	41	50.6	355	1	CKR1_MACMU
19	40	49.4	352	1	C3AR_CANFA
20	40	49.4	371	1	NK6R_MOUSE
21	40	49.4	407	1	IE68_HSVSA
22	40	49.4	416	1	OXIR_RAT
23	40	49.4	425	1	OXIR_HUMAN
24	40	49.4	721	1	ERG7_SCHPO
25	39	48.1	190	1	NODL_RHLV
26	39	48.1	257	1	IOD1_RAT
27	39	48.1	352	1	GPRJ_RAT
28	39	48.1	355	1	CKR1_HUMAN
29	39	48.1	355	1	CKR3_CERAE
30	39	48.1	355	1	CKR3_MACMU
31	39	48.1	371	1	NK6R_RABIT
32	39	48.1	398	1	OPRM_MOUSE
33	39	48.1	409	1	GPRJ_MOUSE

ALIGNMENTS

RESULT	ID	CKR6_HUMAN	STANDARD	PRT	374 AA.
AC	P51684	Q92846	P78553		
DT	01-OCT-1996	(Rel. 36, Last sequence update)			
DT	15-JUL-1998	(Rel. 40, Last annotation update)			
DE	01-OCT-2000	(Rel. 40, Last annotation update)			
DE	C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CCR-6) (IARC				
DE	RECEPTOR) (GPR-CY4) (GPCV4) (CHEMOKINE RECEPTOR-LIKE 3) (CKR-L3)				
DE	(DRY6)				
GN	CKR6 OR CMKBR6 OR STRL22 OR GPR29 OR CKRL3.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A., AND FUNCTION.				
RX	MEDLINE=97313465; PubMed=9169459;				
RA	Baba M., Imai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K.,				
RA	Nomiyama H., Yoshie O.;				
RT	"Identification of CCR6, the specific receptor for a novel				
RT	lymphocyte-directed CC chemokine IARC."				
RL	J. Biol. Chem. 272:14893-14898(1997).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	Lautens L.L., Modi W., Bonner T.I.;				
RL	Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=97040707; PubMed=8886020;				
RA	Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G.;				
RT	"Molecular cloning and RNA expression of two new human chemokine				
RT	receptor-like genes."				
RL	Biochem. Biophys. Res. Commun. 227:846-853(1996).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RA	McCoy R., Perlmuter D.H.;				
RL	Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=97224503; PubMed=9070937;				
RA	Liao F., Lee H.-H., Farber J.M.;				
RT	"Cloning of STRL22, a new human gene encoding a G-protein-coupled				
RT	receptor related to chemokine receptors and located on chromosome				
RT	6q27."				
RL	Genomics 40:175-180(1997).				
CC	-1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-				
CC	ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE				
CC	INTRACELLULAR CALCIUM IONS LEVEL.				
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.				
CC	-1- TISSUE SPECIFICITY: SPLEEN, LYMPH NODES, APPENDIX, AND FETAL				
CC	LIVER. EXPRESSED IN LYMPHOCYTES, T CELLS AND B CELLS BUT NOT IN				
CC	NATURAL KILLER CELLS, MONOCYTES, OR GRANULOCYTES.				
CC	-1- INDUCTION: INTERLEUKIN-2.				
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.				
CC	-1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-6 IS THE INITIATOR.				

Q17094 loligo subu
Q19084 caenorhabdi
P00474 providencia
O75748 homo sapien
P74688 mus musculu
O35786 rattus norv
Q99788 homo sapien
O95867 homo sapien
Q92164 mus musculu
P32239 swinepox vi
P37925 salmonella
P56484 mus musculu

34 39 48.1 439 1 OPSD_LOLSU
35 39 48.1 488 1 YDBM_CAEEL
36 39 48.1 507 1 MTPS_PROST
37 38.5 47.5 371 1 CH23_HUMAN
38 38.5 47.5 371 1 CML1_MOUSE
39 38.5 47.5 371 1 CML1_RAT
40 38.5 47.5 373 1 CML1_HUMAN
41 38 46.9 125 1 NG24_HUMAN
42 38 46.9 126 1 NG24_MOUSE
43 38 46.9 269 1 VC03_SPKA
44 38 46.9 335 1 FIMH_SALTY
45 38 46.9 353 1 CKR8_MOUSE

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 DR EMBL; U45984; AAB62714.1; -
 DR EMBL; 279784; CAB02144.1; ALT_INIT.
 DR EMBL; U60000; AAB06949.1; -
 DR EMBL; U68030; AAC51124.1; -
 DR EMBL; U68032; AAC51125.1; -
 DR HSSP; P34996; 1DDD.
 DR GCRDb; GCR_1037; -
 DR GCRDb; GCR_1075; -
 DR GCRDb; GCR_1906; -
 DR GCRDb; GCR_1919; -
 DR GCRDb; GCR_1941; -
 DR GCRDb; GCR_2110; -
 DR MIM; 601835; -
 DR InterPro: IPR000276; -
 DR Pfam; PF00001; 7tm1.1;
 DR PRINTS; PR00237; GPCRHHODOPS.N.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 47
 FT TRANSMEM 48 74
 FT DOMAIN 75 83
 FT TRANSMEM 84 104
 FT DOMAIN 105 119
 FT TRANSMEM 120 141
 FT DOMAIN 142 159
 FT TRANSMEM 160 180
 FT DOMAIN 181 211
 FT TRANSMEM 212 238
 FT DOMAIN 239 254
 FT TRANSMEM 255 279
 FT DOMAIN 280 303
 FT TRANSMEM 304 321
 FT DOMAIN 322 374
 FT DISULFID 118 197
 FT CARBOHYD 7 7
 FT CARBOHYD 23 23
 FT CONFLICT 60 60
 FT CONFLICT 74 74
 FT CONFLICT 86 86
 FT CONFLICT 164 164
 FT CONFLICT 182 182
 FT CONFLICT 192 192
 FT CONFLICT 206 206
 FT CONFLICT 225 225
 FT CONFLICT 370 374
 FT CONFLICT 374 374
 FT SEQUENCE 374 AA; 42494 MW; D7F963534E990BC4 CRC64;

 Query Match 100.0%; Score 81; DB 1; Length 374;
 Best Local Similarity 100.0%; Pred. No. 4.2e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 HATGAWFSNATCK 14
 Db 106 HATGAWFSNATCK 119

 RESULT 2
 CRR6_MOUSE STANDARD; PRT; 367 AA.
 AC O54689;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)

01-OCT-2000 (Rel. 40, Last annotation update)
 C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CC-CKR-6) (CCR-6) (KY411).
 CCR6 OR CMKBR6.
 Mus musculus (Mouse).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 RN SEQUENCE FROM N.A.
 RA Yanagihara S., Komura E., Yamaguchi Y.;
 RT "Mouse G protein-coupled receptor KY411";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=99077268; PubMed=9862452;
 RA Varona R., Zaballos A., Gutierrez J., Martin P., Roncal F.,
 Albar J.P., Ardavin C., Marquez G.;
 RT "Molecular cloning, functional characterization and mRNA expression
 analysis of the murine chemokine receptor CCR6 and its specific ligand
 MIP-3alpha";
 RT FEBS Lett. 440:188-194(1998).
 RL FEBS Lett. 440:188-194(1998).
 CC !- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-
 ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE
 CC INTRACELLULAR CALCIUM IONS LEVEL.
 CC !- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC !- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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 DR EMBL; AB009369; BAA23776.1; -
 DR EMBL; AJ222714; CAA10956.1; -
 DR MGD; MGI:1333797; Cmkbr6.
 DR InterPro: IPR000276; -
 DR Pfam; PF00001; 7tm1.1;
 DR PRINTS; PR00237; GPCRHHODOPS.N.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 39
 FT TRANSMEM 40 66
 FT DOMAIN 67 75
 FT TRANSMEM 76 96
 FT DOMAIN 97 111
 FT TRANSMEM 112 133
 FT DOMAIN 134 151
 FT TRANSMEM 152 172
 FT DOMAIN 173 203
 FT TRANSMEM 204 230
 FT DOMAIN 231 246
 FT TRANSMEM 247 271
 FT DOMAIN 272 295
 FT TRANSMEM 296 313
 FT DOMAIN 314 367
 FT DISULFID 110 189
 FT CARBOHYD 2 2
 FT CARBOHYD 35 35
 FT SEQUENCE 367 AA; 42102 MW; 6A309AF833B1117E CRC64;

 Query Match 74.1%; Score 60; DB 1; Length 367;
 Best Local Similarity 71.4%; Pred. No. 0.01;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

 Qy 1 HATGAWFSNATCK 14
 Db 98 HATNTWFSALCK 111

RESULT 3
FACA_HUMAN
ID FACA_HUMAN STANDARD; PRT: 1455 AA.
AC O15360; Q92497; Q75266; Q9Y6M2;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE FANCONI ANEMIA GROUP A PROTEIN (FACA PROTEIN).
GN FANCA OR FAA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97312685; PubMed=9169126;
RA Ianzano L., D'Apollito M., Centra M., Savino M., Levran O.,
RA Auerbach A.D., Cleton-Jansen A.M., Doggett N.A., Pronk J.C.,
RA Tipping A.J., Gibson R.A., Mathew C.G., Whitmore S.A., Apostolou S.,
RA Callen F.C., Zelante L., Savoia A.;
RT "The genomic organization of the Fanconi anemia group A (FAA) gene";
RL Genomics 41:309-314(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97051928; PubMed=8996563;
RA Lo Ten Foe J.R., Rooimans M.A., Bosnyan-Collins L., Alon N.,
RA Wijker M., Parker L., Lightfoot J., Carreau M., Callen D.F.,
RA Savoia A., Cheng N.C., van Berkel C.G.M., Strunk M.H.P., Gilie J.J.P.,
RA Pals G., Kruyt F.A.E., Pronk J.C., Arwert F., Buchwald M., Joenje H.;
RT "Expression cloning of a cDNA for the major Fanconi anaemia gene,
RT FAA";
RL Nat. Genet. 14:320-323(1996).
RN [3]
RP SEQUENCE OF 175-834 FROM N.A.
RX MEDLINE=98414611; PubMed=9742112;
RA Naef D., Kupfer G.M., Suliman A., Lambert K., D'Andrea A.D.;
RA Robinson D., Jones M., Buckingham J., Chasteen L., Thompson S.,
RA Goodwin L., Bryant J., Tesmer J., Meincke L., Longmire J., White S.,
RA Ueng S., Tatum O., Campbell C., Fawcett J., Maltbie M., Deaven L.;
RT "Sequencing of human Fanconi anemia complementation group A gene
RT genomic region";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 491-542 FROM N.A.
RX MEDLINE=98375690; PubMed=9711872;
RA Levran O., Doggett N.A., Auerbach A.D.;
RA "Identification of Alu-mediated deletions in the Fanconi anemia gene
RA FAA";
RL Hum. Mutat. 12:145-152(1998).
RN [5]
RP SUBCELLULAR LOCATION, AND MUTAGENESIS.
RX MEDLINE=98414611; PubMed=9742112;
RA Naef D., Kupfer G.M., Suliman A., Lambert K., D'Andrea A.D.;
RA "Functional activity of the Fanconi anemia protein FAA requires FAC
RA binding and nuclear localization";
RL Mol. Cell. Biol. 18:5952-5960(1998).
RN [6]
RP PHOSPHORYLATION.
RX MEDLINE=99007271; PubMed=9789045;
RA Yamashita T., Kupfer G.M., Naf D., Suliman A., Joenje H., Asano S.,
RA D'Andrea A.D.;
RT "The Fanconi anemia pathway requires FAA phosphorylation and FAA/FAC
RT nuclear accumulation";
RL Proc. Natl. Acad. Sci. U.S.A. 95:13085-13090(1998).
RN [7]
RP VARIANTS FA, AND VARIANTS.
RX MEDLINE=98058767; PubMed=9371798;
RA Levran O., Erlich T., Magdalena N., Gregory J.J., Batish S.D.,
RA Verlender P.C., Auerbach A.D.;
RT "Sequence variation in the Fanconi anemia gene FAA";
RL Proc. Natl. Acad. Sci. U.S.A. 94:13051-13056(1997).
RN [8]
RP DNA repair; Nuclear protein; Phosphorylation; Disease mutation;
RN Polymorphism.

VARIANTS FA PRO-1110 AND GLY-1117.
MEDLINE=99225041; PubMed=10210316;
Kupfer G., Naef D., Garcia-Higuera I., Wasik J., Cheng A.,
Yamashita T., Tipping A., Morgan N., Mathew C.G., D'Andrea A.D.;
RT "A patient-derived mutant form of the Fanconi anemia protein, FANCA,
RT is defective in nuclear accumulation.";
RL Exp. Hematol. 27:587-593(1999).
CC -!- FUNCTION: DNA REPAIR PROTEIN THAT MAY OPERATE IN A POSTREPLICATION
CC REPAIR OR A CELL CYCLE CHECKPOINT FUNCTION. MAY BE IMPLICATED IN
CC INTERSTRAND DNA CROSS-LINK REPAIR AND IN THE MAINTENANCE OF NORMAL
CC CHROMOSOME STABILITY.
CC -!- SUBUNIT: BELONGS TO A MULTISUBUNIT COMPLEX COMPOSED OF FANCA,
CC FANCC AND FANCG PROTEINS.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (MAJOR) AND CYTOPLASMIC (MINOR).
CC IS REQUIRED FOR THE FORMATION OF THE NUCLEAR COMPLEX. NOT
CC PHOSPHORYLATED IN CELLS DERIVED FROM GROUPS A, B, C, E, F, G, AND
CC H.
CC -!- DISEASE: DEFECTS IN FANCA ARE THE CAUSE OF ONE OF THE 8
CC COMPLEMENTATION GROUPS OF FANCONI ANEMIA (FA), AN AUTOSOMAL
CC RECESSIVE DISORDER CHARACTERIZED BY PROGRESSIVE PANCYTOPAENIA, A
CC DIVERSE ASSORTMENT OF CONGENITAL MALFORMATIONS, AND A
CC PREDISPOSITION TO THE DEVELOPMENT OF MALIGNANCIES. AT THE CELLULAR
CC LEVEL IT IS ASSOCIATED WITH HYPERSENSITIVITY TO DNA-DAMAGING
CC AGENTS, CHROMOSOMAL INSTABILITY (INCREASED CHROMOSOME BREAKAGE),
CC AND DEFECTIVE DNA REPAIR. FANCA DEFECTS ACCOUNT FOR 65 % OF FA.
CC -!- DATABASE: NAME-Fanconi Anemia Mutation Database;
CC WWW="http://www.rockefeller.edu/fanconi/mutate/";
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; Z83067; CAB05445.1;
CC EMBL; Z83068; CAB05445.1; JOINED.
CC EMBL; Z83069; CAB05445.1; JOINED.
CC EMBL; Z83070; CAB05445.1; JOINED.
CC EMBL; Z83071; CAB05445.1; JOINED.
CC EMBL; Z83072; CAB05445.1; JOINED.
CC EMBL; Z83073; CAB05445.1; JOINED.
CC EMBL; Z83074; CAB05445.1; JOINED.
CC EMBL; Z83075; CAB05445.1; JOINED.
CC EMBL; Z83076; CAB05445.1; JOINED.
CC EMBL; Z83077; CAB05445.1; JOINED.
CC EMBL; Z83078; CAB05445.1; JOINED.
CC EMBL; Z83079; CAB05445.1; JOINED.
CC EMBL; Z83080; CAB05445.1; JOINED.
CC EMBL; Z83081; CAB05445.1; JOINED.
CC EMBL; Z83082; CAB05445.1; JOINED.
CC EMBL; Z83083; CAB05445.1; JOINED.
CC EMBL; Z83084; CAB05445.1; JOINED.
CC EMBL; Z83085; CAB05445.1; JOINED.
CC EMBL; Z83086; CAB05445.1; JOINED.
CC EMBL; Z83087; CAB05445.1; JOINED.
CC EMBL; Z83088; CAB05445.1; JOINED.
CC EMBL; Z83089; CAB05445.1; JOINED.
CC EMBL; Z83090; CAB05445.1; JOINED.
CC EMBL; Z83091; CAB05445.1; JOINED.
CC EMBL; Z83092; CAB05445.1; JOINED.
CC EMBL; Z83093; CAB05445.1; JOINED.
CC EMBL; Z83094; CAB05445.1; JOINED.
CC EMBL; Z83095; CAB05445.1; JOINED.
CC EMBL; Z83151; CAB05445.1; JOINED.
CC EMBL; X99226; CAA67610.1;
CC EMBL; AC005567; AAC33401.1;
CC EMBL; AF054569; AAC28331.1;
CC MIM: 227650;
KW DNA repair; Nuclear protein; Phosphorylation; Disease mutation;
KW Polymorphism.

FT DOMAIN 18 34 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT VARIANT 6 6 V -> D.
FT VARIANT 8 8 /FTID-VAR_009637.
FT POLYMORPHISM).
FT /FTID-VAR_009638.
FT A -> V (IN FA A).
FT /FTID-VAR_009639.
FT L -> F (IN FA A).
FT /FTID-VAR_009640.
FT D -> G (IN FA A).
FT /FTID-VAR_009641.
FT R -> C (IN FA A).
FT /FTID-VAR_009642.
FT H -> R (IN FA A).
FT /FTID-VAR_009643.
FT S -> G.
FT /FTID-VAR_009644.
FT P -> L.
FT /FTID-VAR_009645.
FT G -> D.
FT /FTID-VAR_009646.
FT L -> P (IN FA A).
FT /FTID-VAR_009647.
FT L -> P (IN FA A).
FT /FTID-VAR_009648.
FT R -> L (IN FA A).
FT /FTID-VAR_009649.
FT H -> P (IN FA A; LOSS OF FUNCTION).
FT /FTID-VAR_009650.
FT R -> G (IN FA A; LOSS OF FUNCTION).
FT /FTID-VAR_009651.
FT O -> E (IN FA A).
FT /FTID-VAR_009652.
FT T -> A (IN FA A).
FT /FTID-VAR_009653.
FT MISSING (IN FA A).
FT /FTID-VAR_009654.
FT V -> I.
FT /FTID-VAR_009655.
FT W -> R (IN FA A).
FT /FTID-VAR_009656.
FT T -> A.
FT /FTID-VAR_009657.
FT H -> D (IN FA A).
FT /FTID-VAR_009658.
FT M -> I (IN REF. 2).
FT CONFLICT 717 717
SQ SEQUENCE 1455 AA; 162804 MW; DB43EBDB29DF5C0E CRC64;

Query Match 60.5%; Score 49; DB 1; Length 1455;
Best Local Similarity 53.8%; Pred. No. 2.3;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 HATGAWVFSNATC 13
|||:|:|:|
Db 204 HAVGSWLFRLNLC 216

RESULT 4
CKRV_MOUSE
ID CKRV_MOUSE STANDARD; PRT; 356 AA.
AC P51676;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE C-C CHEMOKINE RECEPTOR (MACROPHAGE INFLAMMATORY PROTEIN-1 ALPHA
DE RECEPTOR-LIKE 1).
GN CMKBR11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

RN SEQUENCE FROM N.A.
RP STRAIN=129/SVJ;
RX MEDLINE=95340546; PubMed=7542241;
RA Gao J.-L., Murphy P.M.;
RT "Cloning and differential tissue-specific expression of three mouse
RT beta chemokine receptor-like genes, including the gene for a
RT functional macrophage inflammatory protein-1 alpha receptor.";
RL J. Biol. Chem. 270:17494-17501(1995).
CC -!- FUNCTION: PROBABLE RECEPTOR FOR A C-C TYPE CHEMOKINE.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: DETECTED IN THE SPLEEN, LIVER AND LEUKOCYTES.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; U28405; AAA89154.1; -;
DR GCRDB; GCR_1696; -;
DR MGD; MGI:104617; Cmkbr11.
DR InterPro; IPR000276; -;
DR InterPro; IPR000355; -;
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSIN.
DR PRINTS; PR00657; CCHEMOKINER.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 32
FT TRANSMEM 33 60
FT DOMAIN 61 67
FT TRANSMEM 68 92
FT DOMAIN 93 108
FT TRANSMEM 109 130
FT DOMAIN 131 147
FT TRANSMEM 148 172
FT DOMAIN 173 198
FT TRANSMEM 199 224
FT DOMAIN 225 240
FT TRANSMEM 241 265
FT DOMAIN 266 282
FT TRANSMEM 283 306
FT DOMAIN 307 356
FT DISULFID 107 184
SQ SEQUENCE 356 AA; 40934 MW; 58C01ABA8D7D4B06 CRC64;

Query Match 58.0%; Score 47; DB 1; Length 356;
Best Local Similarity 63.6%; Pred. No. 1.3;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GAWVFSNATCK 14
|:|:|:|
Db 98 GDWIFGNAMCK 108

RESULT 5
CKR2_HUMAN
ID CKR2_HUMAN STANDARD; PRT; 374 AA.
AC P41597;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 2 (C-C CKR-2) (CCR-2) (CCR2)
DE (MONOCYTE CHEMOATTRACTANT PROTEIN 1 RECEPTOR) (MCP-1-R) (CCR2).
GN CCR2 OR CMKBR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94195821; PubMed=8146186;
 RA Charo I.F., Myers S.J., Herman A., Franci C., Connolly A.J.,
 RA Coughlin S.R.;
 RT "Molecular cloning and functional expression of two monocyte
 RT chemoattractant protein 1 receptors reveals alternative splicing of
 RT the carboxyl-terminal tails.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:2752-2756(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94324942; PubMed=8048929;
 RA Yamagami S., Tokuda Y., Ishii K., Tamaka H., Endo N.;
 RT "cDNA cloning and functional expression of a human monocyte
 RT chemoattractant protein 1 receptor.";
 RL Biochem. Biophys. Res. Commun. 202:1156-1162(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97150864; PubMed=8995400;
 RA Wong L.-M., Myers S.J., Tsou C.-L., Gosling J., Arai H., Charo I.F.;
 RT "Organization and differential expression of the human monocyte
 RT chemoattractant protein 1 receptor gene. Evidence for the role of the
 RT carboxyl-terminal tail in receptor trafficking.";
 RL J. Biol. Chem. 272:1038-1045(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
 RA Nham M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
 RA Guoj L., la Bastide M., Kaplan N., Greco T., Touchman J.,
 RA Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,
 RA Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E.,
 RA Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,
 RA Watanabe M., Doggett N., Garcia D., Sagripanti J.L.;
 RA Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RL FUNCTION: RECEPTOR FOR THE MCP-1, MCP-3 AND MCP-4 CHEMOKINES.
 CC TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS
 CC LEVEL.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U03882; AAA19119.1; -;
 DR EMBL; U03905; AAA19120.1; -;
 DR EMBL; D29984; BAA06253.1; -;
 DR EMBL; U80924; AAC51637.1; -;
 DR EMBL; U80924; AAC51636.1; -;
 DR EMBL; U95626; AAB57791.1; -;
 DR EMBL; U95626; AAB57792.1; -;
 DR GCRdb; GCR_0970; -;
 DR GCRdb; GCR_0989; -;
 DR GCRdb; GCR_1827; -;
 DR GCRdb; GCR_2700; -;
 DR GCRdb; GCR_2701; -;
 DR MIM; 601267; -;
 DR InterPro; IPR000276; -;
 DR InterPro; IPR000355; -;
 DR InterPro; IPR002237; -;
 DR Pfam; PF00001; 7tm_1; 1;
 DR PRINTS; PR00237; GPCRHDOPSN.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01107; CCHEMOKINER2.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.

DR PROSITE; PS00262; G_PROTEIN_RECEP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Alternative splicing.
 FT DOMAIN 1 42 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 43 70 1 (POTENTIAL).
 FT DOMAIN 71 80 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 81 100 2 (POTENTIAL).
 FT DOMAIN 101 114 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 115 136 3 (POTENTIAL).
 FT DOMAIN 137 153 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 154 178 4 (POTENTIAL).
 FT DOMAIN 179 206 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 207 226 5 (POTENTIAL).
 FT DOMAIN 227 243 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 244 268 6 (POTENTIAL).
 FT DOMAIN 269 285 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 286 309 7 (POTENTIAL).
 FT DOMAIN 310 374 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 113 190 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 314 374 BY SIMILARITY.
 FT SLPHIALGCRIPALQKVCVCGPGVRCGNKVVTOGLDGR
 FT GKSGISGRAPASLDQKEGA -> RYLSVFRKHITRRFCK
 FT QCPVYRETVDGVTSNTPTSTGGEQEVSAGL (IN
 FT ISOFORM B).
 SQ SEQUENCE 374 AA; 41914 MW; F865E0D39E74CF0F CRC64;
 FT
 Query Match 58.0%; Score 47; DB 1; Length 374;
 Best Local Similarity 61.5%; Pred. No. 1.4;
 Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 2 ATGAWVFSNATCK 14
 Db 102 AANEVFGNAMCK 114
 | 1111111111
 RESULT 6
 GPRJ_HUMAN STANDARD; PRT; 415 AA.
 ID GPRJ_HUMAN
 AC Q15760;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE PROBABLE G PROTEIN-COUPLED RECEPTOR GPR19 (GPR-NGA).
 GN GPR19.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bonner T.I., Matsuda L.A.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96427280; PubMed=8830667;
 RA O'Dowd B.F., Nguyen T., Lynch K.R., Kolakowski L.F. Jr., Thompson M.,
 RA Cheng R., Marchese A., Ng G.Y.K., Heng H.H.Q., George S.R.;
 RT "A novel gene codes for a putative G protein-coupled receptor with an
 RT abundant expression in brain.";
 RL FEBS Lett. 394:325-329(1996).
 CC -!- FUNCTION: ORPHAN RECEPTOR.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: ABUNDANT EXPRESSION IN THE BRAIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----

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CC EMBL; U55312; AAB00316.1;
CC EMBL; U54871; AAB49751.1;
CC GCRDB; GCR_1914;
CC GCRDB; GCR_1926;
CC MIM; 602927;
CC InterPro; IPR000276;
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
CC PROSITE; PS0262; G-PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 69 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 70 90 1 (POTENTIAL).
FT DOMAIN 91 102 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 103 123 2 (POTENTIAL).
FT DOMAIN 124 143 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 144 161 3 (POTENTIAL).
FT DOMAIN 162 182 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 183 203 4 (POTENTIAL).
FT DOMAIN 204 221 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 222 242 5 (POTENTIAL).
FT DOMAIN 243 277 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 278 298 6 (POTENTIAL).
FT DOMAIN 299 309 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 310 325 7 (POTENTIAL).
FT DOMAIN 326 415 CYTOPLASMIC (POTENTIAL).
FT DISULFID 138 210 BY SIMILARITY.
FT CARBOHYD 25 25 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 415 AA; 47700 MW; 238619E007152ADF CRC64;

Query Match 55.6%; Score 45; DB 1; Length 415;
Best Local Similarity 58.3%; Pred. No. 3.2;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 TGAWVFSNATCK 14
||| |||
DB 128 TGRWTLGSATCK 139

RESULT 7
OPSD_LOLFO STANDARD; PRT; 452 AA.
AC P24603;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE RHODOPSIN.
GN RHO.
OS Loligo forbesi (Northern European squid).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Teuthoidea;
OC Myopsida; Loliginidae; Loligo.
OX NCBI_TaxID=6618;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=91158727; PubMed=1900420;
RA Hall M.D., Hoon M.A., Ryba N.J.P., Pottinger J.D.D., Keen J.N.,
RA Saibil H.R., Findlay J.B.C.;
RT "Molecular cloning and primary structure of squid (Loligo forbesi)
RT rhodopsin, a phospholipase C-directed G-protein-linked receptor.";
RL Biochem. J. 274:35-40(1991).
CC -!- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT
CC MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY
CC LINKED TO CIS-RETINAL. THIS RECEPTOR IS COUPLED TO THE ACTIVATION
CC OF PHOSPHOLIPASE C.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES MAY
CC BE PHOSPHORYLATED.
CC -!- MISCELLANEOUS: THIS RHODOPSIN HAS AN ABSORPTION MAXIMA AT 494 NM.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC -----
CC EMBL; X56788; CAA40108.1;
CC PIR; S14332; S14332.
CC GCRDB; GCR_0239;
CC InterPro; IPR000216;
CC InterPro; IPR000276;
CC InterPro; IPR001760;
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PRINTS; PR00238; RHODOPSNTAIL.
CC PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
CC PROSITE; PS0262; G-PROTEIN_RECEP_FL_2; 1.
CC PROSITE; PS00238; OPSIN; 1.
KW Photoreceptor; Retinal protein; Transmembrane; Glycoprotein; Vision;
KW Phosphorylation; Lipoprotein; Palmitate; G-protein coupled receptor.
FT DOMAIN 1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 58 1 (POTENTIAL).
FT DOMAIN 59 70 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 71 97 2 (POTENTIAL).
FT DOMAIN 98 111 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 112 131 3 (POTENTIAL).
FT DOMAIN 132 151 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 152 175 4 (POTENTIAL).
FT DOMAIN 176 199 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 200 227 5 (POTENTIAL).
FT DOMAIN 228 261 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 262 285 6 (POTENTIAL).
FT DOMAIN 286 294 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 295 318 7 (POTENTIAL).
FT DOMAIN 319 452 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (PROBABLE).
FT DISULFID 108 186 BY SIMILARITY.
FT BINDING 305 305 RETINAL CHROMOPHORE (BY SIMILARITY).
FT LIPID 336 336 PALMITATE (BY SIMILARITY).
FT LIPID 337 337 PALMITATE (BY SIMILARITY).
FT DOMAIN 370 380 MET-RICH.
FT DOMAIN 381 452 GLN/PRO-RICH.
SQ SEQUENCE 452 AA; 50576 MW; 6AA9E2DE4C4DFA4 CRC64;

Query Match 55.6%; Score 45; DB 1; Length 452;
Best Local Similarity 77.8%; Pred. No. 3.4;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 WVFNSNATCK 14
||| |||
DB 101 WVFNGNACK 109

RESULT 8
CKR5_RAT
ID CKR5_RAT STANDARD; PRT; 354 AA.
AC O08556;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35; Last sequence update)
DT 30-MAY-2000 (Rel. 39; Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CC-CKR-5) (MIP-1
DE ALPHA RECEPTOR).
DE CCR5 OR CMKR5.
GN CCR5
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

```

RN RP SEQUENCE FROM N.A.
 RC STRAIN=WISTAR; TISSUE=Brain;
 RX MEDLINE=98334064; PubMed=9670989;
 RA Spleiss O., Gourmal N., Boddeke H.W.G.M., Sauter A., Fiebich B.L.,
 RA Berger M., Gebicke-Haerter P.J.;
 RT "Cloning of rat HIV-1-chemokine coreceptor CKR5 from microglia and
 RT upregulation of its mRNA in ischemic and endotoxinemic rat brain.";
 RL J. Neurosci. Res. 53:16-28(1998).
 RN RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY;
 RX MEDLINE=98318173; PubMed=9655467;
 RA Jiang Y., Salafra M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
 RA Defebvre C.M., Pennell N.A., Streif W.J., Harrison J.K.;
 RT "Chemokine receptor expression in cultured glia and rat experimental
 RT allergic encephalomyelitis";
 RL J. Neuroimmunol. 86:1-12(1998).
 CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC
 CC EMBL; Y12009; CAA72737.1; -;
 CC EMBL; U77350; AAC03243.1; -;
 CC GCRDB; GCR_1470; -;
 CC InterPro; IPR000276; -;
 CC InterPro; IPR000355; -;
 CC InterPro; IPR002240; -;
 CC Pfam; PF00001; 7tm_1; 1;
 CC PRINTS; PR00237; GPCRHHODPSN.
 CC PRINTS; PR00657; CCHEMOKINER.
 CC PRINTS; PR01110; CHEMOKINER5.
 CC PROSITE; PS00237; G-PROTEIN RECEPTOR FL-1; 1.
 CC PROSITE; PS0262; G-PROTEIN RECEPTOR FL-2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein.
 KW DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 33 60 1 (POTENTIAL).
 FT DOMAIN 61 70 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 71 91 2 (POTENTIAL).
 FT DOMAIN 92 104 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 105 126 3 (POTENTIAL).
 FT DOMAIN 127 143 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 144 168 4 (POTENTIAL).
 FT DOMAIN 169 200 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 201 220 5 (POTENTIAL).
 FT DOMAIN 221 237 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 238 262 6 (POTENTIAL).
 FT DOMAIN 263 279 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 280 303 7 (POTENTIAL).
 FT DOMAIN 304 354 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 103 180 BY SIMILARITY.
 FT CARBOHYD 270 270 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 354 AA; 41030 MW; 77EDB368AA4C868D CRC64;

Query Match 54.3%; Score 44; DB 1; Length 354;
 Best Local Similarity 50.0%; Pred. No. 4;
 Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 Oy 1 HATGAWVFSNATCK 14
 : | | | | |
 Db 91 VAANEWVFGNINCK 104

RESULT 9
 CKR2_MOUSE
 ID CKR2_MOUSE STANDARD; PRT; 373 AA.
 AC P51683; O61172;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 2 (C-C CKR-2) (CCR-2) (CCR2)
 DE (JE/FIC RECEPTOR) (MCP-1 RECEPTOR).
 GN CCR2 OR CNKBR2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96205938; PubMed=8631787;
 RA Boring L., Gosling J., Monteciarlo F.S., Lusis A.J., Tsou C.-L.,
 RA Charo I.F.;
 RT "Molecular cloning and functional expression of murine JE (monocyte
 RT chemoattractant protein 1) and murine macrophage inflammatory protein
 RT 1alpha receptors: evidence for two closely linked C-C chemokine
 RT receptors on chromosome 9.";
 RL J. Biol. Chem. 271:7551-7558(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RX MEDLINE=96216064; PubMed=8662823;
 RA Kurihara T., Bravo R.;
 RT "Cloning and functional expression of mCCR2, a murine receptor for
 RT the C-C chemokines JE and FIC";
 RL J. Biol. Chem. 271:11603-11606(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97026720; PubMed=8872898;
 RA Heesen M., Tanabe S., Berman M.A., Yoshizawa I., Luo Y., Kim R.,
 RA Post T.W., Gerard C., Dorf M.E.;
 RT "Mouse astrocytes respond to the chemokines MCP-1 and KC, but reverse
 RT transcriptase-polymerase chain reaction does not detect mRNA for the
 RT KC or new MCP-1 receptor.";
 RL J. Neurosci. Res. 45:382-391(1996).
 CC -!- FUNCTION: RECEPTOR FOR THE MCP-1 (JE), MCP-3 (FIC) AND MCP-5
 CC CHEMOKINES. TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR
 CC CALCIUM IONS LEVEL.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: DETECTED IN MONOCYTE/MACROPHAGE CELL LINES,
 CC BUT NOT IN NONHEMATOPOIETIC CELL LINES.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC
 CC EMBL; U47035; AAC52453.1; -;
 CC EMBL; U51717; AAC52557.1; -;
 CC EMBL; U56819; AAC52784.1; -;
 CC GCRDB; GCR_1649; -;
 CC GCRDB; GCR_1651; -;
 CC GCRDB; GCR_1657; -;
 CC MGI; MGI:106185; Cnkb2.
 CC InterPro; IPR000276; -;
 CC InterPro; IPR000355; -;
 CC InterPro; IPR002237; -;
 CC Pfam; PF00001; 7tm_1; 1;
 CC PRINTS; PR00237; GPCRHHODPSN.
 CC PRINTS; PR00657; CCHEMOKINER.
 CC PRINTS; PR01107; CHEMOKINER2.
 CC PROSITE; PS00237; G-PROTEIN RECEPTOR FL-1; 1.

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DR EMBL: U77349; AAC03242.1; -.
DR InterPro: IPR000276; -.
DR DR InterPro: IPR000355; -.
DR DR InterPro: IPR002237; -.
DR DR Pfam: PF00001; 7tm.1; 1.
DR DR PRINTS: PR00237; GPCRPHODPSN.
DR DR PRINTS: PR00657; CCHEMOKINER.
DR DR PRINTS: PR01107; CHEMOKINER2.
DR DR PROSITE: PS00237; G_PROTEIN_RECP_F1_1; 1.
DR DR PROSITE: PS00262; G_PROTEIN_RECP_F1_2; 1.
DR KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 60 EXTRACELLULAR (POTENTIAL)
FT TRANSMEM 61 81 POTENTIAL.
FT DOMAIN 82 91 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 92 112 POTENTIAL.
FT DOMAIN 113 128 EXTRACELLULAR (POTENTIAL)
FT TRANSMEM 129 149 POTENTIAL.
FT DOMAIN 150 170 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 171 191 POTENTIAL.
FT DOMAIN 192 220 EXTRACELLULAR (POTENTIAL)
FT TRANSMEM 221 241 POTENTIAL.
FT DOMAIN 242 256 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 257 277 POTENTIAL.
FT DOMAIN 278 301 EXTRACELLULAR (POTENTIAL)
FT TRANSMEM 302 322 POTENTIAL.
FT DOMAIN 323 373 CYTOPLASMIC (POTENTIAL).
FT FT DISULFID 126 203 BY SIMILARITY.
SQ SEQUENCE 373 AA; 42763 MW; 2E7BB012F5D6FD09 CRC64;

Query Match 54.3%; Score 44; DB 1; Length 3
Best Local Similarity 50.0%; Pred. No. 4.2;
Matches 7; Conservative 1; Mismatches 6; Indels 0

QY 1 HATCAWVFSNATCK 14
      : ||||| ||
DB 114 YAANEWFGNIMCK 127

RESULT 11
CKR5_MOUSE STANDARD; PRT: 354 AA.
ID CKR5_MOUSE STANDARD; PRT: 354 AA.
AC P51682; Q61867; P97405; O35313; P97308; O35891;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CC-CKR-5) (C-
DE ALPHA RECEPTOR).
DE CCR5 OR CMKBR5.
DE Mus musculus (Mouse).
DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
DE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
OC NCBI_TaxID=10090;
OX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=129/SVJ; TISSUE=Spleen;
RC MEDLINE=96205938; PubMed=8631787;
RX Boring L., Gosling J., Montecarlo F.S., Lusis A.J., Tsch
RA Charo I.F.;
RA "Molecular cloning and functional expression of murine
RT chemoattractant protein 1) and murine macrophage inflama
RT lpha receptors: evidence for two closely linked C-C che
RT receptors on chromosome 9.";
RL J. Biol. Chem. 271:7551-7558(1996).
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6 x CBA; TISSUE=Thymus;
RC MEDLINE=96278910; PubMed=8662890;
RX Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., F
RA "Cloning and characterization of a novel murine macroph
RT inflammatory protein-1 alpha receptor.";
RL J. Biol. Chem. 271:14445-14451(1996).
RN [3]

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RP SEQUENCE FROM N.A.
 RC STRAIN=129/OLA;
 RA Kuziel W.A., Beck M.A., Dawson T.C., Maeda N.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6, AND NIH/SWISS; TISSUE=Liver, Kidney, and Spleen;
 RX MEDLINE=98001387; PubMed=9343222;
 RA Kubmann S.E., Platt E.J., Kozak S.L., Kabat D.;
 RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
 RT implicate specific amino acids in infections by simian and human
 RT immunodeficiency viruses.";
 RL J. Virol. 71:8642-8656(1997).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129;
 RX MEDLINE=97404635; PubMed=9261347;
 RA Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Sharron M., Cen Y.H.,
 RA Wang Z.X., Guo H.H., Du J.G., Accavitti M.A., Doms R.W., Peiper S.C.;
 RT "Two distinct CCR5 domains can mediate coreceptor usage by human
 RT immunodeficiency virus type 1.";
 RL J. Virol. 71:6305-6314(1997).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC Guo B., Kuno K., Harada A., Matsushima K.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: DETECTED IN MONOCYTE/MACROPHAGE CELL LINES,
 CC BUT NOT IN NONHEMATOPOIETIC CELL LINES.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 DR EMBL; U47036; AAC52454.1; -;
 DR EMBL; X94151; CAA63867.1; -;
 DR EMBL; U68565; AAB37273.1; -;
 DR EMBL; U83327; AAC53386.1; -;
 DR EMBL; AF022990; AAC53389.1; -;
 DR EMBL; AF019772; AAB71183.1; -;
 DR EMBL; D83648; BAAL2024.1; -;
 DR GCRDb; GCR_1150; -;
 DR GCRDb; GCR_1645; -;
 DR GCRDb; GCR_1656; -;
 DR GCRDb; GCR_1729; -;
 DR GCRDb; GCR_2449; -;
 DR GCRDb; GCR_2540; -;
 DR GCRDb; GCR_2554; -;
 DR MGD; MGI:107182; Cmkbr5.
 DR InterPro; IPR000276; -;
 DR InterPro; IPR000355; -;
 DR InterPro; IPR002240; -;
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01110; CCHEMOKINER.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
 DR PROSITE; PS0262; G-PROTEIN_RECEP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.
 FT DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 33 60 1 (POTENTIAL).
 FT DOMAIN 61 70 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 71 91 2 (POTENTIAL).
 FT DOMAIN 92 104 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 105 126 3 (POTENTIAL).

FT DOMAIN 127 143 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 144 168 4 (POTENTIAL).
 FT DOMAIN 169 200 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 201 220 5 (POTENTIAL).
 FT DOMAIN 221 237 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 238 262 6 (POTENTIAL).
 FT DOMAIN 263 279 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 280 303 7 (POTENTIAL).
 FT DOMAIN 304 354 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 103 180 BY SIMILARITY.
 FT CARBOHYD 270 270 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 11 11 I -> S.
 FT VARIANT 62 62 K -> R.
 FT VARIANT 66 66 V -> M.
 FT VARIANT 97 97 I -> V.
 FT VARIANT 109 109 V -> L.
 FT VARIANT 156 156 V -> A.
 FT VARIANT 160 160 F -> S.
 FT VARIANT 185 185 P -> L.
 FT VARIANT 213 213 I -> V.
 FT VARIANT 318 318 I -> M.
 FT VARIANT 337 337 V -> A.
 FT CONFLICT 3 3 F -> L (IN REF. 2).
 FT CONFLICT 80 80 L -> F (IN REF. 2).
 FT CONFLICT 190 190 H -> Y (IN REF. 3).
 FT CONFLICT 208 208 P -> S (IN REF. 1).
 FT CONFLICT 145 145 N -> I (IN REF. 5).
 SQ SEQUENCE 354 AA; 40863 MW; B4A6B942E88F9CF0 CRC64;
 Query Match 53.1%; Score 43; DB 1; Length 354;
 Best Local Similarity 42.9%; Pred No. 5.8;
 Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 HATGAWFNSNATCK 14
 Db 91 YAANEWIFGNMCK 104
 RESULT 12
 OPRX_MOUSE
 ID OPRX_MOUSE STANDARD; PRT; 367 AA.
 AC P35377; Q60645;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE NOCICEPTIN RECEPTOR (ORPHANIN FQ RECEPTOR) (KAPPA-TYPE 3 OPIOID
 DE RECEPTOR) (KOR-3) (ORGC) (K3 OPIATE RECEPTOR).
 GN OPR1L OR OPRL OR OOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6N; TISSUE=Brain;
 RA Yasuda K., Jones E., Reisine T., Bell G.I.;
 RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95100967; PubMed=7802669;
 RA Nishi M., Takeshima H., Mori M., Nakagawara K.I., Takeuchi T.;
 RT "Structure and chromosomal mapping of genes for the mouse
 RT kappa-opioid receptor and an opioid receptor homologue (MOR-C).";
 RL Biochem. Biophys. Res. Commun. 205:1353-1357(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=96387345; PubMed=8794880;
 RA Matthes H.W.D., Seward E.P., Kieffer B., North R.A.;
 RT "Functional selectivity of orphanin FQ for its receptor coexpressed
 RT with potassium channel subunits in Xenopus laevis oocytes.";
 RL Mol. Pharmacol. 50:447-450(1996).

[4]
 RP SEQUENCE FROM N.A.
 RA Pan Y.-X., Xu J., Pasternak G.W.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 [5]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=95327076; PubMed=7603458;
 RX Pan Y.-X., Cheng J., Xu J., Rossi G., Jacobson E., Ryan-Moro J.,
 RA Brooks A.I., Dean G.E., Standifer K.M., Pasternak G.W.;
 RT "Cloning and functional characterization through antisense mapping of
 a kappa 3-related opioid receptor";
 RL Mol. Pharmacol. 47:1180-1188(1995).
 [6]
 RP SEQUENCE OF 1-357 FROM N.A.
 RC STRAIN=BALB/C; TISSUE=Spleen;
 RX MEDLINE=95318231; PubMed=7797625;
 RA Halford W.P., Gebhardt B.M., Carr D.J.J.;
 RT "Functional role and sequence analysis of a lymphocyte orphan opioid
 receptor";
 RL J. Neuroimmunol. 59:91-101(1995).
 CC -1- FUNCTION: RECEPTOR FOR THE NEUROPEPTIDE NOCICEPTIN/ORPHANIN FQ.
 CC HAS A POTENTIAL ROLE IN MODULATING A NUMBER OF BRAIN FUNCTIONS,
 CC INCLUDING INSTINCTIVE BEHAVIORS AND EMOTIONS. THE ACTIVITY OF
 CC THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBITS ADENYLATE
 CC CYCLASE.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC or send an email to license@isb-sib.ch).

 DR EMBL; U04952; AAA03730.1; -;
 DR EMBL; D31667; BAA06509.1; -;
 DR EMBL; D31666; BAA06509.1; JOINED.
 DR EMBL; X91813; CAAG2922.1; -;
 DR EMBL; U32932; AAC52669.1; -;
 DR EMBL; U32928; AAC52669.1; JOINED.
 DR EMBL; U32930; AAC52669.1; JOINED.
 DR EMBL; U09421; AAA81333.1; -;
 DR EMBL; U14165; AAA87899.1; -;
 DR HSP; P34996; IIDD.
 DR GCRDB; GCR_0891; -;
 DR GCRDB; GCR_1715; -;
 DR GCRDB; GCR_1716; -;
 DR GCRDB; GCR_1728; -;
 DR GCRDB; GCR_1731; -;
 DR MGD; MGI:97440; Oprl.
 DR InterPro; IPR000276; -;
 DR InterPro; IPR001418; -;
 DR InterPro; IPR001420; -;
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHOPOSPN.
 DR PRINTS; PR00384; OPIOIDR.
 DR PRINTS; PR00547; XOP10DR.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1.1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_F1.2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Phosphorylation; Lipoprotein; Palmitate.
 FT DOMAIN 1 47
 FT TRANSMEM 48 74
 FT DOMAIN 75 84
 FT TRANSMEM 85 106
 FT DOMAIN 107 121
 FT TRANSMEM 122 143
 FT DOMAIN 144 162
 FT TRANSMEM 163 185
 FT DOMAIN 186 208
 FT TRANSMEM 209 233

FT DOMAIN 234 261
 FT TRANSMEM 262 285
 FT DOMAIN 286 319
 FT TRANSMEM 298 320
 FT DOMAIN 320 367
 FT DISULFID 120 137
 FT LIPID 331 331
 FT CARBOHYD 21 21
 FT CARBOHYD 26 26
 FT CARBOHYD 36 36
 FT CONFLICT 348 349
 SQ SEQUENCE 367 AA; 40491 MW; E498CA9FE5276026 CRC64;
 Query Match 51.9%; Score 42; DB 1; Length 367;
 Best Local Similarity 63.6%; Pred. No. 8.7;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 4 GAWVFSNATCK 14
 DB 111 GWPFGNALCK 121
 RESULT 13
 OPRX_RAT STANDARD; PRT; 367 AA.
 AC P35370;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE NOCICEPTIN RECEPTOR (ORPHANIN FQ RECEPTOR) (KAPPA-TYPE 3 OPIOID
 DE RECEPTOR) (KOR-3) (ROR-C) (XOR1).
 GN OPR1 OR OOR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WISTAR; TISSUE=Brain;
 RX MEDLINE=94215703; PubMed=8163014;
 RA Fukuda K., Kato S., Mori K., Nishi M., Takeshima H., Iwabe N.,
 RA Miyata T., Houtani T., Sugimoto T.;
 RT "cDNA cloning and regional distribution of a novel member of the
 RT opioid receptor family";
 RL FEBS Lett. 343:42-46(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Hippocampus;
 RA Meng F., Xie G., Alfred M., Thompson R., Hoversten M., Watson S.,
 RA Akil H.;
 RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
 RX MEDLINE=94307401; PubMed=8034019;
 RA Bunzow J.R., Saez C., Mortrud M., Bouvier C., Williams J.T., Low M.,
 RA Grandy D.K.;
 RT "Molecular cloning and tissue distribution of a putative member of
 RT the rat opioid receptor gene family that is not a mu, delta or kappa
 RT opioid receptor type";
 RL FEBS Lett. 347:284-288(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94307400; PubMed=8034018;
 RA Chen Y., Fan Y., Liu J., Mestek A., Tian M., Kozak C.A., Yu L.;
 RT "Molecular cloning, tissue distribution and chromosomal localization
 RT of a novel member of the opioid receptor gene family";
 RL FEBS Lett. 347:279-283(1994).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=95096849; PubMed=7798930;

RA Lachowicz J.E., Shen Y., Monsma F.J. Jr., Sibley D.R.;
RT "Molecular cloning of a novel G protein-coupled receptor related to
RT the opiate receptor family.";
RL J. Neurochem. 64:34-40(1995).
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=94298959; PubMed=8026588;
RA Wang J.B., Johnson P.S., Imai Y., Persico A.M., Ozenberger B.A.,
RA Eppler C.M., Uhl G.R.;
RT "CDNA cloning of an orphan opiate receptor gene family member and its
RT splice variant.";
RL FEBS Lett. 348:75-79(1994).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
RX MEDLINE=95182817; PubMed=7877452;
RA Wick M.J., Minnerath S.R., Lin X., Elde R.P., Law P.Y., Loh H.H.;
RT "Isolation of a novel cDNA encoding a putative membrane receptor with
RT high homology to the cloned mu, delta, and kappa opioid receptors.";
RL Brain Res. Mol. Brain Res. 27:37-44(1994).
CC -!- FUNCTION: RECEPTOR FOR THE NEUROPEPTIDE NOCICEPTIN/ORPHANIN FQ.
CC HAS A POTENTIAL ROLE IN MODULATING A NUMBER OF BRAIN FUNCTIONS,
CC INCLUDING INSTINCTIVE BEHAVIORS AND EMOTIONS. THE ACTIVITY OF
CC THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBITS ADENYL
CC CYCLASE.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN SEVERAL BRAIN AREAS.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; D16438; BAA03908.1; -
DR EMBL; U05239; AAA16201.1; -
DR EMBL; U01913; AAA21025.1; -
DR EMBL; L28144; AAC37661.1; -
DR EMBL; U07871; AAA69927.1; -
DR EMBL; L33916; AAA50827.1; -
DR EMBL; L29419; AAC42041.1; -
DR PIR; S46238; S46238.
DR PIR; S43655; S43655.
DR HSSP; P34996; IDDD.
DR GCRDB; GCR_0834; -
DR GCRDB; GCR_0898; -
DR GCRDB; GCR_0912; -
DR GCRDB; GCR_1030; -
DR GCRDB; GCR_1455; -
DR GCRDB; GCR_1487; -
DR GCRDB; GCR_1517; -
DR InterPro; IPR000276; -
DR InterPro; IPR001418; -
DR InterPro; IPR001420; -
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR00384; OPIOIDR.
DR PRINTS; PR00547; XPIOIDR.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 47
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 48 74
FT 1 (POTENTIAL).
FT DOMAIN 75 84
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 85 106
FT 2 (POTENTIAL).
FT DOMAIN 107 121
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 122 143
FT 3 (POTENTIAL).
FT DOMAIN 144 162
FT CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 163 185
FT DOMAIN 186 208
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 209 233
FT 5 (POTENTIAL).
FT DOMAIN 234 261
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 262 285
FT 6 (POTENTIAL).
FT DOMAIN 286 297
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 298 319
FT 7 (POTENTIAL).
FT DOMAIN 320 367
FT CYTOPLASMIC (POTENTIAL).
FT DISULFID 120 197
FT BY SIMILARITY.
FT LIPID 331 331
FT PALMITATE (POTENTIAL).
FT CARBOHYD 21 21
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 26 26
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 36 36
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 105 105
FT G -> R (IN REF. 2).
FT CONFLICT 226 226
FT L -> V (IN REF. 2).
FT CONFLICT 246 246
FT S -> P (IN REF. 2).
FT CONFLICT 348 348
FT S -> T (IN REF. 3).
SQ SEQUENCE 367 AA; 40523 MW; EB2637582747B4AD CRC64;

Query Match 51.9%; Score 42; DB 1; Length 367;
Best Local Similarity 63.6%; Pred. No. 8.7;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 GAWVFSNATCK 14
| | | | |
Db 111 GFWPFGNALCK 121

RESULT 14
ID OPRX_HUMAN STANDARD; PRT; 370 AA.
AC P41146;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DE NOCICEPTIN RECEPTOR (ORPHANIN FQ RECEPTOR) (KAPPA-TYPE 3 OPIOID
DE RECEPTOR) (KOR-3).
GN OPR1 OR ORL1 OR OOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain stem;
RX MEDLINE=94185786; PubMed=8137918;
RA Mollereau C., Parmentier M., Mailleux P., Butour J.L., Moisand C.,
RA Chalon P., Caput D., Vassart G., Meunier C.;
RT "ORL1, a novel member of the opioid receptor family. Cloning,
RT functional expression and localization.";
RL FEBS Lett. 341:33-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Lee P.H., Zhu J., Liu-Chen L., Chang K.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 1-333 FROM N.A., AND INDUCTION.
RC TISSUE=Lymphocytes;
RX MEDLINE=96046908; PubMed=7500847;
RA Wick M.J., Minnerath S.R., Roy S., Ramakrishnan S., Loh H.H.;
RT "Expression of alternate forms of brain opioid 'orphan' receptor mRNA
RT in activated human peripheral blood lymphocytes and lymphocytic cell
RT lines.";
RL Brain Res. Mol. Brain Res. 32:342-347(1995).
CC -!- FUNCTION: RECEPTOR FOR THE NEUROPEPTIDE NOCICEPTIN/ORPHANIN FQ.
CC HAS A POTENTIAL ROLE IN MODULATING A NUMBER OF BRAIN FUNCTIONS,
CC INCLUDING INSTINCTIVE BEHAVIORS AND EMOTIONS. THE ACTIVITY OF
CC THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBITS ADENYL
CC CYCLASE.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- INDUCTION: BY PHYTOHEMAGGLUTININ.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:35:12 ; Search time 189.03 Seconds
(without alignments)
8.681 Million cell updates/sec

Title: US-08-887-977-10_COPY_97_110
Perfect score: 81
Sequence: 1 HATGAWVFSNATCK 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues
Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_15:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_unclassified:*
13: sp_vertebrate:*
14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	60	74.1	367	11	Q9R1V0	Q9R1V0 mus musculus
2	49	60.5	236	4	Q9UEA5	Q9UEA5 homo sapien
3	49	60.5	1455	4	O15360	O15360 homo sapien
4	47	58.0	360	6	O18793	O18793 macaca mula
5	44	54.3	319	1	Q07069	Q07069 halobacteri
6	44	54.3	334	10	Q9M7R3	Q9M7R3 phaeodactyl
7	44	54.3	355	6	Q9MYJ8	Q9MYJ8 callithrix
8	44	54.3	373	11	O51913	O51913 rattus norv
9	44	54.3	526	5	O77438	O77438 drosophila
10	44	54.3	581	5	Q9W5D5	Q9W5D5 drosophila
11	44	54.3	581	5	Q9U902	Q9U902 drosophila
12	44	54.3	581	5	Q9NIU0	Q9NIU0 drosophila
13	44	54.3	1009	1	O07971	O07971 halobacteri
14	44	54.3	1073	1	O51965	O51965 halobacteri
15	43	53.1	349	10	Q9SU66	Q9SU66 arabidopsis
16	42	51.9	112	4	O95569	O95569 homo sapien
17	42	51.9	213	11	Q9QUT5	Q9QUT5 mus musculu
18	42	51.9	362	11	Q9JIN4	Q9JIN4 rattus norv
19	41	50.6	103	3	Q04069	Q04069 saccharomyc

20	41	50.6	126	2	Q9KM54	Q9KM54 vibrio chol
21	41	50.6	334	6	O97724	O97724 felis silve
22	41	50.6	351	6	O97774	O97774 felis silve
23	41	50.6	408	10	Q9SF00	Q9SF00 arabidopsis
24	41	50.6	487	10	Q9LY46	Q9LY46 arabidopsis
25	41	50.6	501	10	Q9XEE7	Q9XEE7 arabidopsis
26	41	50.6	646	2	Q9KQK8	Q9KQK8 vibrio chol
27	41	50.6	1998	5	Q9V7A5	Q9V7A5 drosophila
28	41	50.6	2165	5	O19791	O19791 caenorhabdi
29	40	49.4	85	8	Q35796	Q35796 spharagemon
30	40	49.4	297	14	Q9YW65	Q9YW65 melanoplus
31	40	49.4	316	6	Q9TUV7	Q9TUV7 saguinus sp
32	40	49.4	339	6	Q9TUV2	Q9TUV2 saguinus sp
33	40	49.4	339	6	Q9TUV1	Q9TUV1 saguinus sp
34	40	49.4	339	6	Q9TUV0	Q9TUV0 saguinus sp
35	40	49.4	339	6	Q9TUV9	Q9TUV9 saguinus sp
36	40	49.4	339	6	Q9TUV8	Q9TUV8 saguinus sp
37	40	49.4	339	6	Q9TUV6	Q9TUV6 saguinus sp
38	40	49.4	339	6	Q9TUV5	Q9TUV5 saguinus sp
39	40	49.4	339	6	Q9TUV4	Q9TUV4 callithrix
40	40	49.4	339	6	Q9TUV3	Q9TUV3 callithrix
41	40	49.4	339	6	Q9TUV2	Q9TUV2 alouatta ca
42	40	49.4	339	6	Q9TUV1	Q9TUV1 aotus trivi
43	40	49.4	339	6	Q9TUV0	Q9TUV0 aotus trivi
44	40	49.4	339	6	Q9TUV5	Q9TUV5 alouatta ca
45	40	49.4	339	6	Q9TQV5	Q9TQV5 saguinus sp

ALIGNMENTS

RESULT 1
Q9R1V0
ID Q9R1V0 PRELIMINARY: PRT; 367 AA.
AC Q9R1V0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE CC CHEMOKINE LARC SPECIFIC RECEPTOR.
GN MCCR6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Tanaka Y.;
RT "Molecular Cloning of Murine Homologue of CCR6, the Specific Receptor for CC Chemokine LARC";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB016031; BAA02443.1;
DR INTERPRO; IPR000190;
DR INTERPRO; IPR000276;
DR INTERPRO; IPR000355;
DR PRAM; PF00001; 7tm.1.1;
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00635; ANGIOTENSINR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 367 AA; 42082 MW; 207FD98B2F7A6DD3 CRC64;

Query Match 74.1%; Score 60; DB 11; Length 367;
Best Local Similarity 71.4%; Pred. No. 0.016;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HATGAWVFSNATCK 14
||| ||||| ||
Db 98 HATNTWVFSALCK 111

RESULT 2

DR EMBL; 283076; CAB05445.1; JOINED.
 DR EMBL; 283077; CAB05445.1; JOINED.
 DR EMBL; 283078; CAB05445.1; JOINED.
 DR EMBL; 283079; CAB05445.1; JOINED.
 DR EMBL; 283080; CAB05445.1; JOINED.
 DR EMBL; 283081; CAB05445.1; JOINED.
 DR EMBL; 283082; CAB05445.1; JOINED.
 DR EMBL; 283083; CAB05445.1; JOINED.
 DR EMBL; 283084; CAB05445.1; JOINED.
 DR EMBL; 283085; CAB05445.1; JOINED.
 DR EMBL; 283086; CAB05445.1; JOINED.
 DR EMBL; 283087; CAB05445.1; JOINED.
 DR EMBL; 283088; CAB05445.1; JOINED.
 DR EMBL; 283089; CAB05445.1; JOINED.
 DR EMBL; 283090; CAB05445.1; JOINED.
 DR EMBL; 283091; CAB05445.1; JOINED.
 DR EMBL; 283092; CAB05445.1; JOINED.
 DR EMBL; 283093; CAB05445.1; JOINED.
 DR EMBL; 283094; CAB05445.1; JOINED.
 DR EMBL; 283095; CAB05445.1; JOINED.
 DR EMBL; 283151; CAB05445.1; JOINED.
 DR EMBL; X99226; CRA67610.1; -.
 DR EMBL; AC005567; AAC33401.1; -.
 DR EMBL; AF054569; AAC28331.1; -.
 DR MIN; 227650; -.

KW DNA repair; Nuclear protein; Coiled coil; Phosphorylation;
 KW Disease mutation; Polymorphism.

FT DOMAIN 18 34 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT DOMAIN 38 65 COILED COIL (POTENTIAL).
 FT DOMAIN 1069 1090 LEUCINE-ZIPPER (POTENTIAL).
 FT DOMAIN 1235 1258 COILED COIL (POTENTIAL).
 FT VARIANT 6 6 V -> D.
 FT VARIANT 8 8 N -> K.
 FT VARIANT 435 435 R -> C.
 FT VARIANT 492 492 H -> R.
 FT VARIANT 817 817 L -> P.
 FT VARIANT 845 845 L -> P.
 FT VARIANT 1055 1055 R -> L.
 FT VARIANT 1128 1128 Q -> E.
 FT VARIANT 1131 1131 T -> A.
 FT VARIANT 1302 1302 W -> R.
 FT VARIANT 1417 1417 H -> D.
 FT VARIANT 181 181 A -> V.
 FT VARIANT 244 244 L -> F.
 FT VARIANT 252 252 D -> G.
 FT VARIANT 1110 1110 H -> P (IN FA; LOSS OF FUNCTION).
 FT VARIANT 1117 1117 R -> G (IN FA; LOSS OF FUNCTION).
 FT CONFLICT 717 717 M -> I (IN REF. 2).
 FT CONFLICT 501 501 S -> G (IN REF. 3 AND 4).
 SQ SEQUENCE 1455 AA; 162803 MW; DB43EEDB29DF5C0E CRC64;

Query Match 60.5%; Score 49; DB 4; Length 1455;
 Best Local Similarity 53.8%; Pred. No. 4.7;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 HATGAWFSNATC 13
 |||:|:|:|:|
 DB 204 HAVGSLFRNLCC 216

RESULT 4
 OL18793
 ID OL18793 PRELIMINARY; PRT; 360 AA.
 AC OL18793;

DT 01-JAN-1998 (TRENBLrel. 05, Created)
 DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
 DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
 DE CHEMOKINE RECEPTOR.

GN CCR2B.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hauer D.A., Margulies B.J., Clements J.E.;
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF013958; AAD11572.1; -.
 DR INTERPRO; IPR000248; -.
 DR INTERPRO; IPR000276; -.
 DR INTERPRO; IPR000355; -.
 DR INTERPRO; IPR001277; -.
 DR INTERPRO; IPR002236; -.
 DR INTERPRO; IPR002237; -.
 DR INTERPRO; IPR002240; -.
 DR PFAM; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GFCRRHODOPSN.
 DR PRINTS; PR00241; ANGIOTENSINR.
 DR PRINTS; PR00645; LCR1ORPHANR.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01106; CHEMOKINER1.
 DR PRINTS; PR01107; CHEMOKINER2.
 DR PRINTS; PR01110; CHEMOKINER5.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 SQ SEQUENCE 360 AA; 41139 MW; 4B2552BCE913FE9F CRC64;

Query Match 58.0%; Score 47; DB 6; Length 360;
 Best Local Similarity 61.5%; Pred. No. 2.6;
 Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATGAWFSNATCK 14
 | | | | | | | |
 DB 102 AANWVFGNACK 114

RESULT 5
 Q07069
 ID Q07069 PRELIMINARY; PRT; 319 AA.
 AC Q07069;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
 DE HYPOTHETICAL 36.7 KDA PROTEIN.
 OS Halobacterium salinarum.
 OG Plasmid PHH1.
 OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
 OC Halobacterium.
 OX NCBI_TaxID=2242;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93241154; PubMed=8386798;
 RA Pfeiffer F., Ghahraman P.;
 RT "Plasmid pHH1 of Halobacterium salinarum: characterization of the
 RT replicon region, the gas vesicle gene cluster and insertion
 RT elements.";
 RL Mol. Gen. Genet. 238:193-200(1993).
 DR EMBL; X67101; CAA47475.1; -.
 DR Hypothetical protein; Plasmid.
 SQ SEQUENCE 319 AA; 36662 MW; 430F749412F5B082 CRC64;

Query Match 54.3%; Score 44; DB 1; Length 319;
 Best Local Similarity 58.3%; Pred. No. 7.4;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 HATGAWFSNAT 12
 | | | | | | | |
 DB 59 HLTASWVFGST 70

RESULT 6
 Q9M7R3
 ID Q9M7R3 PRELIMINARY; PRT; 334 AA.

AC Q9M7R3;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE CYTOSOLIC GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE.
 GN GAPC2
 OS Phaeodactylum tricornutum.
 OC Eukaryota; stramenopiles; Bacillariophyta; Bacillariophyceae;
 OC Bacillariophycidae; Naviculales; Phaeodactylaceae; Phaeodactylum.
 OX NCBI_TaxID=2850;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Liand M.-F., Lichie C., Apt K., Martin W., Cerff R.;
 RT "Compartment-Specific Isoforms of TPI and GAPDH are Imported into
 RT Mitochondria as a Fusion Protein: Evidence in Favor of a
 RT Mitochondrial Origin of the Eukaryotic Glycolytic Pathway.";
 RL Mol. Biol. Evol. 17:213-223(2000).
 DR EMBL; AF063805; AAF34325.1; -.
 SQ SEQUENCE 334 AA; 35533 MW; 66E1E6821B75F30A CRC64;
 Query Match 54.3%; Score 44; DB 10; Length 334;
 Best Local Similarity 66.7%; Pred. No. 7.7;
 Matches 10; Conservative 1; Mismatches 2; Indels 2; Gaps 1;
 Qy 1 HAT--GAWFSNATC 13
 Db 136 HTYSGATVFSNASC 150
 RESULT 7
 Q9MYJ8 PRELIMINARY; PRT; 355 AA.
 AC Q9MYJ8;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE CHEMOKINE RECEPTOR.
 GN CCRI.
 OS Callithrix jacchus (Common marmoset).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
 OX NCBI_TaxID=9483;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20153429; PubMed=10686294;
 RA Liang M., Rosser M.P., Ng H.P., May K., Bauman J.G., Islam I.,
 RA Ghanam A., Kretscher P.J., Pu H., Dunning L., Snider R.M.,
 RA Morrissey M.M., Hesselgesser J., Perez H.D., Horuk R.;
 RT "Species selectivity of a small molecule antagonist for the CCRI
 RT chemokine receptor.";
 RL Eur. J. Pharmacol. 389:41-49(2000).
 DR EMBL; AF127528; AAF36453.1; -.
 KW Receptor.
 SQ SEQUENCE 355 AA; 40928 MW; 2B01C47E9874A2C1 CRC64;
 Query Match 54.3%; Score 44; DB 6; Length 355;
 Best Local Similarity 77.8%; Pred. No. 8.2;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 6 WVFNSATCK 14
 Db 99 WVFNGAWCK 107
 RESULT 8
 O55193 PRELIMINARY; PRT; 373 AA.
 ID O55193
 AC O55193;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)

DE C-C CHEMOKINE RECEPTOR TYPE 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (CCR2).
 GN CMKBR2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=SPRAGUE DAWLEY;
 RX MEDLINE=98318173; PubMed=9655467;
 RA Jiang Y., Salafranca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
 RA defebvre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
 RT "Chemokine receptor expression in cultured glia and rat experimental
 RT allergic encephalomyelitis.";
 RL J. Neuroimmunol. 86:11-12(1998).
 CC -1- FUNCTION: RECEPTOR FOR THE MCP-1 (JE), MCP-3 (FIC) AND MCP-5
 CC CHEMOKINES. TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR
 CC CALCIUM IONS LEVEL (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LUNG, SPLEEN, KIDNEY, THYMUS AND
 CC MACROPHAGES.
 CC -1- INDUCTION: IN ANIMALS IN WHICH EXPERIMENTAL ALLERGIC
 CC ENCEPHALOMYELITIS (EAE) HAS BEEN INDUCED.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; U77349; AAC03242.1; -.
 DR INTERPRO; IPR000276; -.
 DR INTERPRO; IPR000355; -.
 DR INTERPRO; IPR002237; -.
 DR PFAM; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01107; CHEMOKINER2.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR; UNKNOWN_1.
 KW G-protein coupled receptor; Transmembrane.
 FT DOMAIN 1 60 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 61 81 POTENTIAL.
 FT DOMAIN 82 91 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 92 112 POTENTIAL.
 FT DOMAIN 113 128 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 129 149 POTENTIAL.
 FT DOMAIN 150 170 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 171 191 POTENTIAL.
 FT DOMAIN 192 220 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 221 241 POTENTIAL.
 FT DOMAIN 242 256 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 257 277 POTENTIAL.
 FT DOMAIN 278 301 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 302 322 POTENTIAL.
 FT DOMAIN 323 373 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 126 203 BY SIMILARITY.
 SQ SEQUENCE 373 AA; 42763 MW; 2E7BB012F5D6FD09 CRC64;
 Query Match 54.3%; Score 44; DB 11; Length 373;
 Best Local Similarity 50.0%; Pred. No. 8.6;
 Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 HATGAWFSNATCK 14
 Db 114 YAANEWFGNIMCK 127
 RESULT 9
 O77438 PRELIMINARY; PRT; 526 AA.
 ID O77438
 AC O77438;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE EG:34F3.6 PROTEIN.
 GN EG:34F3.6.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 RN NCBI_TaxID=7227;
 RP SEQUENCE FROM N.A.
 RA Salles C., Valenti P., Darlamitsou A., Henderson N., Campbell L.,
 RA Glover D.;
 RT "Sequencing the distal X chromosome of Drosophila melanogaster";
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Benos P.;
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL031583; CAA20896.1; -
 DR INTERPRO; IPR000024; -
 DR INTERPRO; IPR000539; -
 DR INTERPRO; IPR000832; -
 DR PFAM; PF01392; Fz; 1;
 DR PFAM; PF01534; Frizzled; 2;
 SQ SEQUENCE 526 AA; 58064 MW; 02C225F7740E6152 CRC64;

Query Match 54.3%; Score 44; DB 5; Length 526;
 Best Local Similarity 58.3%; Pred. No. 12;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 TGAWFSNATCK 14
 |||||
 Db 449 TGLWWSRKTC 460

RESULT 10
 Q9W5D5 PRELIMINARY; PRT; 581 AA.
 AC Q9W5D5;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE F23 PROTEIN.
 GN F23.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 RN NCBI_TaxID=7227;
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Gallie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Randell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003418; AAF45547.1; -
 DR FLYBASE; FBgn0027343; Fz3.
 DR INTERPRO; IPR000024; -
 DR INTERPRO; IPR000539; -
 DR PFAM; PF01392; Fz; 1;
 DR PFAM; PF01534; Frizzled; 2;
 DR PRINTS; PR00489; FRIZZLED.
 SQ SEQUENCE 581 AA; 63380 MW; 07A30B442A993938 CRC64;

Query Match 54.3%; Score 44; DB 5; Length 581;
 Best Local Similarity 58.3%; Pred. No. 13;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 TGAWFSNATCK 14
 |||||
 Db 504 TGLWWSRKTC 515

RESULT 11
 Q9U902 PRELIMINARY; PRT; 581 AA.
 AC Q9U902;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE DFRIZZLED-3 PROTEIN.
 GN DFRIZZLED-3.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 RN NCBI_TaxID=7227;
 RP SEQUENCE FROM N.A.
 RA Sato A., Kojima T., Ui-Tei K., Miyata Y., Saigo K.;
 RT "Dfrizzled-3, a new Drosophila Wnt receptor, acting as an attenuator
 of Wingless signaling in wingless hypomorphic mutants.";
 RL Development 126:4421-4430(1999).
 DR EMBL; AB018565; BAA84677.1; -
 DR INTERPRO; IPR000024; -
 DR INTERPRO; IPR000539; -
 DR PFAM; PF01392; Fz; 1;
 DR PFAM; PF01534; Frizzled; 2;
 DR PRINTS; PR00489; FRIZZLED.
 SQ SEQUENCE 581 AA; 63303 MW; 97CDA856A10A976E CRC64;

Query Match 54.3%; Score 44; DB 5; Length 581;
 Best Local Similarity 58.3%; Pred. No. 13;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 TGAWFSNATCK 14
 |||||
 Db 504 TGLWWSRKTC 515

RESULT 12
 Q9NIU0 PRELIMINARY; PRT; 581 AA.
 AC Q9NIU0;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE FRIZZLED 3.
 GN FZ3.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sivasankaran R., Calleja M., Morata G., Basler K.;
 RT "The Wingless target gene Dizz encodes a new member of the Drosophila
 RT Frizzled family.";
 RL Mech. Dev. 91:427-431(2000).
 DR EMBL: AF195242; AAF63250.1; -;
 SQ SEQUENCE 581 AA; 63251 MW; 07A8BBFF2A9E3F93 CRC64;

Query Match 54.3%; Score 44; DB 5; Length 581;
 Best Local Similarity 58.3%; Pred. No. 13;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 TCAGWFSNATCK 14
 |||||
 Db 504 TGLWWSRKTC 515

RESULT 13
 Q07971 PRELIMINARY; PRT; 1009 AA.
 AC Q07971;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE REPH PROTEIN.
 GN REPH.
 OS Halobacterium halobium.
 OG Plasmid pNRC100.
 OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
 OC Halobacterium
 OX NCBI_TaxID=2241;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRC-1;
 RA Ng W.L., Dassarma S.;
 RT "Minimal replication origin of the 200-kilobase Halobacterium plasmid
 RT pNRC100.";
 RL J. Bacteriol. 175:4584-4596(1993).
 DR EMBL: L19296; AAA72017.1; -;
 KW Plasmid.
 SQ SEQUENCE 1009 AA; 113442 MW; A723BDE83FAF7EE1 CRC64;

Query Match 54.3%; Score 44; DB 1; Length 1009;
 Best Local Similarity 58.3%; Pred. No. 23;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 HATGAWFSNAT 12
 |||||
 Db 658 HLTASWFSGST 669

RESULT 14
 O51965 PRELIMINARY; PRT; 1073 AA.
 ID O51965
 AC O51965;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE REPH PROTEIN.
 GN REPH.
 OS Halobacterium halobium.
 OG Plasmid pNRC100.
 OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
 OC Halobacterium
 OX NCBI_TaxID=2241;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRC-1;
 RA Ng W.L., Dassarma S.;
 RT "Minimal replication origin of the 200-kilobase Halobacterium plasmid
 RT pNRC100.";
 RL J. Bacteriol. 175:4584-4596(1993).
 DR EMBL: L19296; AAA72017.1; -;
 KW Plasmid.
 SQ SEQUENCE 1009 AA; 113442 MW; A723BDE83FAF7EE1 CRC64;

Query Match 54.3%; Score 44; DB 1; Length 1009;
 Best Local Similarity 58.3%; Pred. No. 23;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 HATGAWFSNAT 12
 |||||
 Db 658 HLTASWFSGST 669

RESULT 14
 O51965 PRELIMINARY; PRT; 1073 AA.
 ID O51965
 AC O51965;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE REPH PROTEIN.
 GN REPH.
 OS Halobacterium halobium.
 OG Plasmid pNRC100.
 OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
 OC Halobacterium
 OX NCBI_TaxID=2241;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRC-1;
 RA Ng W.L., Dassarma S.;
 RT "Minimal replication origin of the 200-kilobase Halobacterium plasmid
 RT pNRC100.";
 RL J. Bacteriol. 175:4584-4596(1993).
 DR EMBL: L19296; AAA72017.1; -;
 KW Plasmid.
 SQ SEQUENCE 1009 AA; 113442 MW; A723BDE83FAF7EE1 CRC64;

DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-JUN-1998 (TREMBlrel. 06, Last annotation update)
 DE SIMILARITY 100.0.
 OS Halobacterium sp.
 OG Plasmid pNRC100.
 OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
 OC Halobacterium.
 OX NCBI_TaxID=2243;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRC-1;
 RX MEDLINE=88201675; PubMed=348465;
 RA Dassarma S., Damerval T., Jones J.G., Tandeau de Marsac N.;
 RT "A plasmid-encoded gas vesicle protein gene in a halophilic
 RT archaeobacterium.";
 RL Mol. Microbiol. 1:365-370(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRC-1;
 RX MEDLINE=90016863; PubMed=2552415;
 RA Jones J.G., Hackett N.R., Halladay J.T., Scothorn D.J., Yang C.F.,
 RA Ng W.L., Dassarma S.;
 RT "Analysis of insertion mutants reveals two new genes in the pNRC100
 RT gas vesicle gene cluster of Halobacterium halobium.";
 RL Nucleic Acids Res. 17:7785-7793(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRC-1;
 RX MEDLINE=91267967; PubMed=2050644;
 RA Ng W.L., Kothakota S., Dassarma S.;
 RT "Structure of the gas vesicle plasmid in Halobacterium halobium
 RT inversion isomers, inverted repeats, and insertion sequences.";
 RL J. Bacteriol. 173:3933-3933(1991).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRC-1;
 RX MEDLINE=91323716; PubMed=1864501;
 RA Jones J.G., Young D.C., Dassarma S.;
 RT "Structure and organization of the gas vesicle gene cluster on the
 RT Halobacterium halobium plasmid pNRC100.";
 RL Gene 102:117-122(1991).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRC-1;
 RX MEDLINE=93012964; PubMed=1398080;
 RA Halladay J.T., Ng W.L., Dassarma S.;
 RT "Genetic transformation of a halophilic archaeobacterium with a gas
 RT vesicle gene cluster restores its ability to float.";
 RL Gene 119:131-136(1992).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRC-1;
 RX MEDLINE=93139036; PubMed=8423144;
 RA Halladay J.T., Jones J.G., Lin F., MacDonald A.B., Dassarma S.;
 RT "The rightward gas vesicle operon in Halobacterium plasmid pNRC100:
 RT identification of the gvpA and gvpC gene products by use of antibody
 RT probes and genetic analysis of the region downstream of gvpC.";
 RL J. Bacteriol. 175:684-692(1993).
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRC-1;
 RX MEDLINE=93327890; PubMed=8335077;
 RA Dassarma S.;
 RT "Identification and analysis of the gas vesicle gene cluster on an
 RT unstable plasmid of Halobacterium halobium.";
 RL Experimentia 49:482-486(1993).
 RN [8]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRC-1;
 RX MEDLINE=93328662; PubMed=8335618;
 RA Ng W.L., Dassarma S.;
 RT "Minimal replication origin of the 200-kilobase Halobacterium plasmid

RT PNR100.0. ;
 RL J. Bacteriol. 175:4584-4596(1993).
 RN [9]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRC-1;
 RX MEDLINE=95095934; PubMed=8002589;
 RY Dassarma S., Arora P., Lin F., Molinari E., Yin L.R.;
 RT "Wild-type gas vesicle formation requires at least ten genes in the
 RP gvp gene cluster of Halobacterium halobium plasmid pNRC100.0";
 RL J. Bacteriol. 176:7646-7652(1994).
 RN [10]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRC-1;
 RL Ng W.L., Arora P., Dassarma S.;
 RA Syst. Appl. Microbiol. 16:560-568(1994).
 RN [11]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRC-1;
 RA Dassarma S.;
 RL (in) Robb F.T., Place A.R., Sowers K.R., Schreier H.J., Dassarma S.,
 RL Fleischmann E.M. (eds.);
 RL Archaea:
 RL A laboratory manual - halophiles, pp.253-255,
 RL Cold Spring Harbor Laboratory Press, New York (1995).
 RN [12]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRC-1;
 RA Dassarma S., Arora P.;
 RL FEMS Microbiol. Lett. 153:1-10(1997).
 RN [13]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRC-1;
 RA Ng W.L., Ciuffo S.A., Smith T.M., Bumgarner R.E., Loretz C., Baskin D.,
 RA Faust J., Seto J., Slagel J., Hood L., Dassarma S.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 RN [14]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRC-1;
 RA Ng W.L., Ciuffo S.A., Smith T.M., Bumgarner R.E., Loretz C., Baskin D.,
 RA Faust J., Seto J., Slagel J., Hood L., Dassarma S.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF016485; AAC82795.1. ;
 KW Plasmid.
 SQ SEQUENCE 1073 AA; 120578 MW; FBEE9BC662051675 CRC64;
 Query Match 54.3%; Score 44; DB 1; Length 1073;
 Best Local Similarity 58.3%; Pred. No. 24;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 HATGAWFNSAT 12
 | | : ||||| : |
 Db 722 HLTASWFGSGT 733
 RESULT 15
 Q9SU66 PRELIMINARY; PRT; 349 AA.
 AC Q9SU66;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE HYPOTHETICAL 38.7 KDA PROTEIN.
 GN T17F15.100.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Choisine N., Robert C., Brottier P., Wincker P., Cattolico L.,
 RA Artiguenave F., Saurin W., Weissenbach J., Mewes H.W., Mayer K.F.X.,

RA Lemcke K., Schueller C., Quetier F., Salanoubat M.;
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL049658; CAB41136.1. ;
 DR INTERPRO; IPR001841. ;
 DR PFAM; PF00097; zf-C3HC4; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 349 AA; 38686 MW; A080BD4C1D9DEBBE CRC64;
 Query Match 53.1%; Score 43; DB 10; Length 349;
 Best Local Similarity 46.2%; Pred. No. 12;
 Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 1 HATGAWFNSATC 13
 | | : ||||| : |
 Db 233 HCIDTWLLSNSTC 245

Search completed: May 23, 2001, 15:35:13
 Job time: 619 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:28:28 ; Search time 184.73 Seconds
(without alignments)
6.808 Million cell updates/sec

Title: US-08-887-977-10_COPY_111_132

Perfect score: 115

Sequence: 1 LLKGIYAINFCGMLLLTCISM 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235.residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 2: /SID56/gcgdata/geneseq/geneseq/AA1981.DAT:*
- 3: /SID56/gcgdata/geneseq/geneseq/AA1982.DAT:*
- 4: /SID56/gcgdata/geneseq/geneseq/AA1983.DAT:*
- 5: /SID56/gcgdata/geneseq/geneseq/AA1984.DAT:*
- 6: /SID56/gcgdata/geneseq/geneseq/AA1985.DAT:*
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- 13: /SID56/gcgdata/geneseq/geneseq/AA1992.DAT:*
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- 21: /SID56/gcgdata/geneseq/geneseq/AA2000.DAT:*
- 22: /SID56/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	115	100.0	365	19 W48086	Human dendritic ce
2	115	100.0	365	21 Y97077	Primate (human) ch
3	67	58.3	342	19 W80806	STRL33 protein seq
4	67	58.3	342	19 W54041	Human HBMBU14 prot
5	67	58.3	342	20 Y39366	platelet factor-4
6	67	58.3	342	20 W97783	Human HIV/SIV rece
7	67	58.3	342	20 W97784	African green monk
8	66	57.4	342	20 W97785	Pig-tailed macaque
9	64	55.7	378	20 Y41682	Murine D6 protein.
10	62	53.9	302	19 W70001	Rodent chemokine r
11	62	53.9	351	20 Y23825	A7 times membrane

12	61	53.0	359	15 R53747	Seven transmembran
13	61	53.0	359	19 W48728	Murine V31 seven t
14	61	53.0	359	21 B21691	Murine 7TM recepto
15	61	53.0	378	21 B21699	7TM receptor prote
16	57	49.6	358	15 R53745	Partial sequence o
17	57	49.6	358	21 B21689	Human 7TM receptor
18	57	49.6	378	15 R54079	Epstein Barr virus
19	57	49.6	378	15 R53744	Putative seven tra
20	57	49.6	378	19 W48724	Human V31 seven tr
21	57	49.6	378	19 W56164	G-protein coupled
22	57	49.6	378	19 W53622	Epstein Barr virus
23	57	49.6	378	21 B21688	Human 7TM receptor
24	57	49.6	378	21 Y90629	Human G protein-co
25	57	49.6	378	21 Y90663	Human mutant G pro
26	57	49.6	378	22 B50859	Human CCR7. Homo
27	57	49.6	410	15 R53743	Putative seven tra
28	57	49.6	410	19 W48723	Polyptide sequen
29	57	49.6	410	21 B21687	Genomic clone of 7
30	56	48.7	362	21 B01448	Primate GPR2 amino
31	56	48.7	362	21 B01449	Rodent GPR2 protei
32	55.5	48.3	154	15 R53749	Seven transmembran
33	55.5	48.3	154	19 W48730	Human V112 seven t
34	55.5	48.3	154	21 B21694	Human 7TM receptor
35	55.5	48.3	360	20 W97786	Human HIV/SIV rece
36	55.5	48.3	360	21 Y90617	Human G protein-co
37	55.5	48.3	360	21 Y90651	Human mutant G pro
38	52	45.2	479	20 W96320	Glutathione reduct
39	52	45.2	537	19 W4943	Avian infectious b
40	51.5	44.8	360	20 W97787	African green monk
41	51.5	44.8	360	20 W97788	Pig-tailed macaque
42	51	44.3	25	19 W40018	Peptide effecting
43	51	44.3	159	21 B41786	Human ORFX ORF1550
44	51	44.3	246	20 Y57292	Human BGCKr protei
45	51	44.3	263	20 Y30126	A seven-pass trans

ALIGNMENTS

RESULT	1
W48086	W48086 standard; Protein; 365 AA.
ID	W48086;
AC	W48086;
XX	
DT	11-JUN-1998 (first entry)
XX	
DE	Human dendritic cell chemokine receptor.
XX	
KW	Human; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta;
KW	receptor; dendritic cell; macrophage; inflammation; asthma.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	Misc-difference 193
FT	/note= "encoded by CAN"
XX	
PN	WO9801557-A2.
XX	
PD	15-JAN-1998.
XX	
PF	02-JUL-1997; 97WO-US10819.
XX	
PR	04-JUN-1997; 97US-0048593.
PR	05-JUL-1996; 96US-0675814.
PR	11-OCT-1996; 96US-0028329.
XX	
PA	(SCHE) SCHERING CORP.
XX	
PI	Gish KC, Schall TJ, Vicari A, Wang W, Zlotnik A;
XX	
DR	WPI; 1998-101054/09.

DR N-PSDB; V15418.
 XX Novel chemokines, e.g. thymus expressed chemokine - used for
 PT treating inflammatory conditions including asthma.
 XX
 XX Claim 3; Page 94-95; 202pp; English.
 XX
 XX The present sequence represents human dendritic cell chemokine receptor.
 CC Antibodies which bind to the protein can be used in detecting or
 CC diagnosing various immunological conditions related to expression
 CC of the protein. The nucleic acid can be used for screening and
 CC isolating DNA clones for the chemokines, especially from other
 CC species. The chemokine can be used in the treatment of conditions
 CC associated with abnormal physiology or development, including
 CC inflammatory conditions such as asthma.
 XX
 XX Sequence 365 AA;
 SQ

Query Match 100.0%; Score 115; DB 19; Length 365;
 Best Local Similarity 100.0%; Pred. No. 4e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKGIYAINFCGMLLTCISM 22
 DB 111 llkgiyainfcgmltltcism 132

RESULT 2
 Y97077
 ID Y97077 standard; Protein; 365 AA.
 XX AC Y97077;
 XX
 XX 04-DEC-2000 (first entry)
 XX
 XX Primate (human) chemokine receptor CCR6.
 DE
 XX MIP-3-alpha; chemokine; CCR6 receptor; ligand; cytostatic; agonist;
 KW antagonist; anti-psoriatic; dermatological; immunosuppressive;
 KW anti-inflammatory.
 KW
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 193 /note= "Encoded by CAN#"
 FT
 FT
 XX WO200046248-A1.
 PN
 XX 10-AUG-2000.
 XX
 XX 02-FEB-2000; 2000WO-US00511.
 XX
 XX 03-FEB-1999; 99US-0244281.
 XX
 XX (SCHE) SCHERING CORP.
 XX
 XX Oldham ER, Honev B, Dieu-Nosjean M, Caux C, Zlotnik A;
 XX WPI: 2000-543477/49.
 DR N-PSDB; A51971.
 XX
 XX Novel methods for modulating the migration of cells within or to the
 PT skin using MIP-3-alpha or CCR6 agonists or antagonists, useful for
 PT treating skin disorders, e.g. cancer
 XX.
 XX Disclosure; Page 53-54; 61pp; English.
 XX
 XX The MIP-3-alpha chemokine is expressed in inflamed skin cells. This
 CC chemokine is the ligand for the CCR6 receptor. MIP-3-alpha or CCR6
 CC agonists or antagonists can be used to modulate the migration of a cell
 CC within or to the skin of a mammal. MIP-3-alpha can be used to purify a

CC population of cells expressing a MIP-3-alpha receptor. The methods are
 CC useful for treating a mammalian subject with a skin disease or condition,
 CC e.g. cancer, metastasis, psoriasis, atopic or contact dermatitis,
 CC systemic lupus erythematosus and lichen ruber planus, or for treating
 CC skin transplants or grafts.
 XX
 XX Sequence 365 AA;
 SQ

Query Match 100.0%; Score 115; DB 21; Length 365;
 Best Local Similarity 100.0%; Pred. No. 4e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKGIYAINFCGMLLTCISM 22
 DB 111 llkgiyainfcgmltltcism 132

RESULT 3
 W80806
 ID W80806 standard; Protein; 342 AA.
 XX AC W80806;
 XX
 XX 22-JAN-1999 (first entry)
 XX
 XX STRL33 protein sequence.
 DE
 XX STRL33; human; HIV-1; HIV related disorder; therapy; CD4; diagnosis;
 KW fusion accessory factor.
 KW
 XX Homo sapiens.
 OS
 XX WO9844098-A2.
 PN
 XX 08-OCT-1998.
 PD
 XX 31-MAR-1998; 98WO-US06517.
 PF
 XX 31-MAR-1997; 97US-0042880.
 PR
 XX (USSH) US SEC HEALTH & HUMAN SERVICES.
 PA
 XX Alkhatib G, Berger EA, Farber JM, Liao F;
 PI WPI: 1998-557107/47.
 DR N-PSDB; V68515.
 DR
 XX New isolated fusion accessory factor STRL33 - which mediates HIV
 PT infection of cells, used to develop products for the study,
 PT prevention and therapy of HIV-related disorders
 XX
 XX Claim 65; Fig 4; 74pp; English.
 PS
 XX This sequence is the human STRL33 polypeptide that is expressed by
 CC the recombinant cell line of the invention. The STRL33 polypeptide is a
 CC fusion accessory factor that can function with CD4 to mediate fusion with
 CC cells bearing HIV-1 env from both laboratory-adapted TCL-tropic variants
 CC and from M-tropic variants. Agents that suppress STRL33 can be used in a
 CC method to treat HIV-related disorders. The products and methods can be
 CC used for the study, prevention and therapy of HIV-related disorders.
 XX
 XX Sequence 342 AA;
 SQ

Query Match 58.3%; Score 67; DB 19; Length 342;
 Best Local Similarity 61.9%; Pred. No. 0.0034;
 Matches 13; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 LKGIYAINFCGMLLTCISM 22
 DB 105 llgiyinfytsmltltciv 125

```

RESULT 4
W54041
ID W54041 standard; Protein: 342 AA.
XX
AC W54041;
XX
DT 07-AUG-1998 (first entry)
XX
DE Human HBMBU14 protein.
XX
XX Human; 7-transmembrane receptor; HBMBU14; infection; HIV; cancer; asthma;
KW anorexia; Parkinson's disease; acute heart failure; atherosclerosis;
KW osteoporosis; angina pectoris; myocardial infarction; psychotic disorder;
KW benign prostatic hypertrophy; neurological disorder; therapy;
KW Huntington's disease; Gilles de la Tourette's syndrome.
XX
OS Homo sapiens.
XX
PN EP834563-A2.
XX
PD 08-APR-1998.
XX
PF 23-SEP-1997; 97EP-0307428.
XX
PR 26-SEP-1996; 96US-0026669.
XX
PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI Bergsma DJ, Ellis CE, Elshourbagy NA;
XX
DR WPI; 1998-208924/19.
XX
DR N-PSDB; V24017.
XX
XX New isolated human 7-trans-membrane receptor, HBMBU14 - useful for
PT developing products for treating, e.g. infections, pain, cancers,
PT anorexia, hypotension, osteoporosis and asthma
XX
PS Claim 12; Fig 1; 36pp; English.
XX
CC This sequence is the human HBMBU14 protein of the invention. HBMBU14
CC is a human 7-transmembrane (TM) receptor. The products can be used for
CC treating or preventing conditions related to abnormal HBMBU14 expression
CC or activity, e.g. infections such as bacterial, fungal, protozoan and
CC viral infections especially infections caused by HIV-1 and HIV-2, pain,
CC cancers, anorexia, bulimia, asthma, Parkinson's disease, acute heart
CC failure, atherosclerosis, hypotension, hypertension, urinary retention,
CC osteoporosis, angina pectoris, myocardial infarction, ulcers, asthma,
CC allergies, benign prostatic hypertrophy and psychotic and neurological
CC disorders, including anxiety, schizophrenia, manic depression, delirium,
CC dementia or severe mental retardation, and dyskinesias, such as
CC Huntington's disease or Gilles de la Tourette's syndrome. The products
CC can also be used for diagnosing a disease or susceptibility to a disease
CC related to the expression of HBMBU14 and for identifying compounds which
CC bind to and activate or inhibit a receptor for the polypeptide.
XX
SQ Sequence 342 AA;

Query Match 58.3%; Score 67; DB 19; Length 342;
Best Local Similarity 61.9%; Pred. No. 0.0034;
Matches 13; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 LKGIYAINFCGMLLLTCISM 22
| ||| ||| ||:||||:
Db 105 llgiytnfytsmltlctiv 125

RESULT 5
Y39366
ID Y39366 standard; Protein: 342 AA.
XX
AC Y39366;

```

```

XX 05-JAN-2000 (first entry)
XX Platelet factor-4 (PF-4) receptor amino acid sequence.
XX
KW PF-4; platelet factor-4; alpha granules; collagen; thrombotic stimuli;
KW thrombosis; inflammatory activity; chemokine; PF-4 receptor; HBMBU14;
KW BONZO; TYNSTR; agonist; antagonist; HIV; AIDS; rheumatoid arthritis;
KW asthma; psoriasis; atherosclerosis; inflammatory disorder.
XX
OS Homo sapiens.
XX
PN WO9950670-A1.
XX
PD 07-OCT-1999.
XX
PF 26-MAR-1999; 99WO-GB00950.
XX
PR 27-MAR-1998; 98GB-0006677.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC..
XX
PI MacPhee CH, Moores K, Berkhout TA;
XX
DR WPI; 1999-591378/50.
XX
DR N-PSDB; Z28362.
XX
PT Novel PF-4 receptor assays used to identify antagonists and agonists of
PT the receptor for use in therapy
XX
XX Example 1; Page 27-28; 35pp; English.
XX
CC This sequence is the platelet factor-4 (PF-4) receptor amino acid
CC sequence. PF-4 is a 70 residue polypeptide released from alpha-granules
CC when platelets are activated by contacting collagen or other thrombotic
CC stimuli. PF-4 promotes thrombosis at sites of platelet activation, and
CC also exhibits several inflammatory activities. The carboxy terminal
CC tridecapeptide of PF-4 is a potent chemotactic agent for monocytes. PF-4
CC is a CXC chemokine. The PF-4 receptor, also known as HBMBU14, TYNSTR and
CC BONZO, is used in the methods of the invention. The invention relates to
CC a novel screening method for identifying antagonists and agonists of the
CC PF-4 receptor, involving using PF-4 and the PF-4 receptor together. PF-4
CC and the PF-4 receptor are used to identify further chemokine ligands for
CC the receptor using a competitive binding assay and labelled PF-4. PF-4 is
CC used to identify neutralizing or activating antibodies to the PF-4
CC receptor for use in therapy. PF-4 can be used in a screening method for
CC identifying an antagonist of the receptor. Antagonists and agonists may
CC be used for therapeutic purposes, such as treatment of HIV, AIDS,
CC rheumatoid arthritis, asthma, psoriasis, atherosclerosis, and other
CC inflammatory diseases.
XX
SQ Sequence 342 AA;

Query Match 58.3%; Score 67; DB 20; Length 342;
Best Local Similarity 61.9%; Pred. No. 0.0034;
Matches 13; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 LKGIYAINFCGMLLLTCISM 22
| ||| ||| ||:||||:
Db 105 llgiytnfytsmltlctiv 125

RESULT 6
W97783
ID W97783 standard; Protein: 342 AA.
XX
AC W97783;
XX
XX 21-MAY-1999 (first entry)
XX Human HIV/SIV receptor protein Bonzo.
XX

```

KW SIV receptor; HIV receptor; Bonzo; translocation promoting agent;
 KW human; G protein coupled receptor; chemokine receptor; AIDS;
 KW infection; virus transmission.
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH Misc-difference 53 /note= "encoded by TG"
 FT Misc-difference 9..71
 FT /note= "encoded by TG"
 FT Misc-difference 102
 FT /note= "encoded by CG"

XX WO9903888-A1.

XX 28-JAN-1999.

XX PF 17-JUL-1998; 98WO-US14857.

XX PR 17-JUL-1997; 97US-0896155.

XX PA (UYNV) UNIV NEW YORK STATE.

XX PI Deng H, Kewalramani VN, Littman DR, Unutmaz D;

XX WPI; 1999-132164/11.

XX DR N-PSDB; X07289.

XX New nucleic acid encoding the human translocation promoter Bonzo -
 PT used to screen for potential agents for treating acquired immune
 PT deficiency syndrome

XX Claim 4; Page 78-79; 97pp; English.

XX This is the amino acid sequence of human Bonzo, a novel HIV/SIV
 CC translocation promoting agent that acts in conjunction with CD4 to
 CC serve as a receptor for the entry into a cell of a virus having a
 CC specific viral envelope glycoprotein. Bonzo is a member of the
 CC 7-transmembrane G-protein coupled receptor family, is closely
 CC related to the chemokine receptor family, and is expressed in
 CC lymphoid tissues. The invention provides the amino acid sequences
 CC (see W97783-88) and DNA sequences (see X07289-94) of human,
 CC African green monkey and pig-tailed macaque Bonzo and Bob (brother
 CC of Bonzo) translocation promoting agents. These novel receptors
 CC were identified using an expression cloning strategy. They were
 CC found to be used by particular strains of HIV-2 and M-tropic HIV-1.
 CC The invention also includes: mammalian cells transfected with Bonzo
 CC and/or Bob and human CD4, which can be used to screen potential
 CC therapeutic agents and identify ligands; antibodies to Bonzo, which
 CC can be used therapeutically, e.g. as antagonists or to target
 CC toxins or radioisotopes to HIV-permissive cells; transgenic
 CC animals; and antisense and ribozyme molecules, which may also be
 CC used therapeutically, particularly expressed from a gene therapy
 CC vector.

XX SQ Sequence 342 AA;

Query Match 58.3%; Score 67; DB 20; Length 342;
 Best Local Similarity 61.9%; Pred. No. 0.0034;
 Matches 13; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 2 LKGIYAINFCGMILLTICISM 22

Db 105 llgiytnifysmlilciv 125

RESULT 7

W97784

ID W97784 standard; Protein: 342 AA.

XX

AC W97784;

XX 21-MAY-1999 (first entry)

XX African green monkey HIV/SIV receptor protein Bonzo.

XX SIV receptor; HIV receptor; Bonzo; translocation promoting agent;
 KW G protein coupled receptor; chemokine receptor; AIDS; infection;
 KW virus transmission; African green monkey.

XX Cercopithecus aethiops.

XX WO9903888-A1.

XX 28-JAN-1999.

XX PF 17-JUL-1998; 98WO-US14857.

XX PR 17-JUL-1997; 97US-0896155.

XX PA (UYNV) UNIV NEW YORK STATE.

XX PI Deng H, Kewalramani VN, Littman DR, Unutmaz D;

XX WPI; 1999-132164/11.

XX DR N-PSDB; X07290.

XX New nucleic acid encoding the human translocation promoter Bonzo -
 PT used to screen for potential agents for treating acquired immune
 PT deficiency syndrome

XX Disclosure; Page 80-81; 97pp; English.

XX This is the amino acid sequence of African green monkey Bonzo, a
 CC novel HIV/SIV translocation promoting agent that acts in conjunction
 CC with CD4 to serve as a receptor for the entry into a cell of a virus
 CC having a specific viral envelope glycoprotein. Bonzo is a member of
 CC the 7-transmembrane G-protein coupled receptor family, is closely
 CC related to the chemokine receptor family, and is expressed in
 CC lymphoid tissues. The invention provides the amino acid sequences
 CC (see W97783-88) and DNA sequences (see X07289-94) of human,
 CC African green monkey and pig-tailed macaque Bonzo and Bob (brother
 CC of Bonzo) translocation promoting agents. These novel receptors
 CC were identified using an expression cloning strategy. They were
 CC found to be used by particular strains of HIV-2 and M-tropic HIV-1.
 CC The invention also includes: mammalian cells transfected with Bonzo
 CC and/or Bob and human CD4, which can be used to screen potential
 CC therapeutic agents and identify ligands; antibodies to Bonzo, which
 CC can be used therapeutically, e.g. as antagonists or to target
 CC toxins or radioisotopes to HIV-permissive cells; transgenic
 CC animals; and antisense and ribozyme molecules, which may also be
 CC used therapeutically, particularly expressed from a gene therapy
 CC vector.

XX SQ Sequence 342 AA;

Query Match 58.3%; Score 67; DB 20; Length 342;
 Best Local Similarity 61.9%; Pred. No. 0.0034;
 Matches 13; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 2 LKGIYAINFCGMILLTICISM 22

Db 105 llgiytnifysmlilciv 125

RESULT 8

W97785

ID W97785 standard; Protein: 342 AA.

XX

AC W97785;

XX

DT 21-MAY-1999 (first entry)

XX

DE Pig-tailed macaque HIV/SIV receptor protein Bonzo.
 XX
 KW SIV receptor; HIV receptor; Bonzo; translocation promoting agent;
 KW G protein coupled receptor; chemokine receptor; AIDS; infection;
 KW virus transmission; pig-tailed macaque.
 XX
 OS Macaca nemestrina.
 XX
 PN WO9903888-A1.
 XX
 PD 28-JAN-1999.
 XX
 PF 17-JUL-1998; 98WO-US14857.
 XX
 PR 17-JUL-1997; 97US-0896155.
 XX
 PA (UYNV) UNIV NEW YORK STATE.
 XX
 PI Deng H, Kewalramani VN, Littman DR, Unutmaz D;
 DR WPI; 1999-132164/11.
 DR N-PSDB; X07291.
 XX
 PT New nucleic acid encoding the human translocation promoter Bonzo -
 PT used to screen for potential agents for treating acquired immune
 PT deficiency syndrome
 XX
 PS Disclosure; Page 82-83; 97pp; English.
 XX
 CC This is the amino acid sequence of pig-tailed macaque Bonzo, a
 CC novel HIV/SIV translocation promoting agent that acts in conjunction
 CC with CD4 to serve as a receptor for the entry into a cell of a virus
 CC having a specific viral envelope glycoprotein. Bonzo is a member of
 CC the 7-transmembrane G-protein coupled receptor family, is closely
 CC related to the chemokine receptor family, and is expressed in
 CC lymphoid tissues. The invention provides the amino acid sequences
 CC (see 97/783-88) and DNA sequences (see X07289-94) of human,
 CC African green monkey and pig-tailed macaque Bonzo and Bob (brother
 CC of Bonzo) translocation promoting agents. These novel receptors
 CC were identified using an expression cloning strategy. They were
 CC found to be used by particular strains of HIV-2 and M-tropic HIV-1.
 CC The invention also includes: mammalian cells transfected with Bonzo
 CC and/or Bob and human CD4, which can be used to screen potential
 CC therapeutic agents and identify ligands; antibodies to Bonzo, which
 CC can be used therapeutically, e.g. as antagonists or to target
 CC toxins or radioisotopes to HIV-permissive cells; transgenic
 CC animals; and antisense and ribozyme molecules, which may also be
 CC used therapeutically, particularly expressed from a gene therapy
 CC vector.
 XX
 SQ Sequence 342 AA;
 Query Match 57.4%; Score 66; DB 20; Length 342;
 Best Local Similarity 57.1%; Pred. No. 0.005;
 Matches 12; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 OY 2 LKGIYAINFCGMLLTCTISM 22
 Db 105 llgvytinfytmlltctiv 125
 RESULT 9
 Y41682
 ID Y41682 standard; Protein; 378 AA.
 XX
 AC Y41682;
 XX
 DT 06-DEC-1999 (first entry)
 XX
 DE Murine D6 protein.
 XX
 KW D6; G protein-coupled heptahelical receptor; diagnosis; asthma;

KW respiratory inflammatory disorder; identification.
 XX
 OS Mus sp.
 XX
 PN WO9947697-A1.
 XX
 PD 23-SEP-1999.
 XX
 PF 19-MAR-1999; 99WO-US06075.
 XX
 PR 20-MAR-1998; 98US-0045583.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 PA (CRCT-) CRC TECHNOLOGY LTD.
 XX
 PI Graham GJ, Benjamin Nibbs RJ, Gonzalo J, Gutierrez-Ramos J;
 DR WPI; 1999-562123/47.
 DR N-PSDB; Z25023, Z25024.
 XX
 PT Identification of D6 G-protein coupled receptor binding compounds and
 PT modulators, useful in treatment of asthma
 XX
 PS Claim 1; Fig 2; 152pp; English.
 XX
 CC Methods have been developed for identifying a compound, which binds to a
 CC human or murine D6 protein, an allelic variant or a fragment comprises
 CC detecting binding of the test compound to the protein. Also described in
 CC the present invention are: (1) a method for identifying a compound
 CC capable of treating a disorder characterized by aberrant D6 nucleic acid
 CC expression of D6 protein activity; (2) a method for treating a subject
 CC having a disorder characterized by aberrant D6 protein activity or
 CC nucleic acid expression comprising administering to the subject a D6
 CC modulator such that treatment of the subject occurs; and (3) methods for
 CC identifying a compound that modulates the activity of a human or murine
 CC D6 protein, an allelic variant or a fragment. The methods are useful for
 CC identifying compounds capable of treating disorders, especially a
 CC respiratory inflammatory disorder, characterized by aberrant D6 nucleic
 CC acid expression or D6 protein activity. In particular, the disorder is
 CC asthma. D6 modulators are used to treat asthma. The present sequence
 CC represents the murine D6 protein.
 XX
 SQ Sequence 378 AA;
 Query Match 55.7%; Score 64; DB 20; Length 378;
 Best Local Similarity 40.9%; Pred. No. 0.012;
 Matches 9; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
 OY 1 LLKGIYAINFCGMLLTCTISM 22
 Db 118 vistlysinfcgiffitcmsl 139
 RESULT 10
 W70001
 ID W70001 standard; Protein; 302 AA.
 XX
 AC W70001;
 XX
 DT 20-OCT-1998 (first entry)
 XX
 DE Rodent chemokine receptor 941D12 amino acid sequence.
 XX
 KW Chemokine; primate; human; rodent; chemokine receptor; asthma;
 KW inflammatory response; immune response; leukocyte migration; GPCR;
 KW leukocyte adhesion; chemoattractant; modulation; antiviral response;
 KW cellular morphology modification response; G-protein coupled receptor;
 KW phosphoinositide lipid turnover; abnormal proliferation; regeneration;
 KW atrophy; 941D12.
 XX
 OS Mus sp.

PN W09832858-A2.

XX 30-JUL-1998.

XX 22-JAN-1998; 98WO-US00902.

XX 23-JAN-1997; 97US-0036715.

XX (SCHE) SCHERING CORP.

XX Gorman DM, Hedrick JA, Mattson JD, Soto-trejo H;

XX Zlotnik A;

XX WPI; 1998-427954/36.

XX DR N-PSDB; V43795.

XX Rodent and primate chemokines and chemokine receptors - useful

XX PT diagnostically and therapeutically to treat conditions associated

XX PT with abnormal physiology or development e.g. inflammatory conditions

XX PS- Claim 5; Pages 97-99; 105pp; English.

XX This represents a rodent chemokine receptor 941D12 amino acid sequence.
 CC The invention provides novel primate and rodent chemokines and chemokine
 CC receptors. The chemokines, receptors and binding compounds (optionally
 CC antibodies/fragments specifically binding the chemokines) are useful
 CC therapeutically to treat conditions associated with abnormal physiology
 CC or development e.g. inflammatory conditions such as asthma. Chemokines
 CC are important in immune and inflammatory responses in that they induce
 CC leukocyte migration and adhesion. They are also chemoattractants for
 CC several cells involved in inflammation and can induce other biological
 CC responses e.g. modulation of second messenger levels (e.g. Ca⁺⁺),
 CC cellular morphology modification responses, phosphoinositide lipid
 CC turnover, possible antiviral responses etc. The chemokine receptors of
 CC the invention exhibit structural properties of G-protein coupled
 CC receptors (GPCR), although their ligands have not yet been identified.
 CC The chemokine and chemokine receptor polypeptides are useful to produce
 CC ligand:receptor complexes in vivo or in assay techniques. Assays may
 CC also involve chemical antagonists which block complex production or
 CC utilise competitive binding. Binding compounds identified (agonists or
 CC antagonists) can be used to modulate the physiological responses in cells
 CC (especially neurons, macrophages or lymphocytes) to treat e.g. abnormal
 CC proliferation, regeneration, generation and atrophy. The polypeptides
 CC are also used to produce antibodies useful diagnostically, for drug
 CC screening or for polypeptide purification. The polynucleotides are useful
 CC to produce probes for detecting the polypeptides, and to isolate the
 CC polypeptides or related sequences, especially from other species. They
 CC also allow transformation of cells for polypeptide production.

XX Sequence 302 AA;

Query Match 53.9%; Score 62; DB 19; Length 302;
 Best Local Similarity 52.4%; Pred. No. 0.02;
 Matches 11; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 QY 2 LKGIYAINFCGMILLTCISM 22
 Db 114 lrgmytmfysmltctiv 134
 RESULT 11
 Y23825
 ID Y23825 standard; Protein; 351 AA.
 XX AC Y23825;
 XX DT 15-SEP-1999 (first entry)
 XX DE A7 times membrane penetrating type receptor protein ET60.
 XX 7 times membrane-penetrating type receptor protein; ET60;
 KW leukocyte function; control; drug.

XX Sequence 302 AA;

Query Match 53.9%; Score 62; DB 19; Length 302;
 Best Local Similarity 52.4%; Pred. No. 0.02;
 Matches 11; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 LKGIYAINFCGMILLTCISM 22

Db 114 lrgmytmfysmltctiv 134

RESULT 11

ID Y23825 standard; Protein; 351 AA.

XX AC Y23825;

XX DT 15-SEP-1999 (first entry)

XX DE A7 times membrane penetrating type receptor protein ET60.

XX 7 times membrane-penetrating type receptor protein; ET60;

KW leukocyte function; control; drug.

PS

XX Unidentified.

XX JP11155573-A.

XX 15-JUN-1999.

XX 27-NOV-1997; 97JP-0325823.

XX 27-NOV-1997; 97JP-0325823.

XX (ASAH) ASahi KASEI KOGYO KK.

XX WPI; 1999-398070/34.

XX DR N-PSDB; X86032.

XX New 7 times membrane-penetrating type receptor protein ET60 - useful
 XX PT for detecting drug controlling function of leukocyte
 XX PS Claim 1; Page 17-18; 20pp; Japanese.
 XX The present sequence represents a 7 times membrane-penetrating type
 CC receptor protein ET60. The 7 times membrane-penetrating type
 CC receptor protein ET60 can be used for detecting a drug controlling
 CC the function of leukocyte.

XX Sequence 351 AA;

Query Match 53.9%; Score 62; DB 20; Length 351;
 Best Local Similarity 52.4%; Pred. No. 0.024;
 Matches 11; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 QY 2 LKGIYAINFCGMILLTCISM 22
 Db 114 lrgmytmfysmltctiv 134
 RESULT 12
 R53747
 ID R53747 standard; Protein; 359 AA.
 XX AC R53747;
 XX DT 03-FEB-1995 (first entry)
 XX DE Seven transmembrane receptor (V31) partial sequence of mouse.
 XX PR Primer; seven transmembrane receptor; receptor; amplification; PCR;
 KW polymerase chain reaction.

XX Mus musculus.

XX W09412635-A.

XX 09-JUN-1994.

XX 17-NOV-1993; 93WO-US11153.

XX 17-NOV-1992; 92US-0977452.

XX (ICOS-) ICOS CORP.

XX Godiska R, Gray PW, Schweickart VL;

XX WPI; 1994-200264/24.

XX N-PSDB; Q66164.

XX DNA encoding seven transmembrane receptors - used to develop

XX PT prods. for use as therapeutic or diagnostic agents for conditions

XX PT involving the receptors.

XX Example 5; Page 61-62; 100pp; English.

XX Two primers (Q66148, Q66149) were used to amplify human genomic DNA
 CC purified from leukocytes. Approximately 1000 clones were isolated
 CC after the initial amplification reaction and probed with sequences
 CC specific for seven transmembrane receptors IL8R1, AT2R and R20.
 CC Clones which did not hybridise were then chosen for sequence
 CC analysis. Three new clones were identified that appeared to encode
 CC seven transmembrane receptor segments. Two more primers (Q66151,
 CC Q66152) were used to isolate a full length version of one of the
 CC human V31 clone (See Q66153). A fragment of the human clone was used
 CC to isolate a V31 genomic clone of the mouse from a library.
 XX
 XX SQ Sequence 359 AA;

Query Match 53.0%; Score 61; DB 15; Length 359;
 Best Local Similarity 63.2%; Pred. No. 0.036; 4; Indels 0; Gaps 0;
 Matches 12; Conservative 3; Mismatches 4;

QY 4 GIYAINFNCGMLLTCTISM 22
 III :I IIIII III:
 Db 114 giyklfsfsgmlllclisi 132

RESULT 13
 W48728 ID W48728 standard; Protein; 359 AA.
 XX AC W48728;
 XX DT 25-SEP-1998 (first entry)
 XX DE Murine V31 seven transmembrane (7TM) receptor.
 XX KW V28; placenta; seven transmembrane receptor; 7TM; signal transduction;
 KW immunology; inflammation; V31; ss.
 XX OS Mus sp.
 XX PN US5759804-A.
 XX PD 02-JUN-1998.
 XX PF 17-NOV-1993; 93US-0153848.
 XX PR 17-NOV-1992; 92US-0977452.
 XX PA (ICOS-) ICOS CORP.
 XX PI Godiska R, Gray PW, Schweickart VL;
 XX WPI; 1998-332132/29.
 XX DR N-PSDB; V18351.

XX DNA encoding V28 seven transmembrane receptor polypeptide - useful
 PT for producing recombinant polypeptide and anti-V28 antibodies, and
 PT in screening assays for V28 agonists and antagonists
 XX
 XX Example 5; Columns 55-58; 56pp; English.
 XX
 XX The present sequence represents the murine V31 seven transmembrane
 CC (7TM) receptor which is encoded by the murine V31 genomic DNA (V18351)
 CC isolated from a mouse genomic library. The invention claims for the
 CC full length V28 genomic DNA sequence isolated from a human placenta
 CC genomic library. V28 (W48722) and V31 proteins are seven transmembrane
 CC (7TM) receptors which are probably involved in signal transduction.
 CC The invention also claims that cells transformed with V28 DNA can be
 CC used to produce the recombinant polypeptide, to produce anti-V28
 CC antibodies or in screening assays for V28 agonists or antagonists. The
 CC antibodies, agonists and antagonists could then be used to modulate
 CC V28 receptor-ligand binding, for e.g. in immunological and/or
 CC inflammatory events in vivo.
 XX

SQ Sequence 359 AA;
 Query Match 53.0%; Score 61; DB 19; Length 359;
 Best Local Similarity 63.2%; Pred. No. 0.036;
 Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 4 GIYAINFNCGMLLTCTISM 22
 III :I IIIII III:
 Db 114 giyklfsfsgmlllclisi 132

RESULT 14
 B21691 ID B21691 standard; Protein; 359 AA.
 XX AC B21691;
 XX DT 26-JAN-2001 (first entry)
 XX DE Murine 7TM receptor V31cDNA clone protein.
 XX KW Seven transmembrane receptor; 7TM; heptahelical; serpentine;
 KW G-protein-coupled; V28; V31; V112; R20; R2; R12; RM3; gene therapy;
 KW cancer.
 XX OS Mus sp.
 XX PN US6107475-A.
 XX PD 22-AUG-2000.
 XX PF 26-APR-1999; 99US-0299843.
 XX PR 17-MAY-1994; 94US-0245242.
 XX PR 01-JUN-1998; 98US-0088337.
 XX PR 17-NOV-1992; 92US-0977452.
 XX PR 17-NOV-1993; 93US-0153848.
 XX PA (ICOS-) ICOS CORP.
 XX PI Schweickart VL, Gray PW, Godiska R;
 XX WPI; 2000-571335/53.
 XX DR N-PSDB; A91711.

XX Polynucleotide encoding seven transmembrane receptors, antibody
 PT specific to the receptor, agonist and antagonist of the receptor useful
 PT for treating inflammation in a mammal -
 XX Example 4; Columns 57-60; 61pp; English.
 XX
 XX The present sequence is a novel seven transmembrane (7TM) receptors
 CC (also known as heptahelical, serpentine or G-protein-coupled receptors).
 CC The coding sequence for the present sequence may be used for gene
 CC therapy for diseases such as cancer.
 XX
 XX SQ Sequence 359 AA;

Query Match 53.0%; Score 61; DB 21; Length 359;
 Best Local Similarity 63.2%; Pred. No. 0.036;
 Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 GIYAINFNCGMLLTCTISM 22
 III :I IIIII III:
 Db 114 giyklfsfsgmlllclisi 132

RESULT 15
 B21699 ID B21699 standard; Protein; 378 AA.
 XX

AC B21699;
 XX 26-JAN-2001 (first entry)
 XX 7TM receptor protein.
 XX Seven transmembrane receptor; 7TM; heptahelical; serpentine;
 KW G-protein-coupled; V28; V31; V112; R20; R2; R12; RM3; gene therapy;
 KW cancer.
 XX Unidentified.
 XX OS US6107475-A.
 XX PN 22-AUG-2000.
 XX PD 26-APR-1999; 99US-0299843.
 XX PF 17-MAY-1994; 94US-0245242.
 XX PR 01-JUN-1998; 98US-0088337.
 XX PR 17-NOV-1992; 92US-0977452.
 XX PR 17-NOV-1993; 93US-0153848.
 XX PA (ICOS-) ICOS CORP.
 XX PI Schweickart VL, Gray PW, Godiska R;
 XX WPI; 2000-571335/53.
 DR N-PSDB; A91745.
 XX PT Polynucleotide encoding seven transmembrane receptors, antibody
 specific to the receptor, agonist and antagonist of the receptor useful
 for treating inflammation in a mammal -
 XX PS Disclosure; Columns 111-112; 61pp; English.
 XX CC The present sequence is a novel seven transmembrane (7TM) receptors
 (also known as heptahelical, serpentine or G-protein-coupled receptors).
 CC The coding sequence for the present sequence may be used for gene
 CC therapy for diseases such as cancer.
 XX SQ Sequence 378 AA;
 Query Match 53.0%; Score 61; DB 21; Length 378;
 Best Local Similarity 63.2%; Pred. No. 0.038;
 Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 4 GIYAINFCGMLLTCISM 22
 III ::I IIII III;
 Db 134 glyklsffsgmlllcisi 152

Search completed: May 23, 2001, 15:28:28
 Job time: 405 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:30:06 ; Search time 95.91 Seconds
(without alignments)
4.407 Million cell updates/sec

Title: US-08-887-977-10_COPY_111_132
Perfect score: 115
Sequence: 1 LKGIYAINFCNCGMLLTICISM 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pap.*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pap.*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pap.*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pap.*
5: /cgn2_6/ptodata/2/1aa/PTUS_COMB.pap.*
6: /cgn2_6/ptodata/2/1aa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	67	58.3	342	2	US-08-742-011-2
2	61	53.0	359	1	US-08-153-848-24
3	61	53.0	359	3	US-09-299-843A-24
4	61	53.0	359	5	PCT-US93-11153-24
5	61	53.0	378	3	US-09-299-843A-66
6	57	49.6	358	1	US-08-153-848-19
7	57	49.6	358	3	US-09-299-843A-19
8	57	49.6	358	5	PCT-US93-11153-19
9	57	49.6	378	1	US-08-383-750-2
10	57	49.6	378	1	US-08-383-751A-2
11	57	49.6	378	1	US-08-153-848-15
12	57	49.6	378	3	US-08-382-678-2
13	57	49.6	378	3	US-09-299-843A-15
14	57	49.6	378	4	US-09-251-545-1
15	57	49.6	378	5	PCT-US93-09636-2
16	57	49.6	378	5	PCT-US93-11153-15
17	57	49.6	410	1	US-08-153-848-7
18	57	49.6	410	3	US-09-299-843A-7
19	57	49.6	410	5	PCT-US93-11153-7
20	55.5	48.3	154	1	US-08-153-848-36
21	55.5	48.3	154	3	US-09-299-843A-36
22	55.5	48.3	154	5	PCT-US93-11153-36
23	52	45.2	479	4	US-09-126-109-8
24	51	44.3	350	2	US-08-966-316-16
25	51	44.3	368	4	US-08-709-838-2
26	51	44.3	368	4	US-08-829-839-2
27	51	44.3	372	1	US-08-202-056-5

28	51	44.3	372	1	US-08-076-093A-6
29	51	44.3	372	1	US-08-701-265-6
30	51	44.3	372	2	US-08-284-586-6
31	51	44.3	372	2	US-08-805-478-6
32	51	44.3	372	2	US-08-802-627A-6
33	51	44.3	372	2	US-08-801-238-6
34	51	44.3	372	2	US-08-801-228-6
35	51	44.3	372	3	US-09-104-296-6
36	51	44.3	372	4	US-08-982-493-8
37	51	44.3	373	4	US-08-513-974B-373
38	51	44.3	375	1	US-08-442-134A-2
39	51	44.3	375	1	US-08-444-581B-2
40	51	44.3	375	1	US-08-446-088A-2
41	51	44.3	375	2	US-08-559-524A-3
42	51	44.3	375	3	US-08-749-707-3
43	50	43.5	350	2	US-08-966-316-18
44	50	43.5	358	3	US-09-041-545-2
45	50	43.5	358	3	US-09-327-925-2

ALIGNMENTS

RESULT 1
US-08-742-011-2
; Sequence 2, Application US/08742011
; Patent No. 5824504
; GENERAL INFORMATION:
; APPLICANT: Elshourbagy, Nabil A.
; APPLICANT: Bergsma, Derk J.
; APPLICANT: Ellis, Catherine E.
; TITLE OF INVENTION: Human 7-Transmembrane Receptor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742.011
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T.
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: ATG50020P
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-5090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 342 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-742-011-2

Query Match 58.3% Score 67; DB 2; Length 342;
Best Local Similarity 61.9%; Pred. No. 0.0011;
Matches 13; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 LKGIYAINFCNCGMLLTICISM 22

DB 105 LLGIYINFTYMLLTICIV 125

RESULT 2
US-08-153-848-24
; Sequence 24, Application US/08153848
; Patent No. 5759804
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153,848
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5759804and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-153-848-24

Query Match 53.0%; Score 61; DB 1; Length 359;
Best Local Similarity 63.2%; Pred. No. 0.012;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 4 GIYAINFCGMLLLTCISM 22
||| :| |||| |||
Db 114 GIYKLSFFSGMLLLCISI 132

RESULT 3
US-09-299-843A-24
; Sequence 24, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois

COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Jill E. Uhl
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-299-843A-24

Query Match 53.0%; Score 61; DB 3; Length 359;
Best Local Similarity 63.2%; Pred. No. 0.012;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 4 GIYAINFCGMLLLTCISM 22
||| :| |||| |||
Db 114 GIYKLSFFSGMLLLCISI 132

RESULT 4
PCT-US93-11153-24
; Sequence 24, Application PC/TUS9311153
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: Novel Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11153
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-11153-24

Query Match 53.0%; Score 61; DB 5; Length 359;
Best Local Similarity 63.2%; Pred. No. 0.012;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 GIYAINFCGMLLLTCISM 22
||| :| |||| |||
Db 114 GIYKLSFFSGMLLLCISI 132

RESULT 5
US-09-299-843A-66
; Sequence 66, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,843A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/088,337
; FILING DATE: 01-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jill E. Uhl
; REGISTRATION NUMBER: 43,213
; REFERENCE/DOCKET NUMBER: 27866/32059B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX:
; INFORMATION FOR SEQ ID NO: 66:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-299-843A-66

Query Match 53.0%; Score 61; DB 3; Length 378;
Best Local Similarity 63.2%; Pred. No. 0.012;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 GIYAINFCGMLLLTCISM 22
||| :| |||| |||
Db 134 GIYKLSFFSGMLLLCISI 152

RESULT 6
US-08-153-848-19
; Sequence 19, Application US/08153848
; Patent No. 5759804
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153,848
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5759804and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-153-848-19

Query Match 49.6%; Score 57; DB 1; Length 358;
Best Local Similarity 54.5%; Pred. No. 0.055;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 LLKGIYAINFCGMLLLTCISM 22
| :| :| |||| |||
Db 111 LIFAIYKMSFFSGMLLLCISI 132

```

RESULT 7
US-09-299-843A-19
; Sequence 19, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: NO. 6107475el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,843A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/088,337
; FILING DATE: 01-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jill E. Uhl
; REGISTRATION NUMBER: 43,213
; REFERENCE/DOCKET NUMBER: 27866/32059B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-299-843A-19

Query Match 49.6%; Score 57; DB 3; Length 358;
Best Local Similarity 54.5%; Pred. No. 0.055;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 LLKGIYAINFCGMLLLTCISM 22
Db 111 LFAIYKMSFFSGMLLLCISI 132

RESULT 8
PCT-US93-11153-19
; Sequence 19, Application PC/TUS9311153
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: Novel Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

```

```

; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11153
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-11153-19

Query Match 49.6%; Score 57; DB 5; Length 358;
Best Local Similarity 54.5%; Pred. No. 0.055;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 LLKGIYAINFCGMLLLTCISM 22
Db 111 LFAIYKMSFFSGMLLLCISI 132

RESULT 9
US-08-383-750-2
; Sequence 2, Application US/08383750
; Patent No. 5744301
; GENERAL INFORMATION:
; APPLICANT: Birkenbach, Mark
; APPLICANT: Kieff, Elliot
; TITLE OF INVENTION: Epstein Barr Virus Induced Genes
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W.,
; STREET: Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/383,750
; FILING DATE: Herewith
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Fox, Samuel, L.
; REGISTRATION NUMBER: 30,353

```

```

; REFERENCE/DOCKET NUMBER: 0627.3300001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-383-750-2

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```

Query Match 49.6%; Score 57; DB 1; Length 378;
Best Local Similarity 54.5%; Pred. No. 0.059;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

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```

QY 1 LLKGIYAINFCGMLLLTCISM 22
; : : : : : : : : : : : : : : : :
DB 131 LFAIYKMSFFSGMLLLCISI 152

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RESULT 10
US-08-383-751A-2

```

```

; Sequence 2, Application US/08383751A
; Patent No. 5753516
; GENERAL INFORMATION:
; APPLICANT: Heagy, Wyrtta E.
; APPLICANT: Fiberg, Robert W.
; TITLE OF INVENTION: Identification and Uses of Opioid
; TITLE OF INVENTION: Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: US
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/383.751A
; FILING DATE: 03-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: DFCI:001/WIM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; TOPOLOGY: linear
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-383-751A-2

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Query Match 49.6%; Score 57; DB 1; Length 378;
Best Local Similarity 54.5%; Pred. No. 0.059;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

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```

QY 1 LLKGIYAINFCGMLLLTCISM 22
; : : : : : : : : : : : : : : : :
DB 131 LFAIYKMSFFSGMLLLCISI 152

```

RESULT 11

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US-08-153-848-15
; Sequence 15, Application US/08153848
; Patent No. 5759804
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153,848
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5759804and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-153-848-15

```

```

Query Match 49.6%; Score 57; DB 1; Length 378;
Best Local Similarity 54.5%; Pred. No. 0.059;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

```

```

QY 1 LLKGIYAINFCGMLLLTCISM 22
; : : : : : : : : : : : : : : : :
DB 131 LFAIYKMSFFSGMLLLCISI 152

```

```

RESULT 12
US-08-352-678-2

```

```

; Sequence 2, Application US/08352678
; Patent No. 6043351
; GENERAL INFORMATION:
; APPLICANT: Birkenbach, Mark
; APPLICANT: Kieff, Elliott
; TITLE OF INVENTION: EPSTEIN BARR VIRUS INDUCED GENES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

NAME: JILL E. UHL

ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/09636
FILING DATE: herewith
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US93-09636-2

Query Match 49.6%; Score 57; DB 5; Length 378;
Best Local Similarity 54.5%; Pred. No. 0.059;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 LKGIYAINFCGMMLLTCTISM 22
| : || : || || || || || :
Db 131 LIFAIYKMSFFSGMMLLLCISI 152

Search completed: May 23, 2001, 15:30:06
Job time: 413 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 23, 2001, 15:32:00 ; Search time 110.15 Seconds
(without alignments)
13.726 Million cell updates/sec

Title: US-08-887-977-10_COPY_111_132

Perfect score: 115
Sequence: 1 LLKGIYAINFCNCGMLLTTCISM 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.67:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	115	100.0	369	2 JC5068	G protein-coupled
2	61	53.0	378	2 A55735	G protein-coupled
3	57	49.6	378	2 A55680	G protein-coupled
4	57	49.6	378	2 B55735	lymphocyte-specific
5	56	48.7	354	2 B55733	G protein-coupled
6	55.5	48.3	360	2 G02064	G protein-coupled
7	53	46.1	87	2 B41869	pro-sigma K proces
8	52	45.2	374	2 S32785	G protein-coupled
9	52	45.2	479	1 RDHUU	glutathione reduct
10	51	44.3	327	2 S56162	MDCK15 protein - h
11	51	44.3	372	2 S26667	G protein-coupled
12	51	44.3	373	2 A47556	ATP receptor P2u -
13	51	44.3	375	2 A54946	P-2U nucleotide re
14	51	44.3	466	2 S39494	glutathione reduct
15	50	43.5	350	2 JN0621	G protein-coupled
16	49.5	43.0	350	2 A39445	interleukin-8 rece
17	49.5	43.0	360	2 A53611	interleukin-8 rece
18	49	42.6	318	2 T11857	NADH dehydrogenase
19	49	42.6	318	2 T11363	NADH dehydrogenase
20	49	42.6	354	2 A23669	interleukin-8 rece
21	49	42.6	355	2 J01231	interleukin-8 rece
22	49	42.6	358	2 A53752	interleukin-8 rece
23	49	42.6	374	2 S42628	G protein-coupled
24	49	42.6	1162	2 S07421	E2 glycoprotein pr
25	48	41.7	316	1 VNRWMS	nucleocapsid prote
26	48	41.7	480	2 A82033	TLDD protein homol
27	48	41.7	480	2 F81010	tlld protein NMB20
28	47	40.9	367	2 J50349	interferon-inducib
29	46.5	40.4	613	2 T72077	hypothetical prote

30	46	40.0	341	2 I57997	hypothetical calci
31	46	40.0	397	2 S66518	proteinase-activat
32	46	40.0	399	2 I48705	proteinase activat
33	46	40.0	485	2 F82718	tlld protein XF112
34	45	39.1	261	2 F64924	probable thiosulfa
35	45	39.1	300	2 JC5714	G protein-coupled
36	45	39.1	362	2 A39714	G protein-coupled
37	45	39.1	365	2 S68679	G protein-coupled
38	44	38.3	265	2 C72012	CpDiacylglycerol-
39	44	38.3	511	2 T37681	kinesin-like prote
40	44	38.3	533	2 C64706	phosphate permease
41	44	38.3	690	2 T08604	hypothetical prote
42	44	38.3	1162	1 VGIHAK	E2 glycoprotein pr
43	44	38.3	1162	2 S14939	E2 glycoprotein pr
44	44	38.3	1162	2 S14940	E2 glycoprotein pr
45	44	38.3	2052	2 T37711	Probable n-end-rec

ALIGNMENTS

RESULT 1

JC5068

G protein-coupled receptor CKR-L3 - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000

C:Accession: JC5068

R:Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.

Biochem. Biophys. Res. Commun. 227, 846-853, 1996

A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-lik

A:Reference number: JC5067; MUID:97040707

A:Accession: JC5068

A:Molecule type: DNA

A:Residues: 1-369 <ZAB>

A:Cross-references: EMBL:Z79784; NID:gl668737; PIDN:CA802144.1; PID:gl668738

C:Comment: This protein belongs to the family of alpha chemokine receptors.

C:Genetics:

A:Gene: GDB:CMKBR6; STRL22; GPR29; CCR6; CKR-L3; GPR-CY4

A:Cross-references: GDB:5370639; OMIM:601835

A:Map position: 6q27-6q27

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

F;42-68/Domain: transmembrane #status predicted <TM1>

F;79-99/Domain: transmembrane #status predicted <TM2>

F;115-136/Domain: transmembrane #status predicted <TM3>

F;160-180/Domain: transmembrane #status predicted <TM4>

F;212-233/Domain: transmembrane #status predicted <TM5>

F;250-271/Domain: transmembrane #status predicted <TM6>

F;292-315/Domain: transmembrane #status predicted <TM7>

Query Match 100.0%; Score 115; DB 2: Length 369;

Best Local Similarity 100.0%; Pred. No. 1e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLKGIYAINFCNCGMLLTTCISM 22

Db 115 LLKGIYAINFCNCGMLLTTCISM 136

RESULT 2

A55735

G protein-coupled receptor EB11 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 24-Nov-1999

C:Accession: A55735

R:Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T

Genomics 23, 643-650, 1994

A:Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled recep

A:Reference number: A55735; MUID:95154835

A:Accession: A55735

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-378 <SCH>
A:Cross-references: GB:L31580; NID:9468340; PIDN:AAA74232.1; PID:g468341
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

Query Match 53.0%; Score 61; DB 2; Length 378;
Best Local Similarity 63.2%; Pred. No. 0.04;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 GYAINFNCGMLLLTCISM 22
|||:::| ||||| |||:
Db 134 GYKLSFFSGMLLLLCISI 152

RESULT 3

A45680
G protein-coupled peptide receptor EBI 1 - human
C:Species: Homo sapiens (man)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C:Accession: A45680
R:Birkenbach, M.; Josefsen, K.; Yalamanchilli, R.; Lenoir, G.; Kieff, E.
J. Virol. 67, 2209-2220, 1993
A:Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-coupled protein
A:Reference number: A45680; MUID:93188173
A:Accession: A45680
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-378 <BI>
A:Cross-references: GB:L08176; NID:g183484; PID:g183485
A:Experimental source: B-lymphocytes
A:Note: sequence extracted from NCBI backbone (NCBIN:127094, NCBI:P:127095)
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 49.6%; Score 57; DB 2; Length 378;
Best Local Similarity 54.5%; Pred. No. 0.17;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 LLKGIYAINFNCGMLLLTCISM 22
|:::| ||||| |||:
Db 131 LFAIYKMSFFSGMLLLLCISI 152

RESULT 4

B55735
Lymphocyte-specific G protein-coupled receptor EBI1 - human
N:Alternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1
C:Species: Homo sapiens (man)
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 19-May-2000
C:Accession: B55735; S52443
R:Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.
Genomics 23, 643-650, 1994
A:Title: Cloning of human and mouse EBI1, a lymphoid-specific G-protein-coupled receptor
A:Reference number: A55735; MUID:95154835
A:Accession: B55735
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-378 <SCH>
A:Cross-references: GB:L31581; NID:9468319; PIDN:AAA74231.1; PID:g468320
R:Burgstahler, R.; Kempkes, B.; Staube, K.; Lipp, M.
submitted to the EMBL Data Library, February 1995
A:Description: The expression of the chemokine receptor BLR2/EBI1 is specifically trans-
A:Reference number: S52443
A:Accession: S52443
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 21-378 <BUR>
A:Cross-references: EMBL:X84702
C:Genetics:
A:Gene: GDB:CMKBR7; EBI1; BLR2; CCR7
A:Cross-references: GDB:342065; OMIM:600242

A:Map position: 17q12-17q21.2
A:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

Query Match 49.6%; Score 57; DB 2; Length 378;
Best Local Similarity 54.5%; Pred. No. 0.17;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 LLKGIYAINFNCGMLLLTCISM 22
|:::| ||||| |||:
Db 131 LFAIYKMSFFSGMLLLLCISI 152

RESULT 5

B55733
G protein-coupled receptor GPR2 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 26-Aug-1999
C:Accession: B55733
R:Marchese, A.; Docherty, J.M.; Nguyen, T.; Heiber, M.; Cheng, R.; Heng, H.H.Q.; Tsui
Genomics 23, 609-618, 1994
A:Title: Cloning of human genes encoding novel G protein-coupled receptors.
A:Reference number: A55733; MUID:95154831
A:Accession: B55733
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-354 <MAR>
A:Cross-references: GB:U13667
C:Genetics:
A:Gene: GDB:GPR2
A:Cross-references: GDB:371708; OMIM:600240
A:Map position: 17q21.1-17q21.3
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

Query Match 48.7%; Score 56; DB 2; Length 354;
Best Local Similarity 45.0%; Pred. No. 0.23;
Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 2 LKGIYAINFNCGMLLLTCIS 21
|:::| |::| |||
Db 108 ISGLYSASFHAGFLACIS 127

RESULT 6

G02064
G protein-coupled receptor 15 - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 24-Nov-1999
C:Accession: G02064
R:O'Dowd, B.F.
submitted to the EMBL Data Library, August 1995
A:Reference number: H00762
A:Accession: G02064
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-360 <OXD>
A:Cross-references: EMBL:U34806; NID:g1171145; PID:g1171146
C:Genetics:
A:Gene: GDB:GPR15
A:Cross-references: GDB:624476
A:Map position: 3q11.2-3q13.1
C:Superfamily: vertebrate rhodopsin

Query Match 48.3%; Score 55.5; DB 2; Length 360;
Best Local Similarity 44.0%; Pred. No. 0.28;
Matches 11; Conservative 7; Mismatches 4; Indels 3; Gaps 1;

QY 1 LLKG---IYAINFNCGMLLLTCISM 22
|:::| |::| |||:

Db 105 LCKGSSYMAISVNMHCVSLLLTCSMV 129

RESULT 7
B41869
pro-sigma K processing regulatory protein bofa - Bacillus subtilis
N;Alternate names: bypass-of-forespore A; pro-sigma-K processing machinery inhibitor bof
C:Species: Bacillus subtilis
C:Date: 03-May-1994 #sequence_revision 27-Jan-1995 #text_change 15-Oct-1999
C:Accession: B41869; S13789; S66053; H69595
R:Ricca, E.; Cutting, S.; Losick, R.
J. Bacteriol. 174, 3177-3184, 1992
A:Title: Characterization of bofa, a gene involved in intercompartmental regulation of H
A:Reference number: A41869; MUID:92250411
A:Accession: B41869
A:Molecule type: DNA
A:Residues: 1-54, 'G', 56-87 <RIC>
R:Alonso, J.C.; Shirahige, K.; Ogasawara, N.
Nucleic Acids Res. 18, 6771-6777, 1990
A:Title: Molecular cloning, genetic characterization and DNA sequence analysis of the re
A:Reference number: S13786; MUID:91088245
A:Accession: S13789
A:Molecule type: DNA
A:Residues: 1-87 <ALO>
A:Cross-references: EMBL:X17014; NID:g453238; PIDN:CAA34880.1; PID:g40075
R:Ogasawara, N.; Nakai, S.; Yoshikawa, H.
DNA Res. 1, 1-14, 1994
A:Title: Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chrom
A:Reference number: S63967; MUID:96051385
A:Accession: S66053
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-87 <OGA>
A:Cross-references: EMBL:D26185; NID:g467326; PIDN:BAA05259.1; PID:d1005801; PID:g467413
A:Note: The nucleotide sequence was submitted to the EMBL Data Library, December 1993
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Brucher, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funa, S.; Galizzi, A.; Gallier
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033
A:Accession: H69595
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-87 <KUN>
A:Cross-references: GB:Z99104; GB:AL009126; NID:g2632267; PIDN:CAB11799.1; PID:el181956;
A:Experimental source: strain 168
C:Comment: By controlling the proteolytic activation of the precursor of sigma factor K,
factor G in the forespore.
C:Genetics:
A:Gene: bofa
C:Keywords: sporulation; transmembrane protein

Query Match 46.1%; Score 53; DB 2; Length 87;
Best Local Similarity 52.6%; Pred. No. 0.19;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 4 GIYAINFCGMLLTCTISM 22
||| | | ||| |||

Db 31 GITAVKFVAGALLVCVNM 49

RESULT 8
S32785

G protein-coupled receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 24-Nov-1999
C:Accession: S32785
R:Kouba, M.; Vanetti, M.; Wang, X.; Schaefer, M.; Hoellit, V.
FEBS Lett. 321, 173-178, 1993
A:Title: Cloning of a novel putative G-protein-coupled receptor (NLR) which is expres
A:Reference number: S32785; MUID:93238948
A:Accession: S32785
A:Molecule type: mRNA
A:Residues: 1-374 <ROU>
A:Cross-references: GB:X71463; GB:S59748; NID:g599926; PIDN:CAA50582.1; PID:g599927
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 45.2%; Score 52; DB 2; Length 374;
Best Local Similarity 50.0%; Pred. No. 1.1;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 5 IYAINFCGMLLTCTISM 22

Db 130 LHKINFCSSLLACIAV 147
:: ||| | ||| |||

RESULT 9
RDHUU

glutathione reductase (NADPH) (EC 1.6.4.2) - human
C:Species: Homo sapiens (man)
C:Date: 02-Apr-1982 #sequence_revision 22-Apr-1995 #text_change 11-Jun-1999
C:Accession: S08979; A00404; S10730
R:Tutic, M.; Lu, X.; Schirmer, R.H.; Werner, D.
Eur. J. Biochem. 188, 523-528, 1990
A:Title: Cloning and sequencing of mammalian glutathione reductase cDNA.
A:Reference number: S08979; MUID:90235822
A:Accession: S08979
A:Molecule type: mRNA
A:Residues: 1-479 <UT>
A:Cross-references: EMBL:X15722; NID:g31824; PIDN:CAA33744.1; PID:g31825
R:Krauth-Siegel, R.L.; Blatterspiel, R.; Saleh, M.; Schiltz, E.; Schirmer, R.H.; Untu
Eur. J. Biochem. 121, 259-267, 1992
A:Title: Glutathione reductase from human erythrocytes. The sequences of the NADPH do
A:Reference number: A91112; MUID:82138780
A:Accession: A00404
A:Molecule type: protein
A:Residues: 2-479 <KRA>
A:Note: this is the final paper in a series
R:Thieme, R.; Pai, E.F.; Schirmer, R.H.; Schulz, G.E.
J. Mol. Biol. 152, 763-782, 1991

A:Title: Three-dimensional structure of glutathione reductase at 2 angstrom resolution
A:Reference number: A92874; MUID:82145544
A:Contents: annotation; X-ray crystallography, 2 angstroms
R:Arnold, H.H.; Heinze, H.
FEBS Lett. 267, 189-192, 1990
A:Title: Treatment of human peripheral lymphocytes with concanavalin A activates expr
A:Reference number: S10730; MUID:90336771
A:Accession: S10730
A:Molecule type: mRNA
A:Residues: 78-96; 98-116; 118-136; 138-156; 158-176; 178-196; 198-216; 218-236; 238-256; 258-
A:Cross-references: GB:X54507; NID:g31828; PIDN:CAA38367.1; PID:g31829
A:Note: In the displayed figure the last codon of the sequence plus amino acid are sk
C:Genetics:
A:Gene: GDB:GSR
A:Cross-references: GDB:I19288; OMIM:138300
A:Map position: 8p21.1-8p21.1
C:Complex: homodimer
C:Function:
A:Description: catalyzes the reduction of glutathione by NADPH
A:Note: responsible for maintaining high levels of reduced glutathione in the cytopla
C:Superfamily: dihydrolipoamide dehydrogenase; dihydrolipoamide dehydrogenase homolog
C:Keywords: acetylated amino end; FAD; flavoprotein; homodimer; NADP; oxidoreductase;

F:23-51/Region: beta-alpha-beta FAD nucleotide-binding fold
 F:25-475/Domain: dihydrolipoamide dehydrogenase homology <DLD>
 F:190-221/Region: beta-alpha-beta NADP nucleotide-binding fold
 F:2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental
 F:59-64/Disulfide bonds: redox-active #status experimental
 F:91/Disulfide bonds: interchain #status experimental
 F:468/Active site: His #status experimental

Query Match 45.2%; Score 52; DB 1; Length 479;
 Best Local Similarity 47.6%; Pred. No. 1.3;
 Matches 10; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 2 LKGIYAINFCGMLLLTCISM 22
 :||||: |||||
 DB 324 VKGIYAVGDCGKALLTPVAI 344

RESULT 10

MDCR15 protein - human

C:Species: Homo sapiens (man)

C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 08-Oct-1999

C:Accession: S56162

R:Barclia, L.; Loetscher, M.; Tobler, A.; Baggiolini, M.; Moser, B.

Biochem. J. 309, 773-779, 1995

A:Title: Sequence variation of a novel heptahelical leucocyte receptor through alternati

A:Reference number: S56162; MUID:93366951

A:Accession: S56162

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-327 <BAR>

A:Cross-references: EMBL:X68829; NID:g840783; PIDN:CAA48723.1; PID:g840784

C:Superfamily: vertebrate rhodopsin

Query Match 44.3%; Score 51; DB 2; Length 327;
 Best Local Similarity 44.4%; Pred. No. 1.4;
 Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 5 IYAINFCGMLLLTCISM 22
 :|||: |||||
 DB 83 LHKVNFYCSSLLACIAV 100

RESULT 11

S26667

G protein-coupled receptor BLR1 - human

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000

C:Accession: S26667

R:Dobner, T.; Wolf, I.; Emrich, T.; Lipp, M.

Eur. J. Immunol. 22, 2795-2799, 1992

A:Title: Differentiation-specific expression of a novel G protein-coupled receptor from

A:Reference number: S26667; MUID:93049615

A:Accession: S26667

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-372 <DOB>

A:Cross-references: EMBL:X68149; NID:g29459; PIDN:CAA48252.1; PID:g29460

C:Genetics:

A:Gene: GDB:BLR1

A:Map position: 15q26.1-15q26.1

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 44.3%; Score 51; DB 2; Length 372;
 Best Local Similarity 44.4%; Pred. No. 1.5;
 Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 5 IYAINFCGMLLLTCISM 22

Db 128 LHKVNFYCSSLLACIAV 145
 :|||: |||||

RESULT 12

A47556

ATP receptor P2u - mouse

C:Species: Mus musculus (house mouse)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999

C:Accession: A47556

R:Lustig, K.D.; Shiau, A.K.; Brake, A.J.; Julius, D.

Proc. Natl. Acad. Sci. U.S.A. 90, 5113-5117, 1993

A:Title: Expression cloning of an ATP receptor from mouse neuroblastoma cells.

A:Reference number: A47556; MUID:93281707

A:Accession: A47556

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-373 <LUS>

A:Cross-references: GB:L14751; NID:g309457; PIDN:AAA39871.1; PID:g309458

C:Superfamily: ATP receptor P2u

C:Keywords: transmembrane protein

Query Match 44.3%; Score 51; DB 2; Length 373;
 Best Local Similarity 40.9%; Pred. No. 1.5;
 Matches 9; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 LKGIYAINFCGMLLLTCISM 22
 :|||: |||||
 DB 108 LVRFLEYTNLYCSILFLTCISV 129

RESULT 13

A54946

P-2U nucleotide receptor - human

C:Species: Homo sapiens (man)

C:Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 17-Mar-1999

C:Accession: A54946

R:Par, C.E.; Sullivan, D.M.; Paradiso, A.M.; Lazarowski, E.R.; Burch, L.H.; Olsen, J

Proc. Natl. Acad. Sci. U.S.A. 91, 3275-3279, 1994

A:Title: Cloning and expression of a human P-2U nucleotide receptor, a target for cys

A:Reference number: A54946; MUID:94211846

A:Accession: A54946

A:Status: preliminary

A:Molecule type: mRNA; protein

A:Residues: 1-375 <PAR>

A:Cross-references: GB:U07225

A:Note: parts of this sequence were confirmed by protein sequencing

C:Genetics:

A:Gene: GDB:P2RY2; HP20; P2U

A:Cross-references: GDB:362713; OMIM:600041

A:Map position: 11q13.5-11q14.1

C:Superfamily: ATP receptor P2u

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 44.3%; Score 51; DB 2; Length 375;
 Best Local Similarity 40.9%; Pred. No. 1.5;
 Matches 9; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 LKGIYAINFCGMLLLTCISM 22
 :|||: |||||
 DB 108 LVRFLEYTNLYCSILFLTCISV 129

RESULT 14

S39494

glutathione reductase (NADPH) (EC 1.6.4.2) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 22-Jan-1994 #sequence_revision 12-Apr-1996 #text_change 20-Jun-2000

C:Accession: S39494; S39493

R:Tutic, M.; Lu, X.; Schirmer, R.H.; Werner, D.

submitted to the EMBL Data Library, November 1993

Job time: 507 sec

A;Description: Cloning and sequencing of mammalian glutathione reductase cDNA.

A;Reference number: S39494

A;Accession: S39494

A;Molecule type: mRNA

A;Residues: 1-466 <TU1>

A;Cross-references: EMBL:X76341; NID:9433595; PIDN:CAA53959.1; PID:g1334126

R;Tutic, M.; Lu, X.; Schirmer, R.H.; Werner, D.

Eur. J. Biochem. 188, 523-528, 1990

A;Title: Cloning and sequencing of mammalian glutathione reductase cDNA.

A;Reference number: S08979; MUID:90235822

A;Accession: S39493

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 65-306 <TU2>

A;Cross-references: EMBL:X76341

C;Superfamily: dihydrolipoamide dehydrogenase; dihydrolipoamide dehydrogenase homology

C;Keywords: FAD; flavoprotein; NADP; oxidoreductase; redox-active disulfide

F;10-38/Region: beta-alpha-beta FAD nucleotide-binding fold

F;12-462/Domain: dihydrolipoamide dehydrogenase homology <BLD>

F;177-208/Region: beta-alpha-beta NADP nucleotide-binding fold

F;46-51/Disulfide bonds: redox-active #status predicted

F;78/Disulfide bonds: interchain #status predicted

F;455/Active site: His #status predicted

Query Match

Best Local Similarity 44.3%; Score 51; DB 2; Length 466;

Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 2 LKGIYAINFNCGMLLLTCTISM 22

:|:|:|: || ||| :|:

Db 311 VKGVYAVGDCGKALLTPVAI 331

RESULT 15

JN0621

G protein-coupled receptor type B - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 19-May-2000

C;Accession: JN0621

R;Matsuoka, I.; Mori, T.; Aoki, J.; Sato, T.; Kurihara, K.

Biochem. Biophys. Res. Commun. 194, 504-511, 1993

A;Title: Identification of novel members of G-protein coupled receptor superfamily expressed

A;Reference number: JN0621; MUID:93326166

A;Accession: JN0621

A;Molecule type: mRNA

A;Residues: 1-350 <MAT>

A;Cross-references: GB:S63848; NID:9399710; PIDN:AAB27547.1; PID:g399711

A;Experimental source: tongue taste papillae

C;Comment: This protein is involved in modulating taste sensitivity or regeneration of taste

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein

F;42-66/Domain: transmembrane #status predicted <TM1>

F;80-99/Domain: transmembrane #status predicted <TM2>

F;114-135/Domain: transmembrane #status predicted <TM3>

F;154-175/Domain: transmembrane #status predicted <TM4>

F;200-222/Domain: transmembrane #status predicted <TM5>

F;242-265/Domain: transmembrane #status predicted <TM6>

F;284-306/Domain: transmembrane #status predicted <TM7>

F;6,19/Binding site: carbohydrate (Asn) #status predicted

Query Match

Best Local Similarity 43.5%; Score 50; DB 2; Length 350;

Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 5 IYAINFNCGMLLLTCTIS 21

:|:|:|: || ||| :|:

Db 118 LYTQNFVSGMQFLACIS 134

Search completed: May 23, 2001, 15:32:00

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:36:18 ; Search time 62.39 Seconds
(without alignments)
12.079 Million cell updates/sec

Title: US-08-887-977-10_COPY_111_132
Perfect score: 115
Sequence: 1 LKGIYAINFNGCMLLLTCISM 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	115	100.0	374	1 CRR6_HUMAN	P51684 homo sapien
2	102	88.7	367	1 CRR6_MOUSE	O54689 mus musculus
3	67	58.3	342	1 BONZ_CERAE	O18983 cercopithec
4	67	58.3	342	1 BONZ_HUMAN	O00574 homo sapien
5	66	57.4	342	1 BONZ_MACNE	O19024 macaca neme
6	66	57.4	343	1 BONZ_MACMU	O9xt45 macaca mula
7	61	53.0	378	1 CRR7_MOUSE	P47774 mus musculus
8	57	49.6	378	1 CRR7_HUMAN	P32248 homo sapien
9	56	48.7	362	1 CKRA_HUMAN	P45092 homo sapien
10	55.5	48.3	360	1 GPRF_HUMAN	P49685 homo sapien
11	53.5	46.5	360	1 IL8B_BOVIN	O28003 bos taurus
12	53	46.1	87	1 BOFA_BACSU	P24282 bacillus su
13	53	46.1	362	1 CKRA_MOUSE	O9J121 mus musculus
14	52	45.2	374	1 CCR5_RAT	P34997 rattus norv
15	52	45.2	478	1 GSHR_HUMAN	P00390 homo sapien
16	51.5	44.8	360	1 GPRF_CERAE	O18982 cercopithec
17	51.5	44.8	360	1 GPRF_MACMU	O97663 macaca mula
18	51.5	44.8	360	1 GPRF_MACNE	P56412 macaca neme
19	51	44.3	368	1 CCR3_HUMAN	P49682 homo sapien
20	51	44.3	372	1 CCR5_HUMAN	P32302 homo sapien
21	51	44.3	373	1 P2UR_MOUSE	P35383 mus musculus
22	51	44.3	374	1 P2UR_RAT	P41232 rattus norv
23	51	44.3	377	1 P2UR_HUMAN	P41231 homo sapien
24	51	44.3	466	1 GSHR_MOUSE	P47791 mus musculus
25	50	43.5	350	1 GUSB_BOVIN	P33350 bos taurus
26	50	43.5	358	1 GPRK_HUMAN	O99678 homo sapien
27	49.5	43.0	350	1 IL8A_GORGO	P55919 gorilla gor
28	49.5	43.0	350	1 IL8A_HUMAN	P25024 homo sapien
29	49.5	43.0	350	1 IL8A_PANTR	P55920 pan troglod
30	49.5	43.0	353	1 IL8B_GORGO	O28422 gorilla gor
31	49.5	43.0	353	1 IL8B_MACMU	O28519 macaca mula
32	49.5	43.0	353	1 IL8B_PANTR	O28807 pan troglod
33	49.5	43.0	360	1 IL8B_HUMAN	P25025 homo sapien

RESULT 1
CKR6_HUMAN
ID CRR6_HUMAN STANDARD; PRT; 374 AA.
AC P51684; Q92846; P78553;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CC-CKR-6) (CCR-6) (LARC
DE RECEPTOR) (GPR-CY4) (GPCY4) (CHEMOKINE RECEPTOR-LIKE 3) (CKR-L3)
DE (DRY6)
GN CCR6 OR CMKBR6 OR STRL22 OR GPR29 OR CRL3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND FUNCTION.
RX MEDLINE=97313465; PubMed=9169459;
RA Baba M., Inai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K.,
RA Nomiya H., Yoshie O.;
RT "Identification of CCR6, the specific receptor for a novel
RT lymphocyte-directed CC chemokine LARC";
RL J. Biol. Chem. 272:14893-14898(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Lautens L.L., Modi W., Bonner T.I.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97040707; PubMed=8886020;
RA Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G.;
RT "Molecular cloning and RNA expression of two new human chemokine
RT receptor-like genes";
RL Biochem. Biophys. Res. Commun. 227:846-853(1996).
RN [4]
RP SEQUENCE FROM N.A.
RA McCoy R., Perlmutter D.H.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=97224503; PubMed=9070937;
RA Liao F., Lee H.-H., Farber J.M.;
RT "Cloning of STRL22, a new human gene encoding a G-protein-coupled
RT receptor related to chemokine receptors and located on chromosome
RT 6q27";
RL Genomics 40:175-180(1997).
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-
CC ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE
CC INTRACELLULAR CALCIUM IONS LEVEL.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: SPLEEN, LYMPH NODES, APPENDIX, AND FETAL
CC LIVER. EXPRESSED IN LYMPHOCYTES, T CELLS AND B CELLS BUT NOT IN
CC NATURAL KILLER CELLS, MONOCYTES, OR GRANULOCYTES.
CC -!- INDUCTION: INTERLEUKIN-2.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-6 IS THE INITIATOR.

34 49 42.6 318 1 NULM_EQUAS
35 49 42.6 318 1 NULM_HORSE
36 49 42.6 355 1 IL8A_RABIT
37 49 42.6 358 1 IL8B_RABIT
38 49 42.6 374 1 CCR5_MOUSE
39 49 42.6 1162 1 VGL2_IBVM
40 48.5 42.2 349 1 IL8A_RAT
41 48 41.7 316 1 COAT_MSTV
42 47 40.5 367 1 CCR3_MOUSE
43 47 40.5 460 1 DB80_DROME
44 46 40.0 341 1 MO25_MOUSE
45 46 40.0 397 1 PAR2_HUMAN

ALIGNMENTS

P92475 equus asinu
P48652 equus cabal
P21109 oryctolagus
P35344 oryctolagus
Q04683 mus musculus
P12651 avian infec
P70612 rattus norv
P27207 maize strip
O88410 mus musculus
O81305 drosophila
Q06138 mus musculus
P55085 homo sapien


```

RESULT 3
BONZ_CERA 3
ID BONZ_CERA 3 STANDARD; PRT; 342 AA.
AC O18983;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE G PROTEIN-COUPLED RECEPTOR BONZO.
GN BONZO.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97373958; PubMed=9230441;
RA Deng H.K., Unutmaz D., Kewalramani V.N., Littman D.R.;
RT "Expression cloning of new receptors used by simian and human
immunodeficiency viruses.";
RL Nature 388:296-300(1997).
CC -!- FUNCTION: ORPHAN RECEPTOR. COULD BE A CHEMOKINE RECEPTOR. USED AS
A CORRECTOR BY SVIS AND BY STRAINS OF HIV-2 AND M-TROPIC HIV-1.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF007859; AAB64225.1; -
DR GCRDB; GCR_2411; -
DR InterPro; IPR000276; -
DR InterPro; IPR002235; -
DR Pfam; PF00001; 7tm.1.1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PRINTS; PR01105; BONZOORPHANR.
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR_F1_1; 1.
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR_F1_2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 32
FT TRANSMEM 33 59
FT DOMAIN 60 68
FT TRANSMEM 69 89
FT DOMAIN 90 103
FT TRANSMEM 104 125
FT DOMAIN 126 143
FT TRANSMEM 144 164
FT DOMAIN 165 187
FT TRANSMEM 188 215
FT DOMAIN 216 231
FT TRANSMEM 232 259
FT DOMAIN 260 275
FT TRANSMEM 276 293
FT DOMAIN 294 342
FT DISULFID 102 180
FT CARBOHYD 16 16
FT SEQUENCE 342 AA; 39226 MW; 6CBFE389C6E5919E CRC64;

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Query Match 58.3%; Score 67; DB 1; Length 342;
 Best Local Similarity 61.9%; Pred. No. 0.003;
 Matches 13; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

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Oy 2 LKGIYAINPNCGMILLTCTISM 22
| ||| ||| ||| ||| |||
Db 105 LIGIVTINFTSMILITCTIV 125

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RESULT 4
BONZ_HUMAN 4
ID BONZ_HUMAN 4 STANDARD; PRT; 342 AA.
AC O00574; O00575;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE G PROTEIN-COUPLED RECEPTOR BONZO (G PROTEIN-COUPLED RECEPTOR STRL33).
GN BONZO OR STRL33 OR TYMSTR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97373958; PubMed=9230441;
RA Deng H.K., Unutmaz D., Kewalramani V.N., Littman D.R.;
RT "Expression cloning of new receptors used by simian and human
immunodeficiency viruses.";
RL Nature 388:296-300(1997).
CC [2]
CC SEQUENCE FROM N.A.
RX MEDLINE=97373958; PubMed=9166430;
RA Liao F., Alkhatib G., Peden K.W.C., Sharma G., Berger E.A.,
RA Farber J.M.;
RT "STRL33, A novel chemokine receptor-like protein, functions as a
fusion cofactor for both macrophage-tropic and T cell line-tropic
HIV-1.";
RL J. Exp. Med. 185:2015-2023(1997).
CC [3]
CC SEQUENCE FROM N.A.
RX MEDLINE=97431687; PubMed=9285716;
RA Loetscher M., Amara A., Oberlin E., Brass N., Legler D.F.,
RA Loetscher P., D'Apuzzo M., Meese E.U., Rousset D., Virelizier J.L.,
RA Baggiolini M., Arenzana-Seisdedos F., Moser B.;
RT "TYMSTR, a putative chemokine receptor selectively expressed in
activated T cells, exhibits HIV-1 coreceptor function.";
RL Curr. Biol. 7:652-660(1997).
CC -!- FUNCTION: ORPHAN RECEPTOR. COULD BE A CHEMOKINE RECEPTOR. USED AS
A CORRECTOR BY SVIS AND BY STRAINS OF HIV-2 AND M-TROPIC HIV-1.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN LYMPHOID TISSUES AND ACTIVATED T
CELLS.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF007545; AAB64221.1; -
DR EMBL; U73529; AAB61456.1; -
DR EMBL; U73531; AAB61457.1; -
DR EMBL; Y13248; CAA73698.1; -
DR MIN; 605163; -
DR GCRDB; GCR_1328; -
DR GCRDB; GCR_1330; -
DR GCRDB; GCR_2393; -
DR InterPro; IPR000276; -
DR InterPro; IPR002235; -
DR Pfam; PF00001; 7tm.1.1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PRINTS; PR01105; BONZOORPHANR.
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR_F1_1; 1.
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR_F1_2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.
FT DOMAIN 1 32
FT TRANSMEM 33 59
FT TRANSMEM 33 59
FT (POTENTIAL).

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EMBL; AF007858; AAB64224.1; -.
GCRDb; GCR_2409; -.
InterPro; IPR000276; -.
InterPro; IPR002235; -.
Pfam; PF00001; 7tm_1; 1.
PRINTS; P00237; GPCRHHODOPSIN.
PROSITE; PR01105; BONZOORPHANR.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.

DR	EMBL; AF124380; AAD31419.1; -.
DR	InterPro; IPR000276; -.
DR	InterPro; IPR002235; -.
DR	Pfam; PF00001; 7tm1.1.
DR	PRINTS; PR00237; GPCRHOPOPSN.
DR	PRINTS; PR01105; BONZOORPHANR.
DR	PROSITE; PS00237; G_PROTEIN_RECF_F1.1; 1.
DR	PROSITE; PS00262; G_PROTEIN_RECF_F1.2; 1.
KW	G-protein coupled receptor; Transmembrane; Glycoprotein.
FT	DOMAIN 1 33
FT	TRANSMEM 34 60
FT	EXTRACELLULAR (POTENTIAL). 1 (POTENTIAL).

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FT DOMAIN 61 69 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 70 90 2 (POTENTIAL).
FT DOMAIN 91 104 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 105 126 3 (POTENTIAL).
FT DOMAIN 127 144 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 145 165 4 (POTENTIAL).
FT DOMAIN 166 188 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 189 216 5 (POTENTIAL).
FT DOMAIN 217 232 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 233 260 6 (POTENTIAL).
FT DOMAIN 261 276 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 277 294 7 (POTENTIAL).
FT DOMAIN 295 343 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 17 17 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 103 181 BY SIMILARITY.
SQ SEQUENCE 343 AA; 48DB2544949EB83F CRC64;

Query Match 57.4%; Score 66; DB 1; Length 343;
Best Local Similarity 57.1%; Pred. No. 0.0043;
Matches 12; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 LKGIYAINFCGMLLLTICISM 22
| : | | | | | | | | | | | | | |
DB 106 LLGYTINFTSMLTICITY 126

RESULT 7
CKR7_MOUSE STANDARD; PRT; 378 AA.
AC P47774;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 7 PRECURSOR (C-C CKR-7) (CC-CKR-7) (CCR-7)
DE (MIP-3 BETA RECEPTOR) (EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 1)
DE (EBI1).
DE CKR7 OR CMKBR7 OR EB11 OR EB11H.
GN Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6/CBA; TISSUE=Thymus;
RX MEDLINE=95154835; PubMed=7851893;
RA Schweickart V.L., Raport C.J., Godiska R., Byers M.G., Eddy R.L. Jr.,
RA Shows T.B., Gray P.W.;
RT "Cloning of human and mouse EBI1, a lymphoid-specific
RT G-protein-coupled receptor encoded on human chromosome 17q12-q21.2.";
RL Genomics 23:643-650(1994).
CC -1- FUNCTION: RECEPTOR FOR THE MIP-3-BETA CHEMOKINE. PROBABLE MEDIATOR
CC OF EBV EFFECTS ON B LYMPHOCYTES OR OF NORMAL LYMPHOCYTE FUNCTIONS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L31580; AAA74232.1; -
CC MGD; MGI:103011; Cmkbr7.
CC InterPro; IPR000276; -
CC InterPro; IPR001718; -
CC Pfam; PF00001; 7tm1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PRINTS; PR00641; CHEMOKINER7.
CC PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.
CC PROSITE; PS50262; G_PROTEIN_RECEP_FL_2; 1.
```

```
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 378 C-C CHEMOKINE RECEPTOR TYPE 7.
FT DOMAIN 25 59 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 60 86 1 (POTENTIAL).
FT DOMAIN 87 95 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 96 116 2 (POTENTIAL).
FT DOMAIN 117 130 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 131 152 3 (POTENTIAL).
FT DOMAIN 153 170 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 171 191 4 (POTENTIAL).
FT DOMAIN 192 219 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 220 247 5 (POTENTIAL).
FT DOMAIN 248 263 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 264 289 6 (POTENTIAL).
FT DOMAIN 290 313 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 314 331 7 (POTENTIAL).
FT DOMAIN 332 378 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 36 36 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 129 210 BY SIMILARITY.
SQ SEQUENCE 378 AA; 42941 MW; ACBIA422CF54AA54 CRC64;

Query Match 53.0%; Score 61; DB 1; Length 378;
Best Local Similarity 63.2%; Pred. No. 0.028;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 GIYAINFCGMLLLTICISM 22
| | | : | | | | | | | |
DB 134 GIYKLSFFSGMLLLLCISI 152

RESULT 8
CKR7_HUMAN STANDARD; PRT; 378 AA.
AC P32248;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 7 PRECURSOR (C-C CKR-7) (CC-CKR-7) (CCR-7)
DE (MIP-3 BETA RECEPTOR) (EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 1)
DE (EBI1) (BLR2).
DE CKR7 OR CMKBR7 OR EB11 OR EB11.
GN Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93188173; PubMed=8383238;
RA Birkenbach M.P., Josefsen K., Yalamanchili R.R., Lenoir G.M.,
RA Elliott K.;
RT "Epstein-Barr virus-induced genes: first lymphocyte-specific G
RT protein-coupled peptide receptors.";
RL J. Virol. 67:2209-2220(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=95154835; PubMed=7851893;
RA Schweickart V.L., Raport C.J., Godiska R., Byers M.G., Eddy R.L. Jr.,
RA Shows T.B., Gray P.W.;
RT "Cloning of human and mouse EBI1, a lymphoid-specific
RT G-protein-coupled receptor encoded on human chromosome 17q12-q21.2.";
RL Genomics 23:643-650(1994).
CC -1- FUNCTION: RECEPTOR FOR THE MIP-3-BETA CHEMOKINE. PROBABLE MEDIATOR
CC OF EBV EFFECTS ON B LYMPHOCYTES OR OF NORMAL LYMPHOCYTE FUNCTIONS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN VARIOUS LYMPHOID TISSUES AND
CC ACTIVATED B AND T LYMPHOCYTES, STRONGLY UPREGULATED IN B CELLS
CC INFECTED WITH EPSTEIN-BARR VIRUS AND T CELLS INFECTED WITH
CC HERPESVIRUS 6 OR 7.
CC -1- INDUCTION: BY EBV.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
```

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EMBL; L08176; AAA58615.1; -
DR EMBL; L31584; AAA74230.1; -
DR EMBL; L31582; AAA74230.1; JOINED.
DR EMBL; L31583; AAA74230.1; JOINED.
DR EMBL; L31581; AAA74231.1; -
DR PIR; A45680; A45680.
DR HSSP; P34996; 1DDO.
DR GCRDB; GCR_0492; -
DR GCRDB; GCR_0958; -
DR MIM; 600242; -
DR InterPro; IPR000276; -
DR InterPro; IPR001718; -
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR00641; CHEMOKINER7.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 378 C-C CHEMOKINE RECEPTOR TYPE 7.
FT DOMAIN 25 59 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 60 86 1 (POTENTIAL).
FT DOMAIN 87 95 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 96 116 2 (POTENTIAL).
FT DOMAIN 117 130 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 131 152 3 (POTENTIAL).
FT DOMAIN 153 170 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 171 191 4 (POTENTIAL).
FT DOMAIN 192 219 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 220 247 5 (POTENTIAL).
FT DOMAIN 248 263 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 264 289 6 (POTENTIAL).
FT DOMAIN 290 313 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 314 331 7 (POTENTIAL).
FT DOMAIN 332 378 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 129 210 BY SIMILARITY.
FT CONFLICT 182 183 IW -> SA (IN REF. 1).
FT CONFLICT 337 337 L -> I (IN REF. 1).
SQ SEQUENCE 378 AA; 42874 MW; D4CB4213841A1BD4 CRC64;

Query Match 49.6%; Score 57; DB 1; Length 378;
Best Local Similarity 54.5%; Pred. No. 0.12;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 LLKGIYAINFGMGLLLTCISM 22
Db 131 LIFAIYKMSFFSGMLLLCISI 152

RESULT 9
CKRA_HUMAN
ID CKRA_HUMAN STANDARD; PRT: 362 AA.
AC P46092; G9NZG2;
DT 01-NOV-1995 (Rel. 32, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 10 (C-C CKR-10) (CCR-10) (G-
DE PROTEIN COUPLED RECEPTOR 2).
GN CKR10 OR GPR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A., AND CHARACTERIZATION.
RP MEDLINE=20191997; Pubmed=10725696;
RX Jarmin D.I., Rits M., Bota D., Gerard N.P., Graham G.J.,
RA Clark-Lewis I., Gerard C.;
RT "Cutting edge: identification of the orphan receptor G-protein-coupled
receptor 2 as CCR10, a specific receptor for the chemokine ESKINE";
J. Immunol. 164:3460-3464(2000).
[2]
SEQUENCE FROM N.A., AND CHARACTERIZATION.
RP MEDLINE=20191998; Pubmed=10725697;
RX Honey B., Wang W., Soto H., Buchanan M.E., Wiesenborn A., Catron D.,
RA Muller A., McClanahan T.K., Dieu-Nosjean M.C., Orozco R., Ruzicka T.,
RA Lehmann P., Oldham E., Zlotnik A.;
RT "Cutting edge: the orphan chemokine receptor G protein-coupled
receptor-2 (GPR-2, CCR10) binds the skin-associated chemokine CCL27
(CTACK/ALP/ILC).";
J. Immunol. 164:3465-3470(2000).
[3]
SEQUENCE OF 9-362 FROM N.A.
RP MEDLINE=95154831; Pubmed=7851889;
RX Marchese A., Docherty J.M., Nguyen T., Heiber M., Cheng R.,
RA Heng H.H.Q., Tsui L.-C., Shi X., George S.R., O'Dowd B.F.;
RT "Cloning of human genes encoding novel G protein-coupled receptors.";
Genomics 23:609-618(1994).
[4]
LIGAND BINDING, AND TISSUE SPECIFICITY.
RP MEDLINE=20357357; Pubmed=10781587;
RX Wang W., Soto H., Oldham E.R., Buchanan M.E., Honey B., Catron D.,
RA Jenkins N., Copeland N.G., Gilbert D.J., Nguyen N., Abrams J.,
RA Kerzhenovich D., Smith K., McClanahan T., Vicari A.P., Zlotnik A.;
RT "Identification of a novel chemokine (CCL28), which binds CCR10
(GPR2).";
J. Biol. Chem. 275:22313-22323(2000).
[5]
LIGAND BINDING.
RP MEDLINE=20432268; Pubmed=10975800;
RX Pan J., Kunkel E.J., Gossler U., Lazarus N., Langdon P., Broadwell K.,
RA Vierra M.A., Genovese M.C., Butcher E.C., Soler D.;
RT "A novel chemokine ligand for CCR10 and CCR3 expressed by epithelial
cells in mucosal tissues.";
J. Immunol. 165:2943-2949(2000).
CC -1- FUNCTION: RECEPTOR FOR CHEMOKINES SCYA27 AND SCYA28. SUBSEQUENTLY
TRANSDUCE A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS
LEVEL AND STIMULATES CHEMOTAXIS IN A PRE-B CELL LINE.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN ADULT TESTIS,
SMALL INTESTINE, FETAL LUNG, FETAL KIDNEY. WEAKER EXPRESSION WAS
OBSERVED IN MANY OTHER ADULT TISSUES INCLUDING SPLEEN, THYMUS,
LYMPH NODE, PEYER'S PATCHES, COLON, HEART, OVARY, PERIPHERAL BLOOD
LYMPHOCYTES, THYROID AND SPINAL CORD. ALSO EXPRESSED BY
MELANOCYTES, DERMAL FIBROBLASTS, DERMAL MICROVASCULAR ENDOTHELIAL
CELLS. ALSO DETECTED IN T CELLS AND IN SKIN-DERIVED LANGERHANS
CELLS.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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EMBL; AF215981; AAF63709.1; -
DR EMBL; AF208237; AAF72871.1; -
DR EMBL; U13667; AAA64593.1; -
DR MIM; 600240; -
DR InterPro; IPR000276; -
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.

CC	EMBL; U34806; AAC50826.1; -
DR	GCRdb; GCR_1962; -
DR	MIM; 601166; -
DR	InterPro; IPR000276; -
DR	Pfam; PF00001; 7tm1; 1.
DR	PRINTS; P00237; GPCRHHODPSN.
DR	PROSITE; PS00237; G-PROTEIN RECEPT.1; 1.

DR PROSITE: PS00237: C PROTEIN RECD E1 1. 1
 EK FRN1S, FR00427, INKLEUKINOR.

DR PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 Chemotaxis.
 FT DOMAIN 1 48 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 49 75 1 (POTENTIAL).
 FT DOMAIN 76 84 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 85 105 2 (POTENTIAL).
 FT DOMAIN 106 120 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 121 142 3 (POTENTIAL).
 FT DOMAIN 143 163 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 164 183 4 (POTENTIAL).
 FT DOMAIN 184 208 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 209 231 5 (POTENTIAL).
 FT DOMAIN 232 251 6 (POTENTIAL).
 FT TRANSMEM 252 273 7 (POTENTIAL).
 FT DOMAIN 274 294 8 (POTENTIAL).
 FT TRANSMEM 295 315 9 (POTENTIAL).
 FT DOMAIN 316 360 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 119 196 BY SIMILARITY.
 FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 24 24 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 360 AA; 40625 MW; 9A7F70C982A632D1 CRC64;

Query Match 46.5%; Score 53.5; DB 1; Length 360;
 Best Local Similarity 59.1%; Pred. No. 0.39;
 Matches 13; Conservative 2; Mismatches 4; Indels 3; Gaps 1;

OY 1 LKGIYAINFCGMLLLTICISM 22

Db 124 LK----EYFYSGILLACISM 142

RESULT 12

BOFA_BACSU STANDARD; PRT; 87 AA.
 ID BOFA_BACSU STANDARD; PRT; 87 AA.
 AC P24282;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE SIGMA-K FACTOR PROCESSING REGULATORY PROTEIN BOFA (BYPASS-OF-FORESPORE
 DE PROTEIN A).
 GN BOFA.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91088245; PubMed=2124672;
 RA Alonso C., Shirahige K., Ogasawara N.;
 RT "Molecular cloning, genetic characterization and DNA sequence
 RT analysis of the recM region of Bacillus subtilis.";
 RL Nucleic Acids Res. 18:6771-6777(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=168;
 RC MEDLINE=96051385; PubMed=7584024;
 RA Ogasawara N., Nakai S., Yoshikawa H.;
 RT "Systematic sequencing of the 180 kilobase region of the Bacillus
 RT subtilis chromosome containing the replication origin.";
 RL DNA Res. 1:1-14(1994).
 RN [3]
 RP CHARACTERIZATION.
 RX MEDLINE=92250411; PubMed=1577688;
 RA Ricca E., Cutting S.M., Losick R.;
 RT "Characterization of bofa, a gene involved in intercompartmental
 RT regulation of pro-sigma K processing during sporulation in Bacillus
 RT subtilis.";
 RL J. Bacteriol. 174:3177-3184(1992).
 RN [4]
 RP TOPOLOGY.
 RX MEDLINE=97286525; PubMed=9141672;

RA Varcamonti M., Marasco R., de Felice M., Sacco M.;
 RT "Membrane topology analysis of the Bacillus subtilis Bofa protein
 RT involved in pro-sigma K processing.";
 RL Microbiology 143:1053-1058(1997).
 CC -!- FUNCTION: INVOLVED IN THE MEDIATION OF THE INTERCOMPARTMENTAL
 CC COUPLING OF PRO-SIGMA K PROCESSING TO EVENTS IN THE FORESPORE.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC
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 CC
 CC EMBL; X17014; CAA34880.1; -
 CC EMBL; D26185; BAA05259.1; -
 CC EMBL; Z99104; CAB11799.1; -
 CC PIR; S13789; S13789.
 CC PIR; B41869; B41869.
 CC Subtilist; BG10087; bofa.
 KW Sporulation; Transmembrane.
 FT DOMAIN 1 2 EXTRACELLULAR (PROBABLE).
 FT TRANSMEM 3 23 PROBABLE.
 FT DOMAIN 24 36 CYTOPLASMIC (PROBABLE).
 FT TRANSMEM 37 57 PROBABLE.
 FT DOMAIN 58 87 EXTRACELLULAR (PROBABLE).
 FT SEQUENCE 87 AA; 9010 MW; FF1DA14E6826B70E CRC64;

Query Match 46.1%; Score 53; DB 1; Length 87;

Best Local Similarity 52.6%; Pred. No. 0.13;

Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 4 GIYAINFCGMLLLTICISM 22

Db 31 GITAVKEVAGALLVCVNM 49

RESULT 13

CKRA_MOUSE STANDARD; PRT; 362 AA.
 ID CKRA_MOUSE STANDARD; PRT; 362 AA.
 AC Q9JL21; Q9JL20; Q9JTP1;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 10 (C-C CKR-10) (CC-CKR-10) (CCR-10)
 DE (CHEMOKINE C-C RECEPTOR 9) (G-PROTEIN COUPLED RECEPTOR 2).
 GN CCR10 OR CMKBR9 OR GPR2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RX STRAIN=BALB/C; TISSUE=Peyer's patch;
 RC MEDLINE=20191997; PubMed=10725696;
 RA Jarmin D.I., Rits M., Bota D., Gerard N.P., Graham G.J.,
 RA Clark-Lewis I., Gerard C.;
 RT "Cutting edge: Identification of the orphan receptor G-protein-coupled
 RT receptor 2 as CCR10, a specific receptor for the chemokine ESKine.";
 RL J. Immunol. 164:3460-3464(2000).
 RN [2]
 RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND LIGAND BINDING.
 RX TISSUE=Thymocytes;
 RC MEDLINE=20357357; PubMed=10781587;
 RA Wang W., Soto H., Oldham E.R., Buchanan M.E., Homey B., Catron D.,
 RA Jenkins N., Copeland N.G., Gilbert D.J., Nguyen N., Abrams J.,
 RA Kershenovich D., Smith K., McClanahan T., Vicari A.P., Zlotnik A.;
 RT "Identification of a novel chemokine (CCL28), which binds CCR10
 RT (GPR2).";
 RL J. Biol. Chem. 275:22313-22323(2000).

```

CC -!- FUNCTION: RECEPTOR FOR CHEMOKINES SCYA27 AND SCYA28. SUBSEQUENTLY
CC TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS
CC LEVEL.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN SMALL INTESTINE,
CC COLON, LYMPH NODES, Peyer's patches and at lower levels in thymus,
CC LUNG, AND SPLEEN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF215982; AAF63710.1; -
DR EMBL; AF215983; AAF63711.1; -
DR EMBL; AF208238; AAF72872.1; -
DR MGD; MGI:1096320; Cnkbr9.
DR PROSITE; PS00237; G_PROTEIN_RECP_FL1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_FL2_1; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein.
KW DOMAIN 1 48 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 49 69 1 POTENTIAL.
FT DOMAIN 70 80 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 81 101 2 POTENTIAL.
FT DOMAIN 102 115 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 116 136 3 POTENTIAL.
FT DOMAIN 137 159 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 160 180 4 POTENTIAL.
FT DOMAIN 181 208 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 209 229 5 POTENTIAL.
FT DOMAIN 230 247 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 248 268 6 POTENTIAL.
FT DOMAIN 269 291 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 292 312 7 POTENTIAL.
FT DOMAIN 313 362 CYTOPLASMIC (POTENTIAL).
FT DISULFID 113 191 BY SIMILARITY.
FT CONFLICT 135 135 N -> S (IN REF. 2).
SQ SEQUENCE 362 AA; 38926 MW; 0FF4EA2005B94E99 CRC64;

Query Match 46.1%; Score 53; DB 1; Length 362;
Best Local Similarity 40.0%; Pred. No. 0.47; Indels 6; Gaps 0;
Matches 8; Conservative 6; Mismatches 0;

Qy 2 LKGIYAINFCGMLLLTICIS 21
: | | : | | : | | :
Db 116 ISGLYSASFHAGFLEFLACIN 135

RESULT 14
CCR5_RAT STANDARD; PRT; 374 AA.
AC P34997;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-X-C CHEMOKINE RECEPTOR TYPE 5 (CXCR-5) (BURKITT'S LYMPHOMA
DE RECEPTOR 1 HOMOLOG) (NEUROLYMPHATIC RECEPTOR) (NLR).
GN BLR1 OR CXCR5
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=93238948; PubMed=8386678;
RA Kouba M., Vanetti M., Wang X., Schaefer M., Hoell V.;
RT "Cloning of a novel putative G-protein-coupled receptor (NLR) which

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RT is expressed in neuronal and lymphatic tissue.";
RL FEBS Lett. 321:173-178(1993).
CC -!- FUNCTION: CYTOKINE RECEPTOR THAT BINDS TO B LYMPHOCYTE
CC CHEMOATTRACTANT (BLC) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN NEURONAL AND LYMPHATIC TISSUE.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL; X71463; CAA50582.1; -
DR PIR; S32785; S32785.
DR GCRDB; GCR_0648; -
DR InterPro; IPR000276; -
DR InterPro; IPR001053; -
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00564; BURKITTSLYMR.
DR PROSITE; PS00237; G_PROTEIN_RECP_FL1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_FL2_1; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein; B-cell.
KW DOMAIN 1 57 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 58 78 1 POTENTIAL.
FT DOMAIN 79 90 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 91 111 2 POTENTIAL.
FT DOMAIN 112 126 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 127 147 3 POTENTIAL.
FT DOMAIN 148 169 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 170 190 4 POTENTIAL.
FT DOMAIN 191 221 5 POTENTIAL.
FT TRANSSEM 222 242 6 POTENTIAL.
FT DOMAIN 243 261 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 262 282 7 POTENTIAL.
FT DOMAIN 283 306 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 307 327 7 POTENTIAL.
FT DOMAIN 328 374 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 28 28 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 124 204 POTENTIAL.
SQ SEQUENCE 374 AA; 42012 MW; D87A3AC816207319 CRC64;

Query Match 45.2%; Score 52; DB 1; Length 374;
Best Local Similarity 50.0%; Pred. No. 0.68;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 5 IYAINFCGMLLLTICISM 22
: | | | | | | | | | |
Db 130 LHKINFCSSLLLIACIAV 147

RESULT 15
GSHR_HUMAN STANDARD; PRT; 478 AA.
AC P00390;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE GLUTATHIONE REDUCTASE (EC 1.6.4.2) (GR) (GRASE).
GN GSR OR GIUR OR GRDI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;

```

RX MEDLINE=90235822; PubMed=2185014;
RA Tutic M., Lu X.A., Schirmer R.H., Werner D.;
RT "Cloning and sequencing of mammalian glutathione reductase cDNA.";
RL Eur. J. Biochem. 188:523-528(1990).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=20175207; PubMed=10708558;
RX Kelnner M.J., Montoya M.A.;
RT "Structural organization of the human glutathione reductase (GSR)
gene: determination of correct cDNA sequence and identification of a
mitochondrial leader sequence.";
RL Biochem. Biophys. Res. Commun. 269:366-368(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Reichwald K., Blechschmidt K., Schilhabel M., Baumgart C., Menzel U.,
RA Dette M., Jahn N., Korenberg J.R., Schlegelberger B., Rosenthal A.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE.
RX MEDLINE=82138780; PubMed=7060551;
RA Krauth-Siegel R.L., Blatterspiel R., Saleh M., Schiltz E.,
RA Schirmer R.H., Untucht-Grau R.;
RT "Glutathione reductase from human erythrocytes. The sequences of the
NADPH domain and of the interface domain.";
RL Eur. J. Biochem. 121:259-267(1982).
RN [5]
RP SEQUENCE OF 54-66.
RC TISSUE=Erythrocyte;
RX MEDLINE=78043204; PubMed=923580;
RA Kröhne-Ehrich G., Schirmer R.H., Untucht-Grau R.;
RT "Glutathione reductase from human erythrocytes. Isolation of the
enzyme and sequence analysis of the redox-active peptide.";
RL Eur. J. Biochem. 80:65-71(1977).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2 ANGSTROMS).
RX MEDLINE=82145544; PubMed=7334521;
RA Thieme R., Pai E.F., Schirmer R.H., Schulz G.E.;
RT "Three-dimensional structure of glutathione reductase at 2-A
resolution.";
RL J. Mol. Biol. 152:763-782(1981).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (1.57 ANGSTROMS).
RX MEDLINE=88011277; PubMed=3656429;
RA Karplus P.A., Schulz G.E.;
RT "Refined structure of glutathione reductase at 1.54-A resolution.";
RL J. Mol. Biol. 195:701-729(1987).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 18-478.
RX MEDLINE=98206290; PubMed=9546215;
RA Becker K., Savvides S.N., Keese M., Schirmer R.H., Karplus P.A.;
RT "Enzyme inactivation through sulphydryl oxidation by physiologic NO-
carriers.";
RL Nat. Struct. Biol. 5:267-271(1998).
RN
CC -1- FUNCTION: MAINTAIN HIGH LEVELS OF REDUCED GLUTATHIONE IN THE
CYTOSOL.
CC -1- CATALYTIC ACTIVITY: NADPH + OXIDIZED GLUTATHIONE = NADP(+) +
2 GLUTATHIONE.
CC -1- COFACTOR: FAD.
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- DOMAIN: EACH SUBUNIT CAN BE DIVIDED INTO 4 DOMAINS THAT ARE
CONSECUTIVE ALONG THE POLYPEPTIDE CHAIN. DOMAINS 1 & 2 BIND FAD
AND NADPH, RESPECTIVELY. DOMAIN 4 FORMS THE INTERFACE
-1- MISCELLANEOUS: THE ACTIVE SITE IS A REDOX-ACTIVE DISULFIDE BOND.
CC -1- SIMILARITY: BELONGS TO THE PYRIDINE NUCLEOTIDE-DISULFIDE
OXIDOREDUCTASES CLASS-1.
CC
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CC EMBL; X15722; CAA33744.1; -
DR EMBL; AF228703; AAF37573.1; -
DR EMBL; AF215848; AAF20007.1; -
DR PIR; A00404; RDHUU.
DR PIR; S08979; S08979.
DR PDB; 4GR1; 31-JUL-94.
DR PDB; 1GRA; 31-JAN-94.
DR PDB; 1GRB; 31-JAN-94.
DR PDB; 1GRG; 31-JAN-94.
DR PDB; 1GRF; 31-JAN-94.
DR PDB; 1GRG; 31-JAN-94.
DR PDB; 1GRH; 31-JAN-94.
DR PDB; 3GRS; 16-APR-88.
DR PDB; 1GRT; 16-JUN-97.
DR PDB; 2GRT; 12-AUG-97.
DR PDB; 3GRT; 12-AUG-97.
DR PDB; 4GRT; 12-AUG-97.
DR PDB; 5GRT; 12-AUG-97.
DR PDB; 1ALG; 15-OCT-97.
DR PDB; 1XAN; 11-JUL-96.
DR PDB; 1DNC; 27-MAY-98.
DR PDB; 1GSN; 27-MAY-98.
DR MIM; 138300; -
DR InterPro; IPR001100; -
DR InterPro; IPR001327; -
DR Pfam; PF00070; PYR_redox; 1.
DR PRINTS; PR00368; FADPNR.
DR PRINTS; PR00411; PNDRTASEI.
DR PROSITE; PS00076; PYRIDINE_REDOX_1; 1.
KW Redox-active center; Oxidoreductase; Flavoprotein; FAD; NADP;
KW Acetylation; 3D-structure.
FT INIT_MET 0
FT MOD_RES 1
FT NP_BIND 22 52 ACETYLATION.
FT DISULFID 58 63 FAD (ADP PART) (PROBABLE).
FT DISULFID 90 90 REDOX-ACTIVE.
FT NP_BIND 321 331 INTERCHAIN (WITH DIMER).
FT ACT_SITE 467 467 FAD (FLAVIN PART) (BY SIMILARITY).
FT STRAND 19 20
FT STRAND 23 26
FT HELIX 30 41
FT TURN 42 43
FT TURN 46 50
FT TURN 54 55
FT HELIX 56 61
FT TURN 81 82
FT HELIX 83 85
FT TURN 86 86
FT HELIX 96 120
FT TURN 121 122
FT STRAND 124 127
FT STRAND 131 132
FT STRAND 139 142
FT TURN 143 144
FT STRAND 145 148
FT STRAND 152 154
FT STRAND 158 160
FT TURN 165 167
FT TURN 169 170
FT HELIX 171 173
FT STRAND 175 175
FT HELIX 177 180
FT TURN 181 182
FT STRAND 189 193
FT HELIX 197 208
FT TURN 209 210
FT STRAND 212 216
FT TURN 224 225
FT HELIX 228 240
FT TURN 241 242

FT STRAND 244 246
FT TURN 247 248
FT STRAND 249 257
FT TURN 258 259
FT STRAND 260 267
FT TURN 270 271
FT STRAND 275 282
FT STRAND 284 287
FT STRAND 291 293
FT TURN 296 299
FT TURN 300 302
FT TURN 303 304
FT STRAND 307 307
FT TURN 309 310
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FT TURN 317 318
FT STRAND 320 320
FT TURN 324 325
FT STRAND 326 328
FT TURN 330 333
FT STRAND 334 334
FT TURN 339 354
FT TURN 358 359
FT TURN 365 366
FT STRAND 369 371
FT STRAND 377 381
FT TURN 384 391
FT TURN 393 395
FT STRAND 396 403
FT TURN 406 410
FT STRAND 417 424
FT TURN 425 428
FT STRAND 429 436
FT TURN 438 439
FT TURN 440 452
FT TURN 453 454
FT STRAND 456 456
FT TURN 457 461
FT TURN 462 462
FT TURN 471 475

Query Match 45.2%; Score 52; DB 1; Length 478;
Best Local Similarity 47.6%; Pred. No. 0.86;
Matches 10; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 2 LKGIYAINFCGMLLTICISM 22
:||||: || ||| ::
Db 323 VKGIYAVGDCGKALLTPVAI 343

Search completed: May 23, 2001, 15:36:18
Job time: 649 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:35:13 ; Search time 189.03 Seconds
(without alignments)
13.641 Million cell updates/sec

Title: US-08-887-977-10_COPY_111_132
Perfect score: 115
Sequence: 1 LLKGIYAINFCNCGMLLTICISM 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues
Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_15: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phase: *
10: sp_plant: *
11: sp_rodent: *
12: sp_unclassified: *
13: sp_vertebrate: *
14: sp_virus: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	102	88.7	367	11	Q9RLV0 mus musculus
2	67	58.3	342	6	Q9TV16 pan troglod
3	66	57.4	343	6	Q9XT45 macaca mula
4	66	57.4	343	6	Q9N020 cercocebus
5	64	55.7	378	11	Q08707 mus musculus
6	63	54.8	382	11	Q09027 rattus norv
7	58	50.4	368	13	Q42444 oncorhynch
8	56	48.7	361	4	Q9NZG2 homo sapien
9	56	48.7	362	11	Q9JI11 mus musculus
10	53	46.1	360	11	Q9JL20 mus musculus
11	53	46.1	362	11	Q9JL21 mus musculus
12	52	45.2	522	4	Q9NP63 homo sapien
13	51.5	44.8	360	6	Q97663 macaca mula
14	51.5	44.8	360	6	Q9TV17 macaca mula
15	51	44.3	350	4	Q9NPB9 homo sapien
16	51	44.3	415	4	O15185 homo sapien
17	51	44.3	420	11	P70619 rattus norv
18	50	43.5	353	11	O35797 rattus norv
19	49.5	43.0	111	4	Q9P2T7 homo sapien

20	49	42.6	384	4	O00537	000537 homo sapien
21	49	42.6	384	4	O00590	000590 homo sapien
22	49	42.6	553	14	Q9Q3F4	Q9Q3F4 avian infec
23	49	42.6	553	14	Q9IWU9	Q9IWU9 avian infec
24	49	42.6	1153	14	O66178	Q66178 avian infec
25	48	41.7	342	13	O93239	Q93239 cyprinus ca
26	48	41.7	480	2	Q9JXG0	Q9JXG0 neisseria m
27	48	41.7	480	2	Q9JWH8	Q9JWH8 neisseria m
28	47	40.9	367	11	O88410	O88410 mus musculu
29	47	40.9	367	11	Q9QWN6	Q9QWN6 mus musculu
30	47	40.9	367	11	Q9JLI9	Q9JLI9 rattus norv
31	46.5	40.4	613	5	Q9XXQ9	Q9XXQ9 caenorhabdi
32	46	40.0	216	10	Q9LUB4	Q9LUB4 arabidopsis
33	46	40.0	337	11	Q9QX13	Q9QX13 rattus norv
34	46	40.0	341	4	Q9Y376	Q9Y376 homo sapien
35	46	40.0	485	2	Q9PEA1	Q9PEA1 xylella fas
36	46	40.0	1061	5	O96998	O96998 leishmania
37	46	40.0	1090	10	Q9LQK8	Q9LQK8 arabidopsis
38	45	39.1	361	11	O35811	O35811 rattus norv
39	45	39.1	361	11	Q9JJS7	Q9JJS7 mus musculu
40	45	39.1	452	5	O25631	O25631 onchocerca
41	45	39.1	462	5	O01412	O01412 onchocerca
42	45	39.1	552	14	Q9Q6Q7	Q9Q6Q7 avian infec
43	44.5	38.7	115	8	Q9MJJ4	Q9MJJ4 carabus gen
44	44.5	38.7	246	10	Q9ZQP8	Q9ZQP8 arabidopsis
45	44	38.3	265	2	Q9Z6S6	Q9Z6S6 chlamydia p

ALIGNMENTS

RESULT 1
Q9RLV0 Q9RLV0 PRELIMINARY; PRT; 367 AA.
AC Q9RLV0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE CC CHEMOKINE LARC SPECIFIC RECEPTOR.
GN MCCR6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Tanaka Y.;
RT "Molecular Cloning of Murine Homologue of CCR6, the Specific Receptor
for CC Chemokine LARC."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB016031; BAA82443.1; -
DR INTERPRO; IPR000190; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR000355; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR00635; ANGIOTENSINR.
DR PRINTS; PR00637; CCHEMOKINER.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 367 AA; 42082 MW; 207FD98B2F7A6DD3 CRC64;

Query Match 88.7%; Score 102; DB 11; Length 367;
Best Local Similarity 81.8%; Pred. No. 1.9e-08;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LLKGIYAINFCNCGMLLTICISM 22

Db 112 LMKGTAYVNFNCGMLLTICISM 133

RESULT 2

[illegible]

DR EMBL; Y12879; CAA73379.1; -
DR MGD; MGI:1096320; Cmkbr9.
DR INTERPRO; IPR000276; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
SQ SEQUENCE 378 AA; 43255 MW; 7A125F3C7B2F5E0 CRC64;

Query Match 55.7%; Score 64; DB 11; Length 378;
Best Local Similarity 40.9%; Pred. No. 0.022;
Matches 9; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

OY 1 LLKGIYAINFCGMLLLTCISM 22
:: :||| ||: :||:|
Db 118 VISTLYSINFCGIFITCMLS 139

RESULT 6
O09027 ID O09027 PRELIMINARY; PRT; 382 AA.
AC O09027;

DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE CCRI0-RELATED RECEPTOR.
GN RCCR10RR.

OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]

RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RA Bonini J.A., Steiner D.F.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U92803; AAB61572.1; -
DR INTERPRO; IPR000276; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
SQ SEQUENCE 382 AA; 43293 MW; E8714CE23DB96772 CRC64;

Query Match 54.8%; Score 63; DB 11; Length 382;
Best Local Similarity 50.0%; Pred. No. 0.033;
Matches 9; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY 5 IYAINFCGMLLLTCISM 22
:||| ||: :||:|
Db 123 LYSINFCGIFITCMLS 140

RESULT 7
O42444 ID O42444 PRELIMINARY; PRT; 368 AA.
AC O42444;

DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE INTERLEUKIN-8-LIKE RECEPTOR.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
[1]

RP SEQUENCE FROM N.A.
RA Zou J., Daniels G.D., Cunningham C., Secombes C.J.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ003159; CAA05917.1; -
DR INTERPRO; IPR000276; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.

SQ SEQUENCE 368 AA; 41523 MW; BE28E2D4C47E821A CRC64;

Query Match 50.4%; Score 58; DB 13; Length 368;
Best Local Similarity 70.6%; Pred. No. 0.2;
Matches 12; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 6 YAINFCGMLLLTCISM 22
| ||| ||| ||| |||
Db 126 YKINFFSMLLLTCISV 142

RESULT 8

O9NZG2 ID O9NZG2 PRELIMINARY; PRT; 361 AA.
AC O9NZG2;

DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE 7-TRANSMEMBRANE G-PROTEIN COUPLED RECEPTOR 2.
GN GPR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]

RP SEQUENCE FROM N.A.
RX MEDLINE=20191998; PubMed=10725697;
RA Honey B., Wang W., Buchanan M., Wisenborn A., Soto H., Catron D.,
RA Orozco R., Ruzicka T., Lehmann P., Oldham E., Zlotnik A.;
RT "Cutting edge: the orphan chemokine receptor G protein-coupled
RT receptor-2 (GPR-2, CCR10) binds the skin-associated chemokine CCL27
RT (CTACK/ALP/ILC)";
RL J. Immunol. 164:3465-3470(2000).
DR EMBL; AF208237; AAF72871.1; -
KW Receptor; Transmembrane.
SQ SEQUENCE 361 AA; 38302 MW; F8AA749118E3926F CRC64;

Query Match 48.7%; Score 56; DB 4; Length 361;
Best Local Similarity 45.0%; Pred. No. 0.41;
Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY 2 LKGIYAINFCGMLLLTCIS 21
: ||: | : | | |||
Db 116 ISGLYSASFHAGFLFLACIS 135

RESULT 9

O9JIP1 ID O9JIP1 PRELIMINARY; PRT; 362 AA.
AC O9JIP1;

DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE 7-TRANSMEMBRANE G-PROTEIN COUPLED RECEPTOR 2.
GN GPR2.
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]

RP SEQUENCE FROM N.A.
RA Wang W., Soto H., Oldham E.R., Buchanan M.E., Honey B., Catron D.,
RA Jenkins N., Copeland N.G., Gilbert D.J., Nguyen N., Abrams J.,
RA Kershenovich D., Smith K., McClanahan T., Vicari A.P., Zlotnik A.;
RT "Identification of a novel chemokine (CCL28), which binds CCR10
RT (GPR2)";
RL J. Biol. Chem. 275:22313-22323(2000).
DR EMBL; AF208238; AAF72872.1; -
KW Receptor; Transmembrane.
SQ SEQUENCE 362 AA; 38899 MW; 13C4292859C376CE CRC64;

Query Match 48.7%; Score 56; DB 11; Length 362;
Best Local Similarity 45.0%; Pred. No. 0.41;
Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 2 LKGIYAINFCGMLLTCIS 21
:|:::|:::|:::|:::|:::
DB 116 ISGLYSASFAGFLACIN 135

RESULT 10

Q9JL20
ID Q9JL20 PRELIMINARY; PRT; 360 AA.
AC Q9JL20;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CC CHEMOKINE RECEPTOR 10B (FRAGMENT).
GN CCR10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RX MEDLINE=20191997; PubMed=10725696;
RA Jarmin D.I., Rits M., Bota D., Gerard N.P., Graham G.J.,
RA Clark-Lewis I., Gerard C.;
RT "Cutting edge: identification of the orphan receptor G-protein-coupled
RT receptor 2 as CCR10, a specific receptor for the chemokine ESkin.";
RL J. Immunol. 164:3460-3464(2000).
DR EMBL; AF215983; AAF63711.1; -;
KW Receptor.
FT NON_TER
SQ SEQUENCE 360 AA; 38738 MW; 16CBFF69F785BA23 CRC64;

Query Match 46.1%; Score 53; DB 11; Length 360;
Best Local Similarity 40.0%; Pred. No. 1.2;
Matches 8; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 2 LKGIYAINFCGMLLTCIS 21
:|:::|:::|:::|:::|:::
DB 114 ISGLYSASFAGFLACIN 133

RESULT 11

Q9JL21
ID Q9JL21 PRELIMINARY; PRT; 362 AA.
AC Q9JL21;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CC CHEMOKINE RECEPTOR 10A.
GN CCR10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RX MEDLINE=20191997; PubMed=10725696;
RA Jarmin D.I., Rits M., Bota D., Gerard N.P., Graham G.J.,
RA Clark-Lewis I., Gerard C.;
RT "Cutting edge: identification of the orphan receptor G-protein-coupled
RT receptor 2 as CCR10, a specific receptor for the chemokine ESkin.";
RL J. Immunol. 164:3460-3464(2000).
DR EMBL; AF215982; AAF63710.1; -;
KW Receptor.
SQ SEQUENCE 362 AA; 38926 MW; 0FF4EA2005B94E99 CRC64;

Query Match 46.1%; Score 53; DB 11; Length 362;
Best Local Similarity 40.0%; Pred. No. 1.2;
Matches 8; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 2 LKGIYAINFCGMLLTCIS 21
:|:::|:::|:::|:::|:::
DB 116 ISGLYSASFAGFLACIN 135

RESULT 12

Q9NP63
ID Q9NP63 PRELIMINARY; PRT; 522 AA.
AC Q9NP63;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE MITOCHONDRIAL GLUTATHIONE REDUCTASE PRECURSOR.
GN GRD1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kelner M.J., Montoya M.A.;
RT "Structural organization of the human glutathione reductase (GSR)
RT gene: determination of correct cDNA sequence and identification of a
RT mitochondrial leader sequence.";
RL Biochem. Biophys. Res. Commun. 0:0-0(2000).
DR EMBL; AF228704; AAF37574.1; -;
DR EMBL; AF228703; AAF37572.1; -;
KW Transmembrane; Mitochondrion.
FT TRANSIT
SQ SEQUENCE 522 AA; 56257 MW; DD8E2BA9D8E3757B CRC64;

Query Match 45.2%; Score 52; DB 4; Length 522;
Best Local Similarity 47.6%; Pred. No. 2.5;
Matches 10; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 2 LKGIYAINFCGMLLTCISM 22
:|:::|:::|:::|:::|:::
DB 367 VKGIYAVGDVCGKALLTPVAI 387

RESULT 13

O97663
ID O97663 PRELIMINARY; PRT; 360 AA.
AC O97663;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE PUTATIVE CHEMOKINE RECEPTOR.
GN GPR15.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Margulies B.J., Hauer D.A., Clements J.E.;
RT "Identification and characterization of thirteen rhesus macaque
RT chemokine receptors and chemokine receptor homologues.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99335217; PubMed=10408732;
RA Pretet J.L., Brussel A., Guillet J.G., Butor C.;
RT "Two alleles for rhesus macaque GPR15.";
RL AIDS Res. Hum. Retroviruses 15:945-947(1999).

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF100203; AAC72401.1; -
DR EMBL: AF084226; AAD52038.1; -
DR INTERPRO: IPR000248; -
DR INTERPRO: IPR000276; -
DR PFAM: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODOPSN.
DR PRINTS: PR00241; ANGIOTENSINR.
DR PROSITE: PS00237; G-PROTEIN_RECEPTOR; 1.
KW Receptor; G-protein coupled receptor; Transmembrane; Glycoprotein.
SQ SEQUENCE 360 AA; 40787 MW; ECCEDID0BC34E959 CRC64;

Query Match 44.8%; Score 51.5; DB 6; Length 360;
Best Local Similarity 40.0%; Pred. No. 2.1;
Matches 10; Conservative 7; Mismatches 5; Indels 3; Gaps 1;

QY 1 LLKG---IYAINFCGMLLLTCISM 22
| | | : : | : | | | : |
Db 105 LCKGSSYMSVNMHCVFLLTCMSV 129

RESULT 14

Q9TV17 PRELIMINARY; PRT; 360 AA.
AC Q9TV17;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
DE G PROTEIN-COUPLED RECEPTOR GPR15.
GN GPR15.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A. PubMed=10408732;
RX MEDLINE=99335217; PubMed=10408732;
RA Pretet J.L., Brussel A., Guillet J.G., Butor C.;
RT "two alleles for rhesus macaque GPR15 (BOB).";
RL AIDS Res. Hum. Retroviruses 15:945-947(1999).
DR EMBL: AF084227; AAD52039.1; -
DR INTERPRO: IPR000248; -
DR INTERPRO: IPR000276; -
DR PFAM: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODOPSN.
DR PRINTS: PR00241; ANGIOTENSINR.
DR PROSITE: PS00237; G-PROTEIN_RECEPTOR; 1.
KW Receptor.
SQ SEQUENCE 360 AA; 40806 MW; 96F0BBE1CBIDA4 CRC64;

Query Match 44.8%; Score 51.5; DB 6; Length 360;
Best Local Similarity 40.0%; Pred. No. 2.1;
Matches 10; Conservative 7; Mismatches 5; Indels 3; Gaps 1;

QY 1 LLKG---IYAINFCGMLLLTCISM 22
| | | : : | : | | | : |
Db 105 LCKGSSYMSVNMHCVFLLTCMSV 129

RESULT 15

Q9NPB9 PRELIMINARY; PRT; 350 AA.
AC Q9NPB9;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TRENBLrel. 15, Last annotation update)
DE CHEMOKINE RECEPTOR (CC CHEMOKINE RECEPTOR) (ORPHAN SEVEN-TRANSMEMBRANE RECEPTOR).
GN CCR11 OR CCR2 OR VSHK1.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Schweickart V.L., Epp A., Raport C.J., Gray P.W.;
RT "CCR11 is a Functional Receptor for the Monocyte Chemoattractant Protein Family of Chemokines";
RL J. Biol. Chem. 275:9550-9556(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20171478; PubMed=10706668;
RA Gosling J., Dairaghi D.J., Wang Y., Hanley M., Talbot D., Miao Z., Schall T.J.;
RT "Cutting edge: identification of a novel chemokine receptor that binds dendritic cell- and T cell-active chemokines including ELC, SLC, and TECK";
RL J. Immunol. 164:2851-2856(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Khoja H., Wang G., Lee Ng C.-T., Tucker J., Brown T., Shymala V.;
RT "Cloning of CCRL1, an orphan seven transmembrane receptor related to chemokine receptors, expressed abundantly in heart";
RL Gene 246:229-238(2000).
RN [4]
RP SEQUENCE FROM N.A.
RA Shymala V., Khoja H.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF193507; AAF61299.1; -
DR EMBL: AF233281; AAF44751.1; -
DR EMBL: AF110640; AAF59827.1; -
KW Receptor; Transmembrane.
SQ SEQUENCE 350 AA; 39913 MW; 8E26049D2D5757C8 CRC64;

Query Match 44.3%; Score 51; DB 4; Length 350;
Best Local Similarity 40.9%; Pred. No. 2.5;
Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 1 LLKGIYAINFCGMLLLTCISM 22
| | | : : | : | | | : |
Db 114 ITSALYTLNFVSGMQLACISI 135

Search completed: May 23, 2001, 15:35:14
Job time: 620 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:28:28 ; Search time 184.73 Seconds
(without alignments)
5.570 Million cell updates/sec

Title: US-08-887-977-10_COPY_133_150

Perfect score: 86
Sequence: 1 DRYIAIVQATKSFRLRSR 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_0401.*
1: /SID56/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID56/gcgdata/geneseq/geneseq/AA1981.DAT.*
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5: /SID56/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SID56/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SID56/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SID56/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SID56/gcgdata/geneseq/geneseq/AA1988.DAT.*
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11: /SID56/gcgdata/geneseq/geneseq/AA1990.DAT.*
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13: /SID56/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SID56/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SID56/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SID56/gcgdata/geneseq/geneseq/AA1995.DAT.*
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20: /SID56/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID56/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID56/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	100.0	365	19 W48086	Human dendritic ce
2	86	100.0	365	21 Y97077	Primate (human) ch
3	55	64.0	358	15 R53745	Partial sequence o
4	55	64.0	358	21 B21689	Human 7TM receptor
5	55	64.0	361	20 W97348	An Epstein-barr vi
6	55	64.0	378	15 R54079	Epstein Barr virus
7	55	64.0	378	15 R53744	Putative seven tra
8	55	64.0	378	19 W48724	Human V31 seven tr
9	55	64.0	378	19 W56164	G-protein coupled
10	55	64.0	378	19 W53622	Epstein Barr virus
11	55	64.0	378	21 B21688	Human 7TM receptor

12	55	64.0	378	21 Y90629	Human G protein-co
13	55	64.0	378	21 Y90663	Human mutant G pro
14	55	64.0	378	22 B50859	Human CCR7. Homo
15	55	64.0	410	15 R53743	Putative seven tra
16	55	64.0	410	19 W48723	Polypeptide sequen
17	55	64.0	410	21 B21687	Genomic clone of 7
18	53	61.6	302	19 W70001	Rodent chemokine r
19	53	61.6	351	20 Y23825	A7-times membrane
20	53	61.6	359	15 R53747	Seven transmembran
21	53	61.6	359	19 W48728	Marine V31 seven t
22	53	61.6	359	21 B21691	Murine 7TM recepto
23	53	61.6	378	21 B21699	7TM receptor prote
24	49	57.0	337	15 R53753	Seven transmembran
25	49	57.0	337	18 W08141	G-protein receptor
26	49	57.0	337	19 W69997	Primate chemokine
27	49	57.0	337	19 W48734	Human RM3 seven tr
28	49	57.0	337	21 B21698	Human 7TM receptor
29	49	57.0	337	21 B02847	Human G protein co
30	49	57.0	337	21 B02856	Human G protein co
31	49	57.0	352	13 R27792	New platelet facto
32	49	57.0	352	16 R68812	Human monocyte PF4
33	49	57.0	352	16 R80757	Chemokine superfam
34	49	57.0	352	20 Y39993	Human CXCR4 protel
35	49	57.0	352	21 Y52507	Human CXCR4-chemok
36	49	57.0	356	20 W97362	G-protein coupled
37	49	57.0	359	19 W64778	A murine CXCR4 chemo
38	49	57.0	359	20 Y39994	Mouse CXCR4 protel
39	48	55.8	73	19 W69998	Rodent chemokine r
40	48	55.8	418	14 R39263	Human somatostatini
41	48	55.8	428	14 R39264	Murine somatostatini
42	47	54.7	244	19 W69996	Primate chemokine
43	47	54.7	339	15 R53752	Seven transmembran
44	47	54.7	339	18 W07617	Human G-protein th
45	47	54.7	339	19 W48733	Human R12 seven tr

ALIGNMENTS

RESULT	1
W48086	
ID	W48086 standard; Protein; 365 AA.
XX	XX
AC	W48086;
XX	XX
DT	11-JUN-1998 (first entry)
XX	XX
DE	Human dendritic cell chemokine receptor.
DE	XX
DE	XX
KW	Human; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta;
KW	receptor; dendritic cell; macrophage; inflammation; asthma.
XX	XX
OS	Homo sapiens.
XX	XX
XX	XX
PH	Key Location/Qualifiers
FT	Misc-difference 193
FT	/note= "encoded by CAN"
XX	XX
PN	W09801557-A2.
XX	XX
PD	15-JAN-1998.
XX	XX
PF	02-JUL-1997; 97WO-US10819.
XX	XX
PR	04-JUN-1997; 97US-0048593.
PR	05-JUL-1996; 96US-0675814.
PR	11-OCT-1996; 96US-0028329.
XX	XX
PA	(SCHE) SCHERING CORP.
XX	XX
PI	Gish KC, Schall TJ, Vicari A, Wang W, Zlotnik A;
XX	XX
DR	WPI; 1998-101054/09.

DR N-PSDB; V15418.

PT Novel chemokines, e.g. thymus expressed chemokine - used for
treating inflammatory conditions including asthma.

XX Claim 3; Page 94-95; 202pp; English.

CC The present sequence represents human dendritic cell chemokine receptor.
CC Antibodies which bind to the protein can be used in detecting or
CC diagnosing various immunological conditions related to expression
CC of the protein. The nucleic acid can be used for screening and
CC isolating DNA clones for the chemokines, especially from other
CC species. The chemokine can be used in the treatment of conditions
CC associated with abnormal physiology or development, including
CC inflammatory conditions such as asthma.

XX Sequence 365 AA;

Query Match 100.0%; Score 86; DB 19; Length 365;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLRSR 18

DB 133 dryiaivqatksfrlrsr 150

RESULT 2

Y97077
ID Y97077 standard; Protein; 365 AA.

AC Y97077;

DT 04-DEC-2000 (first entry)

DE Primate (human) chemokine receptor CCR6.

XX MIP-3-alpha; chemokine; CCR6 receptor; ligand; cytostatic; agonist;
KW antagonist; anti-psoriatic; dermatological; immunosuppressive;
KW anti-inflammatory.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 193
FT /note= "Encoded by CAN#"

XX WO2000046248-A1.

XX 10-AUG-2000.

XX 02-FEB-2000; 2000WO-US00511.

XX 03-FEB-1999; 99US-0244281.

XX (SCHE) SCHERING CORP.

XX Oldham ER, Homey B, Dieu-Nosjean M, Caux C, Zlotnik A;

XX WPI; 2000-543477/49.

XX N-PSDB; A51971.

PT Novel methods for modulating the migration of cells within or to the
PT skin using MIP-3-alpha or CCR6 agonists or antagonists, useful for
PT treating skin disorders, e.g. cancer

XX Disclosure; Page 53-54; 61pp; English.

XX The MIP-3-alpha chemokine is expressed in inflamed skin cells. This
CC chemokine is the ligand for the CCR6 receptor. MIP-3-alpha or CCR6
CC agonists or antagonists can be used to modulate the migration of a cell
CC within or to the skin of a mammal. MIP-3-alpha can be used to purify a

CC population of cells expressing a MIP-3-alpha receptor. The methods are
CC useful for treating a mammalian subject with a skin disease or condition,
CC e.g. cancer, metastasis, psoriasis, atopic or contact dermatitis,
CC systemic lupus erythematosus and lichen ruber planus, or for treating
CC skin transplants or grafts.

XX Sequence 365 AA;

Query Match 100.0%; Score 86; DB 21; Length 365;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLRSR 18

DB 133 dryiaivqatksfrlrsr 150

RESULT 3

R53745
ID R53745 standard; Protein; 358 AA.

XX R53745;

XX 02-FEB-1995 (first entry)

XX Partial sequence of seven transmembrane receptor (V31).

XX Primer; seven transmembrane receptor; receptor; amplification; PCR;
KW polymerase chain reaction.

XX Homo sapiens.

XX WO9412635-A.

XX 09-JUN-1994.

XX 17-NOV-1993; 93WO-US111153.

XX 17-NOV-1992; 92US-0977452.

XX (ICOS-) ICOS CORP.

XX Godiska R, Gray PW, Schweickart VL;

XX WPI; 1994-200264/24.

XX N-PSDB; Q66162.

XX DNA encoding seven transmembrane receptors - used to develop
PT prods. for use as therapeutic or diagnostic agents for conditions
PT involving the receptors.

XX Example 3; Page 56-57; 100pp; English.

XX Two primers (Q66148, Q66149) were used to amplify human genomic DNA
CC purified from leukocytes. Approximately 1000 clones were isolated
CC after the initial amplification reaction and probed with sequences
CC specific for seven transmembrane receptors IL8R1, AT2R and R20.

CC Clones which did not hybridise were then chosen for sequence
CC analysis. Three new clones were identified that appeared to encode
CC seven transmembrane receptor segments. Two more primers (Q66151,
CC Q66152) were used to isolate a full length version of one of these
CC clones designated V31 (See Q66153). This is the sequence encoded
CC by exon 3 of the V31 genomic clone

XX Sequence 358 AA;

Query Match 64.0%; Score 55; DB 15; Length 358;

Best Local Similarity 61.1%; Pred. No. 0.047;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLRSR 18

```

Db      133 dryvaivqavsahrhr 150
      |||:||||| : | | : |
RESULT  4
B21689
ID      B21689 standard; Protein; 358 AA.
XX
AC      B21689;
XX
DT      26-JAN-2001 (first entry)
XX
DE      Human 7TM receptor V31-B cDNA clone exon 1 protein.
XX
KW      Seven transmembrane receptor; 7TM; heptahelical; serpentine;
KW      G-protein-coupled; V28; V31; V112; R20; R2; R12; RM3; gene therapy;
KW      cancer.
XX
OS      Homo sapiens.
XX
PN      US6107475-A.
XX
PD      22-AUG-2000.
XX
PF      26-APR-1999; 99US-0299843.
XX
PR      17-MAY-1994; 94US-0245242.
PR      01-JUN-1998; 98US-0088337.
PR      17-NOV-1992; 92US-0977452.
PR      17-NOV-1993; 93US-0153848.
XX
PA      (ICOS-) ICOS CORP.
XX
PI      Schweickart VL, Gray PW, Godiska R;
XX
DR      WPI; 2000-571335/53.
XX
N-PSDB; A91709.
XX
PT      Polynucleotide encoding seven transmembrane receptors, antibody
PT      specific to the receptor, agonist and antagonist of the receptor useful
PT      for treating inflammation in a mammal -
XX
PS      Example 3; Columns 49-52; 61pp; English.
XX
CC      The present sequence is a novel seven transmembrane (7TM) receptors
CC      (also known as heptahelical, serpentine or G-protein-coupled receptors).
CC      The coding sequence for the present sequence may be used for gene
CC      therapy for diseases such as cancer.
XX
SQ      Sequence 358 AA;

Query Match      64.0%; Score 55; DB 21; Length 358;
Best Local Similarity 61.1%; Pred. NO. 0.047;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      1 DRYIAIVQATKSFRLRSR 18
      |||:||||| : | | : |
DB      133 dryvaivqavsahrhr 150

RESULT  5
W97348
ID      W97348 standard; Protein; 361 AA.
XX
AC      W97348;
XX
DT      12-MAY-1999 (first entry)
XX
DE      An Epstein-barr virus-induced G-protein coupled receptor.
XX
KW      Epstein-barr virus-induced G-protein coupled receptor; EBI 3;
KW      splicing variant; EBI 1; vaccine; infection; HIV-1; HIV-2; pain;
KW

cancer; anorexia; bulimia; asthma; Parkinson's disease;
acute heart failure; hypotension; hypertension; urinary retention;
osteoporosis; angina pectoris; myocardial infarction; ulcer; allergy;
benign prostatic hypertrophy; psychotic disorder; neurological disorder;
anxiety; schizophrenia; manic depression; delirium; dementia;
severe mental retardation; dyskinesias; Huntington's disease;
Gilles de la Tourette's syndrome.
Homo sapiens.
EP894854-A2.
03-FEB-1999.
04-DEC-1997; 97EP-0309791.
29-JUL-1997; 97US-0902294.
(SMIK ) SMITHKLINE BEECHAM CORP.
Zhu Y;
WPI; 1999-108346/10.
N-PSDB; X15857.
New Epstein-barr virus-induced G-protein coupled receptor (EBI 3)
gene and protein - useful as diagnostic reagents and for prevention
and treatment of HIV infections and cancer
Claim 2; Page 7; 20pp; English.

The present sequence represents a Epstein-barr virus-induced G-protein
coupled receptor (EBI 3), which is a splicing variant of EBI 1. EBI 3
antibodies are useful for inducing an immune response to immunize and
prevent disease, and for isolating EBI 3 clones or purifying the
polypeptides by affinity chromatography. EBI 3 polypeptides can be
administered directly or as a vaccine to inoculate against disease.
Diseases diagnosed, prevented and treated include: bacterial, fungal,
viral and protozoan infections, particularly infections caused by HIV-1
or HIV-2; pain; cancers; anorexia; bulimia; asthma; Parkinson's disease;
acute heart failure; hypotension; hypertension; urinary retention;
osteoporosis; angina pectoris; myocardial infarction; ulcers; allergies;
benign prostatic hypertrophy; and psychotic and neurological disorders,
including anxiety, schizophrenia, manic depression, delirium, dementia,
severe mental retardation and dyskinesias, such as Huntington's disease
or Gilles de la Tourette's syndrome.
Sequence 361 AA;

Query Match      64.0%; Score 55; DB 20; Length 361;
Best Local Similarity 61.1%; Pred. NO. 0.048;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      1 DRYIAIVQATKSFRLRSR 18
      |||:||||| : | | : |
DB      136 dryvaivqavsahrhr 153

RESULT  6
R54079
ID      R54079 standard; Protein; 378 AA.
XX
AC      R54079;
XX
DT      03-FEB-1995 (first entry)
XX
DE      Epstein Barr virus induced (EBI-1) polypeptide.
XX
KW      Epstein Barr virus; EBV; induction; detection; diagnosis;
KW      lymphocytes; antigen; growth; differentiation; mediator;
KW      infectious mononucleosis.
KW

```

OS Homo sapiens.
 XX Key
 FH Region
 FT 1..24 Location/Qualifiers
 FT /label= Hydrophobic region.
 FT /note= "Predicted to be a signal peptide for
 FT membrane translocation."
 FT Modified-site 36
 FT /note= "Potential N-linked glycosylation site."
 FT Region 60..86
 FT /label= Hydrophobic region.
 FT Region 96..116
 FT /label= Hydrophobic region.
 FT Region 131..152
 FT /label= Hydrophobic region.
 FT Region 151..159
 FT /note= "This sequences motif
 FT (S-[I/V]-D-R-[V/F]-X-X-X) is highly
 FT conserved among a large number of G-protein
 FT coupled receptors."
 FT Region 171..191
 FT /label= Hydrophobic region.
 FT Region 220..247
 FT /label= Hydrophobic region.
 FT Region 284..289
 FT /label= Hydrophobic region.
 FT Modified-site 292
 FT /note= "Potential N-linked glycosylation site."
 FT Region 314..331
 FT /label= Hydrophobic region.
 XX
 PN W09412519-A.
 XX
 PD 09-JUN-1994.
 XX
 PF 08-OCT-1993; 93WO-US09636.
 XX
 PR 25-NOV-1992; 92US-0980518.
 XX
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
 XX
 PI Birkenbach M, Kieff E;
 XX
 DR WPI; 1994-200183/24.
 DR N-PSDB; Q64125.
 XX
 PT DNA coding for Epstein Barr Virus induced (EBI) polypeptide(s)
 PT and antibodies to EB1, 2 and 3 - useful for detecting EBV by
 PT hybridisation or by immunoassay
 XX
 PS Claim 8; Page 54-56; 84pp; English.
 XX
 CC EBV infected B lymphocytes recapitulate features of antigen
 CC stimulation in enlarging, increasing RNA synthesis, expressing
 CC activation antigens and adhesion molecules, secreting Ig and
 CC proliferating. Unlike antigen stimulated B lymphocytes, EBV
 CC infected B lymphocytes continue to proliferate (in vitro) as
 CC immortalised lymphoblastoid cell lines. Because of the similar
 CC effects of EBV and antigen, EBV induced genes are likely to include
 CC mediators of antigen induced B lymphocyte growth or differentiation.
 XX
 SQ Sequence 378 AA;

Query Match 64.0%; Score 55; DB 15; Length 378;
 Best Local Similarity 61.1%; Pred. No. 0.05;
 Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 DRYIAIVQATKSFRLRSR 18
 |||:||||| : | : |
 Db 153 dryvaivqavsahrhr 170

OS Homo sapiens.
 XX
 KW V28; placenta; seven transmembrane receptor; 7TM; signal transduction;
 KW immunology; inflammation; V31.
 XX
 OS

RESULT 7
 R53744
 ID R53744 standard; Protein; 378 AA.
 XX
 AC R53744;
 XX
 DT 02-FEB-1995 (first entry)
 XX
 DE Putative seven transmembrane receptor (V31).
 XX
 KW Primer; seven transmembrane receptor; receptor; amplification; PCR;
 KW polymerase chain reaction.
 XX
 OS Homo sapiens.
 XX
 PN W09412635-A.
 XX
 PD 09-JUN-1994.
 XX
 PF 17-NOV-1993; 93WO-US11153.
 XX
 PR 17-NOV-1992; 92US-0977452.
 XX
 PA (ICOS-) ICOS CORP.
 XX
 PI Godiska R, Gray PW, Schweickart VL;
 XX
 DR WPI; 1994-200264/24.
 DR N-PSDB; Q66160.
 XX
 PT DNA encoding seven trans:membrane receptors - used to develop
 PT prods. for use as therapeutic or diagnostic agents for conditions
 PT involving the receptors.
 XX
 PS Claim 1; Page 52-53; 100pp; English.
 XX
 CC A human cDNA encoding the seven transmembrane receptor V31 was
 CC isolated by first amplifying a partial cDNA clone from a human
 CC tonsil cDNA library using two primers (Q66154, Q66155). The resulting
 CC amplified products were probed using two radioactively labelled
 CC sequences (Q66156, Q66157). A hybridising band was isolated from the
 CC gel and cloned. The resulting clone was named pv31-5'end (Q66158). A
 CC full length cDNA clone was isolated from a peripheral blood
 CC mononuclear cell library using V31 specific primers (Q66159, Q66152).
 CC Clone PBMC75 was isolated and the V31 cDNA insert in the clone was
 CC designated cDNA V31-B (Q66160).
 XX
 SQ Sequence 378 AA;

Query Match 64.0%; Score 55; DB 15; Length 378;
 Best Local Similarity 61.1%; Pred. No. 0.05;
 Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 DRYIAIVQATKSFRLRSR 18
 |||:||||| : | : |
 Db 153 dryvaivqavsahrhr 170

RESULT 8
 W48724
 ID W48724 standard; Protein; 378 AA.
 XX
 AC W48724;
 XX
 DT 25-SEP-1998 (first entry)
 XX
 DE Human V31 seven transmembrane receptor.
 XX

XX FH Key Location/Qualifiers
 FT Domain 58..86
 FT FT /note= "Transmembrane domain 1"
 FT Domain 96..119
 FT FT /note= "Transmembrane domain 2"
 FT Domain 131..152
 FT FT /note= "Transmembrane domain 3"
 FT Domain 171..196
 FT FT /note= "Transmembrane domain 4"
 FT Domain 219..247
 FT FT /note= "Transmembrane domain 5"
 FT Domain 264..285
 FT FT /note= "Transmembrane domain 6"
 FT Domain 306..331
 FT FT /note= "Transmembrane domain 7"

XX US5759804-A.

XX 02-JUN-1998.

XX 17-NOV-1993; 93US-0153848.

XX 17-NOV-1992; 92US-0977452.

XX (ICOS-) ICOS CORP.

XX Godiska R, Gray PW, Schweickart VL;

XX WPI; 1998-332132/29;

XX N-PSDB; V18347.

XX DNA encoding V28 seven transmembrane receptor polypeptide - useful
 PT for producing recombinant polypeptide and anti-V28 antibodies, and
 PT in screening assays for V28 agonists and antagonists

XX Example 3; Columns 39-42; 56pp; English.

XX The present sequence represents the V31 seven transmembrane (7TM)
 CC receptor encoded by the V31 cDNA (V18347). The invention claims for
 CC a full length V28 genomic DNA (V18343) and the V28 protein it
 CC encodes (W48722). V28 and V31 proteins are 7TM receptors which
 CC are probably involved in signal transduction. The invention also
 CC claims that cells transformed with V28 DNA can be used to produce the
 CC recombinant polypeptide, to produce anti-V28 antibodies or in screening
 CC assays for V28 agonists or antagonists. The antibodies, agonists and
 CC antagonists could then be used to modulate V28 receptor-ligand binding,
 CC for e.g. in immunological and/or inflammatory events in vivo.

XX SQ Sequence 378 AA;

Query Match 64.0%; Score 55; DB 19; Length 378;

Best Local Similarity 61.1%; Pred. No. 0.05;

Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYIAIVQATKSFRLRSR 18

Db 153 dryvaivqavsahrhrar 170

RESULT 9

ID W56164 standard; Protein; 378 AA.

XX AC W56164;

XX 20-JUL-1998 (first entry)

XX G-protein coupled receptor (R7G) designated EB11.

XX Lymphocyte R7G; EB11; G-protein coupled receptor;

XX opiate/opioid recognition site; opiate; opioid; opioid binding protein;

KW screening; lymphocyte receptor; compound; agonist; antagonist;
 KW lymphocyte receptor protein; immune-cell specific lymphocyte receptor;
 KW neuronal type opioid receptor.

XX Homo sapiens.

OS US5753516-A.

XX 19-MAY-1998.

XX 03-FEB-1995; 95US-0383751.

XX 03-FEB-1995; 95US-0383751.

XX (FINB/) FINBERG R W.

XX (HEAG/) HEAGY W E.

XX Finberg RW, Heagy WE;

XX WPI; 1998-311410/27.

XX N-PSDB; V22684.

XX Screening assay for lymphocyte opioid receptor ligands - using
 PT recombinant receptor protein

XX Claim 1; Columns 87-88; 70pp; English.

XX The present sequence represents a novel lymphocyte R7G, termed EB11. R7G
 CC proteins are part of the G-protein coupled receptor superfamily. EB11 is
 CC a functional opiate/opioid recognition site that probably plays a major
 CC role in mediating the effects that opiate/opioids have on lymphocytes.
 CC The EB11 protein is an opioid binding protein that is displayed on the
 CC surface of lymphocytes. A process for screening a candidate substance for
 CC ability to interact with a lymphocyte receptor comprises selecting a
 CC candidate substance having a chemical structure or biological activity
 CC suggestive of an ability to mimic the biological activity of an
 CC opiate, opioid drug or opioid peptide having known binding affinity for
 CC EB11. The ability of the candidate substance is tested to interact with
 CC the lymphocyte receptor protein. This method can be used to screen for
 CC agonists or antagonists to the lymphocyte receptor protein. The method
 CC can be modified and used to screen for agonists or antagonists to the
 CC immune-cell specific lymphocyte receptor polypeptide or the neuronal type
 CC opioid receptor polypeptide.

XX SQ Sequence 378 AA;

Query Match 64.0%; Score 55; DB 19; Length 378;

Best Local Similarity 61.1%; Pred. No. 0.05;

Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYIAIVQATKSFRLRSR 18

Db 153 dryvaivqavsahrhrar 170

RESULT 10

ID W53622 standard; Protein; 378 AA.

XX AC W53622;

XX 09-JUL-1998 (first entry)

XX Epstein Barr virus induced protein 1 (EBI-1).

XX Assessing; monitoring; foetal development; placental development;

XX Epstein Barr virus; EBV; induced gene 1; EBI-1.

XX Homo sapiens.

XX OS US5744301-A.

XX PN

PD 28-APR-1998.
 XX
 PF 02-FEB-1995; 95US-0383750.
 XX
 PR 02-FEB-1995; 95US-0383750.
 PR 25-NOV-1992; 92US-0980518.
 PR 30-NOV-1994; 94US-0352678.
 XX
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
 XX
 XX Birkenbach M, Kieff E;
 XX WPI; 1998-271060/24.
 DR N-PSDB; V25490.
 XX
 XX Assessing or monitoring foetal or placental development - comprises
 PT detecting the level or size of Epstein Barr virus induced nucleic
 PT acid or protein in maternal serum samples
 XX
 PS Example 2; Columns 37-40; 45pp; English.
 XX
 CC The present sequence was used in the development of a novel method
 CC for assessing or monitoring foetal or placental development. the
 CC method comprises taking a maternal serum sample, and detecting the
 CC level or size of Epstein Barr virus (EBV) induced gene or protein 3
 CC (EBI-3) to obtain a result, which can be compared to a control to
 CC assess or monitor foetal or placental development.
 XX
 XX Sequence 378 AA;

Query Match 64.0%; Score 55; DB 19; Length 378;
 Best Local Similarity 61.1%; Pred. No. 0.05;
 Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLRSR 18
 |||:||||| : | : |
 Db 153 dryvaivqavsahrhrar 170

RESULT 11
 B21688
 ID B21688 standard; Protein; 378 AA.
 XX
 AC B21688;
 XX
 DT 26-JAN-2001 (first entry)
 XX
 DE Human 7TM receptor V31-B cDNA clone protein.
 XX
 KW Seven transmembrane receptor; 7TM; heptahelical; serpentine;
 KW G-protein-coupled; V28; V31; V112; R20; R2; R12; RM3; gene therapy;
 KW cancer.
 XX
 OS Homo sapiens.
 XX
 PN US6107475-A.
 XX
 PD 22-AUG-2000.
 XX
 PF 26-APR-1999; 99US-0299843.
 XX
 PR 17-MAY-1994; 94US-0245242.
 PR 01-JUN-1998; 98US-0083337.
 PR 17-NOV-1992; 92US-0977452.
 PR 17-NOV-1993; 93US-0153848.
 XX
 PA (ICOS-) ICOS CORP.
 XX
 XX Schweickart VL, Gray PW, Godiska R;
 PI WPI; 2000-571335/53.
 DR N-PSDB; A91707.

XX
 PT Polynucleotide encoding seven transmembrane receptors, antibody
 PT specific to the receptor, agonist and antagonist of the receptor useful
 PT for treating inflammation in a mammal
 XX
 PS Example 3; Columns 41-44; 61pp; English.
 XX
 CC The present sequence is a novel seven transmembrane (7TM) receptors
 CC (also known as heptahelical, serpentine or G-protein-coupled receptors).
 CC The coding sequence for the present sequence may be used for gene
 CC therapy for diseases such as cancer.
 XX
 XX Sequence 378 AA;

Query Match 64.0%; Score 55; DB 21; Length 378;
 Best Local Similarity 61.1%; Pred. No. 0.05;
 Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLRSR 18
 |||:||||| : | : |
 Db 153 dryvaivqavsahrhrar 170

RESULT 12
 Y90629
 ID Y90629 standard; Protein; 378 AA.
 XX
 AC Y90629;
 XX
 DT 21-AUG-2000 (first entry)
 XX
 DE Human G protein-coupled receptor EB11.
 XX
 KW G protein-coupled receptor; GPCR; constitutively active;
 KW intracellular loop 3; transmembrane domain 6; drug screening;
 KW agonist; antagonist.
 XX
 OS Homo sapiens.
 XX
 PN WO200022129-A1.
 XX
 PD 20-APR-2000.
 XX
 PF 12-OCT-1999; 99WO-US23938.
 XX
 PR 13-OCT-1998; 98US-0170496.
 XX
 PA (AREN-) ARENA PHARM INC.
 XX
 PI Behan DP, Chalmers DT, Liaw CW;
 XX WPI; 2000-329165/28.
 DR N-PSDB; A30632.
 XX
 PT Non-endogenous constitutively activated human G protein-coupled
 PT receptors, useful for identifying agonists for use as pharmaceutical
 PT agents
 XX
 PS Example 1; Page 158-159; 341pp; English.
 XX
 CC The invention relates to constitutively active, non-endogenous versions
 CC of endogenous human orphan G protein-coupled receptors (GPCRs, Y90643-
 CC Y90677 and Y90683-Y90687), and to DNA encoding them (A30709-A30743 and
 CC A30775-A30779). The mutant proteins of the invention contain a
 CC mutation in a portion of the protein comprising intracellular loop 3
 CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
 CC is substituted for an endogenous residue in IC3 at a position 16 amino
 CC acids N-terminal of an endogenous proline in TM6 to form a sequence
 CC X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or
 CC Ala, and is preferably Lys. When the endogenous residue at this position
 CC is Lys, this residue is replaced by His, Arg or preferably Ala. The 15
 CC amino acid stretch between the substituted amino acid and the Pro may be

CC endogenous, non-endogenous, or a mixture of endogenous and non-endogenous
 CC residues. The constitutively active GPCRs are useful for identifying
 CC antagonists, agonists and partial agonists for use as pharmaceutical
 CC agents. The mutant proteins are also useful in research settings for
 CC elucidating the roles of the receptors in normal and diseased conditions.
 CC Antagonists for a particular GPCR are useful for treating diseases and
 CC disorders associated with that receptor. Because the novel mutant GPCRs
 CC are constitutively active, they can be used directly for screening of
 CC compounds without the need for endogenous ligands. The present
 CC sequence represents a human wild-type GPCR referred to in an
 CC exemplification of the invention.

XX SQ Sequence 378 AA;

Query Match 64.0%; Score 55; DB 21; Length 378;
 Best Local Similarity 61.1%; Pred. No. 0.05;
 Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYIAIVQATKSFRLRSR 18
 |||:||||| : | : |
 Db 153 dryvaivqavsahrhrar 170

RESULT 13
 Y90663
 ID Y90663 standard; Protein; 378 AA.

XX AC Y90663;
 XX DT 21-AUG-2000 (first entry)
 XX DE Human mutant G protein-coupled receptor EB11 (I262K).

XX KW G protein-coupled receptor; GPCR; constitutively active;
 KW intracellular loop 3; transmembrane domain 6; drug screening;
 KW agonist; antagonist; mutant; mutein.

XX OS Homo sapiens.
 OS Synthetic.

XX PN WO2000022129-A1.

XX PD 20-APR-2000.

XX PF 12-OCT-1999; 99WO-US23938.

XX PR 13-OCT-1998; 98US-0170496.

XX PA (AREN-) ARENA PHARM INC.

XX PI Behan DP, Chalmers DT, Liaw CW;

XX DR WPI; 2000-329165/28.

XX DR N-PSDB; A30729.

XX PT Non-endogenous constitutively activated human G protein-coupled
 PT receptors, useful for identifying agonists for use as pharmaceutical
 PT agents

XX PS Example 2; Page 259-260; 341pp; English.

XX CC The invention relates to constitutively active, non-endogenous versions
 CC of endogenous human orphan G protein-coupled receptors (GPCRs, Y90643-
 CC Y90677 and Y90683-Y90687), and to DNA encoding them (A30709-A30743 and
 CC A30775-A30779). The mutant proteins of the invention contain a
 CC mutation in a portion of the protein comprising intracellular loop 3
 CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
 CC is substituted for an endogenous residue in IC3 at a position 16 amino
 CC acids N-terminal of an endogenous proline in TM6 to form a sequence
 CC X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or
 CC Ala, and is preferably Lys. When the endogenous residue at this position
 CC is Lys, this residue is replaced by His, Arg or preferably Ala. The 15

CC amino acid stretch between the substituted amino acid and the pro may be
 CC endogenous, non-endogenous, or a mixture of endogenous and non-endogenous
 CC residues. The constitutively active GPCRs are useful for identifying
 CC antagonists, agonists and partial agonists for use as pharmaceutical
 CC agents. The mutant proteins are also useful in research settings for
 CC elucidating the roles of the receptors in normal and diseased conditions.
 CC Antagonists for a particular GPCR are useful for treating diseases and
 CC disorders associated with that receptor. Because the novel mutant GPCRs
 CC are constitutively active, they can be used directly for screening of
 CC compounds without the need for endogenous ligands. Sequences Y90643-
 CC Y90677 and Y90683-Y90687 the mutant human GPCRs of the invention.

XX SQ Sequence 378 AA;

Query Match 64.0%; Score 55; DB 21; Length 378;
 Best Local Similarity 61.1%; Pred. No. 0.05;
 Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYIAIVQATKSFRLRSR 18
 |||:||||| : | : |
 Db 153 dryvaivqavsahrhrar 170

RESULT 14
 B50859
 ID B50859 standard; protein; 378 AA.

XX AC B50859;

XX DT 16-MAR-2001 (first entry)
 XX DE Human CCR7.

XX KW Human; chemokine receptor 7; CCR7; chemokine beta-9; Ckbeta-9;
 KW allergy; autoimmune disease; ischaemia; atherosclerosis; cancer;
 KW chronic inflammatory disorder; organ transplant; tissue graft;
 KW chronic myelogenous leukaemia; Infection.

XX OS Homo sapiens.

XX PN US6153441-A.

XX PD 28-NOV-2000.

XX PF 17-FEB-1999; 99US-0251545.

XX PR 17-FEB-1998; 98US-0074883.

XX PA (SMIK) SMITHKLINE BEECHAM CORP.

XX PI Appelbaum ER, White JR, Sarau HM;

XX DR WPI; 2001-049151/06.

XX PT Identifying agonists or antagonists of interaction between human
 PT protein, chemokine beta-9 and human CC chemokine receptor 7, by
 PT contacting cell expressing receptor with test compound

XX PS Claim 1; Fig 1; 20pp; English.

XX CC The present sequence is human chemokine receptor 7 (CCR7), a cellular
 CC receptor for chemokine beta-9 (Ckbeta-9). The sequence may be
 CC used in a method for discovering agonists and antagonists of the
 CC interaction between Ckbeta-9 and CCR7. A cell expressing CCR7
 CC polypeptide on its surface, associated with a component capable of
 CC providing a detectable signal in response to binding of Ckbeta-9, is
 CC contacted with a compound in the presence of labelled or unlabelled
 CC Ckbeta-9. The compound is identified as an agonist/antagonist by
 CC determining whether it activates or inhibits the detectable signal.
 CC The method is useful for identifying agonists and antagonists of the
 CC interaction between Ckbeta-9 and CCR7 which are useful for treating
 CC diseases including allergic disorders, autoimmune diseases,

CC ischaemia/reperfusion injury, development of atherosclerotic plaques,
CC cancer, chronic inflammatory disorders, chronic rejection of
CC transplanted organs or tissue grafts, chronic myelogenous leukaemia, and
CC infection by HIV and other pathogens.
XX
SQ Sequence 378 AA;

Query Match 64.0%; Score 55; DB 22; Length 378;
Best Local Similarity 61.1%; Pred. No. 0.05;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLRSR 18
 | | | : | | | | : | | : |
Db 153 dryvaivqavsahrhrar 170

RESULT 15
R53743
ID R53743 standard; Protein; 410 AA.
XX AC R53743;
XX DT 02-FEB-1995 (first entry)
XX DE Putative seven transmembrane receptor (V31).
XX KW Primer; seven transmembrane receptor; receptor; amplification; PCR;
XX KW polymerase chain reaction.
XX OS Homo sapiens.
XX PN W09412635-A.
XX PD 09-JUN-1994.
XX PF 17-NOV-1993; 93WO-US11153.
XX PR 17-NOV-1992; 92US-0977452.
XX PA (ICOS-) ICOS CORP.
XX PI Godiska R, Gray PW, Schweickart VL;
XX DR WPI; 1994-200264/24.
XX DR N-PSDB; Q66153.
XX PT DNA encoding seven transmembrane receptors - used to develop
XX PT prods. for use as therapeutic or diagnostic agents for conditions
XX PT involving the receptors.
XX PS Example 2; Page 46-48; 100pp; English.
XX CC Two primers (Q66148, Q66149) were used to amplify human genomic DNA
XX CC purified from leukocytes. Approximately 1000 clones were isolated
XX CC after the initial amplification reaction and probed with sequences
XX CC specific for seven transmembrane receptors IL8R1, A2R and R20.
XX CC Clones which did not hybridise were then chosen for sequence
XX CC analysis. Three new clones were identified that appeared to encode
XX CC seven transmembrane receptor segments. Two more primers (Q66151,
XX CC Q66152) were used to isolate a full length version of one of these
XX CC clones, one of which was designated V31 and encoded this
XX CC polypeptide.
XX SQ Sequence 410 AA;

Query Match 64.0%; Score 55; DB 15; Length 410;
Best Local Similarity 61.1%; Pred. No. 0.055;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLRSR 18
 | | | : | | | | : | | : |

Db 185 dryvaivqavsahrhrar 202

Search completed: May 23, 2001, 15:28:29
Job time: 406 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:30:06 ; Search time 95.91 Seconds
(without alignments)
3.605 Million cell updates/sec

Title: US-08-887-977-10_COPY_133_150

Perfect score: 86

Sequence: 1 DRYTAIVQATKSFRLRSR 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA:*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PCOMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	64.0	358	1 US-08-153-848-19	Sequence 19, Appl
2	55	64.0	358	3 US-09-299-843A-19	Sequence 19, Appl
3	55	64.0	358	5 PCT-US93-11153-19	Sequence 19, Appl
4	55	64.0	361	2 US-08-902-294-2	Sequence 2, Appl
5	55	64.0	361	3 US-09-178-637-2	Sequence 2, Appl
6	55	64.0	378	1 US-08-383-750-2	Sequence 2, Appl
7	55	64.0	378	1 US-08-383-751A-2	Sequence 2, Appl
8	55	64.0	378	1 US-08-153-848-15	Sequence 15, Appl
9	55	64.0	378	3 US-08-352-678-2	Sequence 2, Appl
10	55	64.0	378	3 US-09-299-843A-15	Sequence 15, Appl
11	55	64.0	378	4 US-09-251-545-1	Sequence 1, Appl
12	55	64.0	378	5 PCT-US93-09636-2	Sequence 2, Appl
13	55	64.0	378	5 PCT-US93-11153-15	Sequence 15, Appl
14	55	64.0	410	1 US-08-153-848-7	Sequence 7, Appl
15	55	64.0	410	3 US-09-299-843A-7	Sequence 7, Appl
16	55	64.0	410	5 PCT-US93-11153-7	Sequence 7, Appl
17	53	61.6	359	1 US-08-153-848-24	Sequence 24, Appl
18	53	61.6	359	3 US-09-299-843A-24	Sequence 24, Appl
19	53	61.6	359	5 PCT-US93-11153-24	Sequence 24, Appl
20	53	61.6	378	3 US-09-299-843A-66	Sequence 66, Appl
21	49	57.0	337	1 US-08-153-848-46	Sequence 46, Appl
22	49	57.0	337	3 US-09-299-843A-46	Sequence 46, Appl
23	49	57.0	337	5 PCT-US93-11153-46	Sequence 46, Appl
24	49	57.0	352	1 US-08-202-056-3	Sequence 3, Appl
25	49	57.0	352	1 US-08-076-093A-4	Sequence 4, Appl
26	49	57.0	352	1 US-08-450-393A-6	Sequence 6, Appl
27	49	57.0	352	1 US-08-701-265-4	Sequence 4, Appl

28	49	57.0	352	2 US-08-284-586-4	Sequence 4, Appl
29	49	57.0	352	2 US-08-805-478-4	Sequence 4, Appl
30	49	57.0	352	2 US-08-802-627A-4	Sequence 4, Appl
31	49	57.0	352	2 US-08-801-238-4	Sequence 4, Appl
32	49	57.0	352	2 US-08-801-228-4	Sequence 4, Appl
33	49	57.0	352	3 US-09-104-296-4	Sequence 4, Appl
34	49	57.0	352	4 US-08-446-669-6	Sequence 6, Appl
35	49	57.0	352	5 PCT-US95-00476-6	Sequence 6, Appl
36	48	55.8	418	1 US-07-816-283-10	Sequence 10, Appl
37	48	55.8	418	1 US-08-417-103-10	Sequence 10, Appl
38	48	55.8	428	1 US-07-816-283-12	Sequence 12, Appl
39	48	55.8	428	1 US-08-417-103-12	Sequence 12, Appl
40	47	54.7	339	1 US-08-153-848-44	Sequence 44, Appl
41	47	54.7	339	2 US-08-812-871-3	Sequence 3, Appl
42	47	54.7	339	3 US-09-299-843A-44	Sequence 44, Appl
43	47	54.7	339	5 PCT-US93-11153-44	Sequence 44, Appl
44	47	54.7	339	5 PCT-US95-07180-2	Sequence 2, Appl
45	47	54.7	360	4 US-08-875-573-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1

US-08-153-848-19
; Sequence 19, Application US/08153848
; Patent No. 5759804
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153,848
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5759804and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-153-848-19

Query Match 64.0%; Score 55; DB 1; Length 358;
Best Local Similarity 61.1%; Pred No. 0.041;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYAIVQATKSFRLRSR 18
| | | : | | | : | | |
Db 133 DRYAIVQAVSAHRHRAR 150

RESULT 2

US-09-299-843A-19
; Sequence 19, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,843A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/088,337
; FILING DATE: 01-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992

; ATTORNEY/AGENT INFORMATION:
; NAME: Jill E. Uhl
; REGISTRATION NUMBER: 43,213
; REFERENCE/DOCKET NUMBER: 27866/32059B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-299-843A-19

Query Match 64.0%; Score 55; DB 3; Length 358;
Best Local Similarity 61.1%; Pred. No. 0.041;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYAIVQATKSFRLRSR 18
| | | : | | | : | | |
Db 133 DRYAIVQAVSAHRHRAR 150

RESULT 3

PCR-US93-11153-19
; Sequence 19, Application PC/TUS9311153
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald

; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: Novel Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11153
; FILING DATE:
; CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

PCT-US93-11153-19

Query Match 64.0%; Score 55; DB 5; Length 358;
Best Local Similarity 61.1%; Pred. No. 0.041;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYAIVQATKSFRLRSR 18
| | | : | | | : | | |
Db 133 DRYAIVQAVSAHRHRAR 150

RESULT 4

US-08-902-294-2
; Sequence 2, Application US/08902294
; Patent No. 5874252
; GENERAL INFORMATION:

; APPLICANT: ZHU, YUAN
; TITLE OF INVENTION: A NOVEL SPLICING VARIANT OF
; TITLE OF INVENTION: THE EPSTEIN-BARR VIRUS-INDUCED G-PROTEIN COUPLED
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/902,294
FILING DATE: 29-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-70177
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-902-294-2

Query Match 64.0%; Score 55; DB 2; Length 361;
Best Local Similarity 61.1%; Pred. No. 0.042;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYAIVQATKSFRLRSR 18
DB 136 DRYVAIVQAVSAHRHRAR 153

RESULT 5
US-09-178-637-2
Sequence 2, Application US/09178637
Patent No. 6001972
GENERAL INFORMATION:
APPLICANT: ZHU, YUAN
TITLE OF INVENTION: A No. 6001972el Splicing Variant of
the Epstein-Barr Virus-Induced G-Protein Coupled Receptor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/178,637
FILING DATE: 26-OCT-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/902,294
FILING DATE: 29-JUL-1998
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-70177-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-178-637-2

Query Match 64.0%; Score 55; DB 3; Length 361;
Best Local Similarity 61.1%; Pred. No. 0.042;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYAIVQATKSFRLRSR 18
DB 136 DRYVAIVQAVSAHRHRAR 153

RESULT 6
US-08-383-750-2
Sequence 2, Application US/08383750
Patent No. 5744301
GENERAL INFORMATION:
APPLICANT: Birkenbach, Mark
APPLICANT: Kieff, Elliot
TITLE OF INVENTION: Epstein Barr Virus Induced Genes
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W.,
SUITE: Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/383,750
FILING DATE: Herewith
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Fox, Samuel, L.
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 0627.3300001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-383-750-2

Query Match 64.0%; Score 55; DB 1; Length 378;
Best Local Similarity 61.1%; Pred. No. 0.044;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYAIVQATKSFRLRSR 18
DB 153 DRYVAIVQAVSAHRHRAR 170

RESULT 7
US-08-383-751A-2
Sequence 2, Application US/08383751A
Patent No. 5753516
GENERAL INFORMATION:
APPLICANT: Heagy, Wyrta E.
APPLICANT: Finberg, Robert W.
TITLE OF INVENTION: Identification and Uses of Opioid

;; TITLE OF INVENTION: Receptors
;; NUMBER OF SEQUENCES: 8
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Arnold, White & Durkee
;; STREET: P.O. Box 4433
;; CITY: Houston
;; STATE: Texas
;; COUNTRY: US
;; ZIP: 77210
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/383,751A
;; FILING DATE: 03-FEB-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Wilson, Mark B.
;; REGISTRATION NUMBER: 37,259
;; REFERENCE/DOCKET NUMBER: DFCI:001/WIM
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (512) 418-3000
;; TELEFAX: (512) 474-7577
;; TELEX: 79-0924
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 378 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-383-751A-2

Query Match 64.0%; Score 55; DB 1; Length 378;
Best Local Similarity 61.1%; Pred. No. 0.044;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSPRLRSR 18
| | | | | : | : |
Db 153 DRYVAIVQAVSAHRHRAR 170

RESULT 8
US-08-153-848-15
; Sequence 15, Application US/08153848
; Patent No. 5759804
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153,848
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992

;; ATTORNEY/AGENT INFORMATION:
;; NAME: No. 5759804and, Greta E.
;; REGISTRATION NUMBER: 35,302
;; REFERENCE/DOCKET NUMBER: 31794
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312) 474-6300
;; TELEFAX: (312) 474-0448
;; TELEX: 25-3856
;; INFORMATION FOR SEQ ID NO: 15:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 378 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-153-848-15

Query Match 64.0%; Score 55; DB 1; Length 378;
Best Local Similarity 61.1%; Pred. No. 0.044;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSPRLRSR 18
| | | | | : | : |
Db 153 DRYVAIVQAVSAHRHRAR 170

RESULT 9
US-08-352-678-2
; Sequence 2, Application US/08352678
; Patent No. 6043351
; GENERAL INFORMATION:
; APPLICANT: Birkenbach, Mark
; APPLICANT: Kieff, Elliott
; TITLE OF INVENTION: EPSTEIN BARR VIRUS INDUCED GENES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/352,678
; FILING DATE: 30-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/980,518
; FILING DATE: 25-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gates, Edward R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: B0801/7044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-352-678-2

Query Match 64.0%; Score 55; DB 3; Length 378;
Best Local Similarity 61.1%; Pred. No. 0.044;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Qy 1 DRYIAIVQATKSFRLRSR 18
    |||:||||| : ||:|
Db 153 DRYVAIVQAVSAHRHRAR 170

RESULT 10
US-09-299-843A-15
; Sequence 15, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,843A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/088,337
; FILING DATE: 01-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jill E. Uhl
; REGISTRATION NUMBER: 43,213
; REFERENCE/DOCKET NUMBER: 27866/32059B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-299-843A-15

Query Match 64.0%; Score 55; DB 3; Length 378;
Best Local Similarity 61.1%; Pred. No. 0.044;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYIAIVQATKSFRLRSR 18
    |||:||||| : ||:|
Db 153 DRYVAIVQAVSAHRHRAR 170

RESULT 11
US-09-251-545-1
; Sequence 1, Application US/09251545
; Patent No. 6153441
; GENERAL INFORMATION:
; APPLICANT: Edward R. Appelbaum
; APPLICANT: Henry M. Sarau
; APPLICANT: John R. White
; TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND
; TITLE OF INVENTION: ANTAGONISTS OF THE INTERACTION BETWEEN HUMAN CCR7 RECEPTOR
; TITLE OF INVENTION: AND CK(-9 LIGAND AND INTERACTION THEREOF
; FILE REFERENCE: P50753
; CURRENT APPLICATION NUMBER: US/09/251,545
; CURRENT FILING DATE: 1999-02-17
; EARLIER APPLICATION NUMBER: 60/074,883
; EARLIER FILING DATE: 1998-02-17
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Human
US-09-251-545-1

Query Match 64.0%; Score 55; DB 4; Length 378;
Best Local Similarity 61.1%; Pred. No. 0.044;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYIAIVQATKSFRLRSR 18
    |||:||||| : ||:|
Db 153 DRYVAIVQAVSAHRHRAR 170

RESULT 12
PCT-US93-09636-2
; Sequence 2, Application PC/TUS9309636
; GENERAL INFORMATION:
; APPLICANT: Birkenbach, Mark
; APPLICANT: Kieff, Elliot
; TITLE OF INVENTION: Epstein Barr Virus Induced Genes
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/09636
; FILING DATE: herewith
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
PCT-US93-09636-2

Query Match 64.0%; Score 55; DB 5; Length 378;
Best Local Similarity 61.1%; Pred. No. 0.044;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYIAIVQATKSFRLRSR 18
    |||:||||| : ||:|
Db 153 DRYVAIVQAVSAHRHRAR 170

RESULT 11
US-09-251-545-1
; Sequence 1, Application US/09251545
; Patent No. 6153441
; GENERAL INFORMATION:
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RESULT 13
PCT-US93-11153-15
; Sequence 15, Application PC/TUS9311153
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: Novel Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11153
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 07/977,452
; APPLICATION NUMBER: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-11153-15

Query Match 64.0%; Score 55; DB 5; Length 378;
Best Local Similarity 61.1%; Pred. No. 0.044;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 DRYIAIVQATKSFRLRSR 18
|||:||||:|:|:
Db 153 DRYAIVQAVSAHRHR 170

RESULT 14
US-08-153-848-7
; Sequence 7, Application US/08153848
; Patent No. 5759804
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153,848
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA: US 07/977,452
; APPLICATION NUMBER: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5759804and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 410 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-153-848-7

Query Match 64.0%; Score 55; DB 1; Length 410;
Best Local Similarity 61.1%; Pred. No. 0.048;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 DRYIAIVQATKSFRLRSR 18
|||:||||:|:|:
Db 185 DRYAIVQAVSAHRHR 202

RESULT 15
US-09-299-843A-7
; Sequence 7, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,843A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: US 09/088,337
; APPLICATION NUMBER: 01-JUN-1998
; FILING DATE: 01-JUN-1998
; PRIOR APPLICATION DATA: US 08/153,848
; APPLICATION NUMBER: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452

```
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jill E. Uhl
; REGISTRATION NUMBER: 43,213
; REFERENCE/DOCKET NUMBER: 27866/32059B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 410 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-299-843A-7

Query Match      64.0%; Score 55; DB 3; Length 410;
Best Local Similarity 61.1%; Pred. No. 0.048;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYAIVQATKSFRLRSR 18
   |||:|||||:|:|
Db 185 DRYAIVQAVSAHRHR 202
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Search completed: May 23, 2001, 15:30:06
Job time: 413 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 23, 2001, 15:32:00 ; Search time 110.15 Seconds
(without alignments)
11.230 Million cell updates/sec

Title: US-08-887-977-10_COPY_133_150

Perfect score: 86
Sequence: 1 DRYIAIVQATKSPRLRSR 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR-67: *
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86	100.0	369	2 JC5068	G protein-coupled
2	55	64.0	378	2 A45680	G protein-coupled
3	55	64.0	378	2 B55735	lymphocyte-specific
4	53	61.6	378	2 A55735	G protein-coupled
5	49	57.0	352	2 G00048	fusin (LESTRA) - c
6	49	57.0	352	2 A45747	neuropeptide Y/pep
7	48	55.8	418	2 A46226	somatostatin recep
8	48	55.8	428	2 A44021	somatostatin recep
9	48	55.8	428	2 S30508	probable G protein
10	47	54.7	360	2 A57160	chemokine (C-C) re
11	47	54.7	374	2 S42628	G protein-coupled
12	47	54.7	374	2 S32785	G protein-coupled
13	47	54.7	380	2 I38435	angiotensin recept
14	46	53.5	327	2 S6162	MDCK15 protein - h
15	46	53.5	353	2 S28787	neuropeptide Y/pep
16	46	53.5	354	2 A23669	interleukin-8 rece
17	46	53.5	372	2 S26667	G protein-coupled
18	45	52.3	349	2 I59336	galanin receptor 1
19	45	52.3	355	2 G02436	chemokine (C-C) re
20	45	52.3	355	2 A45177	chemokine (C-C) re
21	45	52.3	355	2 I49339	macrophage inflamm
22	45	52.3	359	2 I49341	MIP-1 alpha recept
23	45	52.3	367	2 J50349	interferon-inducib
24	45	52.3	383	2 S55594	G protein-coupled
25	44	51.2	350	2 A39445	interleukin-8 rece
26	44	51.2	355	2 J01231	interleukin-8 rece
27	44	51.2	358	2 A53752	interleukin-8 rece
28	44	51.2	360	2 A53611	interleukin-8 rece
29	44	51.2	360	2 JC4587	chemokine (C-C) re

30	43	50.0	355	2 JC5067	G protein-coupled
31	43	50.0	391	2 A41795	somatostatin recep
32	43	50.0	391	2 C41795	somatostatin recep
33	43	50.0	391	2 A39297	somatostatin recep
34	43	50.0	444	2 T27866	hypothetical prote
35	42.5	49.4	359	2 JC1104	angiotensin II rec
36	42.5	49.4	359	2 JC1194	angiotensin II rec
37	42.5	49.4	359	2 A48857	angiotensin II rec
38	42.5	49.4	359	2 A42656	angiotensin II rec
39	42.5	49.4	359	2 JQ1516	angiotensin II rec
40	42.5	49.4	359	2 S15403	angiotensin II rec
41	42.5	49.4	359	2 I39418	angiotensin II rec
42	42.5	49.4	359	2 JH0621	angiotensin II rec
43	42.5	49.4	359	2 JC2134	angiotensin II rec
44	42	48.8	72	2 PH0848	somatostatin recep
45	42	48.8	356	2 S42096	interleukin-8 rece

ALIGNMENTS

RESULT 1

JC5068
G protein-coupled receptor CKR-L3 - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
C:Accession: JC5068
R:Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
Biochem. Biophys. Res. Commun. 227, 846-853, 1996
A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-lik
A:Reference number: JC5067; MUID:97040707
A:Accession: JC5068
A:Molecule type: DNA
A:Residues: 1-369 <ZAB>
A:Cross-references: EMBL:279784; NID:g1668737; PIDN:CAB02144.1; PID:g1668738
C:Comment: This protein belongs to the family of alpha chemokine receptors.
C:Genetics:
A:Gene: GDB:CMK9R6; STRL22; GPR29; CCR6; CKR-L3; GPR-CY4
A:Cross-references: GDB:5370639; OMIM:601835
A:Map position: 6q27-6q27
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein
F:42-68/Domain: transmembrane #status predicted <TM1>
F:79-99/Domain: transmembrane #status predicted <TM2>
F:115-136/Domain: transmembrane #status predicted <TM3>
F:160-180/Domain: transmembrane #status predicted <TM4>
F:212-233/Domain: transmembrane #status predicted <TM5>
F:250-271/Domain: transmembrane #status predicted <TM6>
F:292-315/Domain: transmembrane #status predicted <TM7>

Query Match 100.0%; Score 86; DB 2; Length 369;
Best Local Similarity 100.0%; Pred. No. 3.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSPRLRSR 18

Db 137 DRYIAIVQATKSPRLRSR 154

RESULT 2

A45680
G protein-coupled peptide receptor EBI 1 - human
C:Species: Homo sapiens (man)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C:Accession: A45680
R:Birkenbach, M.; Josefsen, K.; Yalamanchili, R.; Lenoir, G.; Kieff, E.
J. Virol. 67, 2209-2220, 1993
A:Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-couple
A:Reference number: A45680; MUID:93188173
A:Accession: A45680
A>Status: preliminary
A:Molecule type: nucleic acid

A;Residues: 1-378 <BIR>
A;Cross-references: GB:L08176; NID:g183484; PID:g183485
A;Experimental source: B-lymphocytes
A;Note: sequence extracted from NCBI backbone (NCBIN:127094, NCBI:127095)
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 64.0%; Score 55; DB 2; Length 378;
Best Local Similarity 61.1%; Pred. No. 0.023;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYIAIVQATKSFRLRSR 18
| | | : | | | | | : | | : |
Db 153 DRYVAIVQAVSAHRHRAR 170

RESULT 3
Lymphocyte-specific G protein-coupled receptor EB11 - human
N:Alternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1
C:Species: Homo sapiens (man)
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 19-May-2000
C:Accession: B55735; S52443
R:Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.
Genomics 23, 643-650, 1994
A:Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor
A:Reference number: A55735; MUID:95154835
A:Accession: B55735
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-378 <SCH>
A;Cross-references: GB:L31581; NID:g468319; PIDN:AAA74231.1; PID:g468320
R:Burgstahler, R.; Kempkes, B.; Staube, K.; Lipp, M.
submitted to the EMBL Data Library, February 1995
A:Description: The expression of the chemokine receptor BLR2/EB11 is specifically trans
A:Reference number: S52443
A:Accession: S52443
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 21-378 <BUR>
A;Cross-references: EMBL:X84702
C:Genetics:
A:Gene: GDB:CMKBR7; EB11; BLR2; CCR7
A;Cross-references: GDB:342065; OMIM:600242
A:Map position: 17q12-17q21.2
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor

Query Match 64.0%; Score 55; DB 2; Length 378;
Best Local Similarity 61.1%; Pred. No. 0.023;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYIAIVQATKSFRLRSR 18
| | | : | | | | | : | | : |
Db 153 DRYVAIVQAVSAHRHRAR 170

RESULT 4
A55735
G protein-coupled receptor EB11 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 24-Nov-1999
C:Accession: A55735
R:Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.
Genomics 23, 643-650, 1994
A:Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor
A:Reference number: A55735; MUID:95154835
A:Accession: A55735
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-378 <SCH>

A;Cross-references: GB:L31580; NID:g468340; PIDN:AAA74232.1; PID:g468341
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor

Query Match 61.6%; Score 53; DB 2; Length 378;
Best Local Similarity 61.1%; Pred. No. 0.054;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DRYIAIVQATKSFRLRSR 18
| | | : | | | | | : | | : |
Db 153 DRYVAIVQAVSAHRHRAR 170

RESULT 5
G00048
fusin (LESTRA) - crab-eating macaque
C:Species: Macaca fascicularis (crab-eating macaque)
C:Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 26-Aug-1999
C:Accession: G00048
R:Tatsumi, M.
submitted to GenBank, July 1996
A:Reference number: H00048
A:Accession: G00048
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-352 <TAT>
A;Cross-references: GB:D86579; NID:g1468948; PID:g1468949
C;Superfamily: vertebrate rhodopsin

Query Match 57.0%; Score 49; DB 2; Length 352;
Best Local Similarity 68.8%; Pred. No. 0.28;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYIAIVQATKSFRLR 16
| | | : | | | | | : | | : |
Db 133 DRYLAIVHATNSQRPR 148

RESULT 6
A45747
neuropeptide Y/peptide YY receptor Y3 - human
N:Alternate names: fusin; HM89; leukocyte-derived seven-transmembrane receptor LESTR;
C:Species: Homo sapiens (man)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 05-Nov-1999
C:Accession: A45747; A53103; I53006; I59444; I69203; S32761
R:Federspiel, B.; Melhado, I.G.; Duncan, A.M.V.; Delaney, A.; Schappert, K.; Clark-L
Genomics 16, 707-712, 1993
A:Title: Molecular cloning of the cDNA and chromosomal localization of the gene for a
A:Reference number: A45747; MUID:93315164
A:Accession: A45747
A:Molecule type: mRNA
A:Residues: 1-352 <FED>
A;Cross-references: GB:M99293; NID:g292516; PIDN:AAA16617.1; PID:g292517
R:Loetscher, M.; Geiser, T.; O'Reilly, T.; Zwaalen, R.; Baggiolini, M.; Moser, B.
J. Biol. Chem. 269, 232-237, 1994
A:Title: Cloning of a human seven-transmembrane domain receptor, LESTR, that is highl
A:Reference number: A53103; MUID:94103215
A:Accession: A53103
A:Molecule type: mRNA
A:Residues: 1-352 <LOE>
A;Cross-references: EMBL:X71635; NID:g297099; PIDN:CAA50641.1; PID:g297100
R:Herzog, H.; Hort, Y.J.; Shine, J.; Selbie, L.A.
DNA Cell Biol. 12, 465-471, 1993
A:Title: Molecular cloning, characterization, and localization of the human homolog t
A:Reference number: I53006; MUID:93319629
A:Accession: I53006
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-352 <HER>
A;Cross-references: GB:L06797; NID:g414929; PIDN:AAA03209.1; PID:g414928
R:Jazin, E.E.; Yoo, H.; Blomqvist, A.G.; Yee, F.; Weng, G.; Walker, M.W.; Salton, J.;

Regul. Pept. 47, 247-258, 1993
A:Title: A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its human homolo
A:Reference number: I59444; MUID:94052833
A:Accession: I59444
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-352 <RE2>
A:Cross-references: GB:L01639; NID:g189313; PIDN:AAA16594.1; PID:g189314
R:Nomura, H.; Nielsen, B.W.; Matsushima, K.
Int. Immunol. 5, 1239-1249, 1993
A:Title: Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte chem
A:Reference number: I54751; MUID:94092629
A:Accession: I69203
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-352 <RES>
A:Cross-references: GB:D10924; NID:g219868; PIDN:BAA01722.1; PID:g219869
C:Genetics:
A:Gene: GDB:NPY3R; NPY3
A:Cross-references: GDB:230002; OMIM:162643
A:Map position: 2q21-2q21
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 57.0%; Score 49; DB 2; Length 352;
Best Local Similarity 68.8%; Pred. No. 0.28;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYAIVQATKSFRLR 16
|||:|:| | | | |
Db 133 DRYLAIVHATNSQRPR 148

RESULT 7
A46226
somatostatin receptor 3 - human
C:Species: Homo sapiens (man)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C:Accession: A46226; S32501
R:Yamada, Y.; Reisine, T.; Law, S.F.; Ihara, Y.; Kubota, A.; Kagimoto, S.; Seino, M.; Se
Mol. Endocrinol. 6, 2136-2142, 1992
A:Title: Somatostatin receptors, an expanding gene family: cloning and functional charac
A:Reference number: A46226; MUID:93149123
A:Accession: A46226
A:Molecule type: DNA
A:Residues: 1-418 <YAM>
A:Cross-references: GB:M96738; NID:g338498; PIDN:AAA60592.1; PID:g338499
A:Note: sequence extracted from NCBI backbone (NCBIN:123685, NCBIPI:123690)
R:Corneiss, J.D.; Demchyshyn, L.L.; Seeman, P.; van Tol, H.H.M.; Srikant, C.B.; Kent, G.;
FEBS Lett. 321, 279-284, 1993
A:Title: A human somatostatin receptor (SSTR3), located on chromosome 22, displays prefe
A:Reference number: S32501; MUID:93238970
A:Accession: S32501
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-418 <COR>
C:Genetics:
A:Gene: GDB:SSTR3
A:Cross-references: GDB:I34187; OMIM:182453
A:Map position: 22q13.1-22q13.1
A:Introns: #status absent
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot
F:44-70/Domain: transmembrane #status predicted <TM1>
F:81-106/Domain: transmembrane #status predicted <TM2>
F:118-139/Domain: transmembrane #status predicted <TM3>
F:159-181/Domain: transmembrane #status predicted <TM4>
F:203-233/Domain: transmembrane #status predicted <TM5>
F:255-282/Domain: transmembrane #status predicted <TM6>
F:289-316/Domain: transmembrane #status predicted <TM7>
F:17-30/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:116-191/Disulfide bonds: #status predicted

F:151-251,317,332/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #sta
F:251/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status pre
F:256/Binding site: phosphate (Thr) (covalent) (by CAMP-dependent kinase) #status pre
F:412/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicte

Query Match 55.8%; Score 48; DB 2; Length 418;
Best Local Similarity 52.9%; Pred. No. 0.51;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYAIVQATKSFRLRS 17
|||:|:| | | | |
Db 140 DRYLAVVHPTR SARWRT 156

RESULT 8
A44021
somatostatin receptor SSTR3 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 11-Jan-2000
C:Accession: A44021
R:Yasuda, K.; Rens-Domiano, S.; Breder, C.D.; Law, S.F.; Saper, C.B.; Reisine, T.; Be
J. Biol. Chem. 267, 20422-20428, 1992
A:Title: Cloning of a novel somatostatin receptor, SSTR3, coupled to adenylylcyclase.
A:Reference number: A44021; MUID:93015924
A:Accession: A44021
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-428 <YAS>
A:Cross-references: GB:M91000; NID:g201065; PIDN:AAA40144.1; PID:g201066
A:Note: sequence extracted from NCBI backbone (NCBIPI:115746)
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 55.8%; Score 48; DB 2; Length 428;
Best Local Similarity 52.9%; Pred. No. 0.52;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYAIVQATKSFRLRS 17
|||:|:| | | | |
Db 141 DRYLAVVHPTR SARWRT 157

RESULT 9
S30508
probable G protein-coupled receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 11-Jan-2000
C:Accession: S30508
R:Meyerhof, W.; Wulfsen, I.; Schoenrock, C.; Fehr, S.; Richter, D.
Proc. Natl. Acad. Sci. U.S.A. 89, 10267-10271, 1992
A:Title: Molecular cloning of a somatostatin-28 receptor and comparison of its expres
A:Reference number: S30508; MUID:93066220
A:Accession: S30508
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-428 <MEY>
A:Cross-references: EMBL:X63574; NID:g56315; PIDN:CAA45130.1; PID:g56316
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 55.8%; Score 48; DB 2; Length 428;
Best Local Similarity 52.9%; Pred. No. 0.52;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYAIVQATKSFRLRS 17
|||:|:| | | | |
Db 141 DRYLAVVHPTR SARWRT 157

RESULT 10

A57160

Chemokine (C-C) receptor 4 - human
 N:Alternate names: C-C CR-4
 C:Species: Homo sapiens (man)
 C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
 C:Accession: A57160
 R:Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.; W
 J. Biol. Chem. 270, 19495-19500, 1995
 A:Title: Molecular cloning and functional expression of a novel CC chemokine receptor cd
 A:Reference number: A57160; MUID:95370289
 A:Accession: A57160
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-360 <POM>
 A:Cross-references: GB:X85740; NID:g1370103; PIDN:CAA59743.1; PID:g971452
 A:Note: source clone K5-5
 C:Genetics:
 A:Gene: GDB:CMKBR4
 A:Cross-references: GDB:677463
 A:Map position: 3p21-3p21
 C:Superfamily: G protein-coupled rhodopsin
 F:40-65/Domain: transmembrane #status predicted <TM1>
 F:76-97/Domain: transmembrane #status predicted <TM2>
 F:112-133/Domain: transmembrane #status predicted <TM3>
 F:151-175/Domain: transmembrane #status predicted <TM4>
 F:208-226/Domain: transmembrane #status predicted <TM5>
 F:243-264/Domain: transmembrane #status predicted <TM6>
 F:291-308/Domain: transmembrane #status predicted <TM7>
 F:23-276,110-187/Disulfide bonds: #status predicted
 F:72,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
 F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
 F:183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 54.7%; Score 47; DB 2; Length 360;
 Best Local Similarity 58.8%; Pred. No. 0.67;
 Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLRS 17
 |||:|||||:|:|:
 Db 134 DRYLAIVHAVFSRLART 150

RESULT 11

S42628
 G protein-coupled receptor Gpcr6 - mouse
 N:Alternate names: Interleukin-8 receptor homolog; muBLR1 protein
 C:Species: Mus musculus (house mouse)
 C:Date: 07-Sep-1994 #sequence_revision 26-May-1995 #text_change 21-Jul-2000
 C:Accession: S42628; C48909
 R:Kaiser, E.; Foerster, R.; Wolf, I.; Ebensperger, C.; Kuehl, W.M.; Lipp, M.
 Eur. J. Immunol. 23, 2532-2539, 1993
 A:Title: The G protein-coupled receptor BLR1 is involved in murine B cell differentiation
 A:Reference number: S42628; MUID:94009211
 A:Accession: S42628
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-374 <KAI>
 A:Cross-references: EMBL:X71788; NID:g2598563; PIDN:CAA50673.1; PID:g433947
 R:Wilkie, T.M.; Chen, Y.; Gilbert, D.J.; Moore, K.J.; Yu, L.; Simon, M.I.; Copeland, N.G
 Genomics 18, 175-184, 1993
 A:Title: Identification, chromosomal location, and genome organization of mammalian G-pr
 A:Reference number: A48909; MUID:94116980
 A:Accession: C48909
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 151-269 <WIL>
 A:Cross-references: GB:L20332; NID:g438798; PIDN:AAA16852.1; PID:g438799
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 54.7%; Score 47; DB 2; Length 374;
 Best Local Similarity 56.2%; Pred. No. 0.7;
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLR 16
 |||:|||||:|:|:
 Db 148 DRYLAIVHAVYARRR 163

RESULT 12

S32785
 G protein-coupled receptor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 24-Nov-1999
 C:Accession: S32785
 R:Kouba, M.; Vanetti, M.; Wang, X.; Schaefer, M.; Hoeltt, V.
 FEBS Lett. 321, 173-178, 1993
 A:Title: Cloning of a novel putative G-protein-coupled receptor (NLR) which is expres
 A:Reference number: S32785; MUID:93238948
 A:Accession: S32785
 A:Molecule type: mRNA
 A:Residues: 1-374 <KOU>
 A:Cross-references: GB:X71463; GB:S59748; NID:g599926; PIDN:CAA50582.1; PID:g599927
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 54.7%; Score 47; DB 2; Length 374;
 Best Local Similarity 56.2%; Pred. No. 0.7;
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLR 16
 |||:|||||:|:|:
 Db 148 DRYLAIVHAVYARRR 163

RESULT 13

I38435
 angiotensin receptor homolog APJ - human
 C:Species: Homo sapiens (man)
 C:Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 21-Jul-2000
 C:Accession: I38435
 R:O'Dowd, B.F.; Heiber, M.; Chan, A.; Heng, H.H.; Tsui, L.; Kennedy, J.L.; Shi, X.; P
 Gene 136, 355-360, 1993
 A:Title: A human gene that shows identity with the gene encoding the angiotensin rece
 A:Reference number: I38435; MUID:94124031
 A:Accession: I38435
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-380 <RES>
 A:Cross-references: EMBL:U03642; NID:g425351; PIDN:AAA18954.1; PID:g425352
 C:Genetics:
 A:Gene: APJ
 A:Map position: 11q12
 A:Introns: #status absent
 C:Superfamily: vertebrate rhodopsin

Query Match 54.7%; Score 47; DB 2; Length 380;
 Best Local Similarity 55.6%; Pred. No. 0.71;
 Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLSR 18
 |||:|||||:|:|:
 Db 126 DRYLAIVRPVANARLRL 143

RESULT 14

S56162
 MDCR15 protein - human
 C:Species: Homo sapiens (man)
 C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 08-Oct-1999

C;Accession: S56162
R;Barella, L.; Loetscher, M.; Tobler, A.; Baggiolini, M.; Moser, B.
Biochem. J. 309, 773-779, 1995
A;Title: Sequence variation of a novel heptahelical leucocyte receptor through alternati
A;Reference number: S56162; MUID:95366951
A;Accession: S56162
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-327 <BAR>
A;Cross-references: EMBL:X68829; NID:g840783; PIDN:CAA48723.1; PID:g840784
C;Superfamily: vertebrate rhodopsin

Query Match 53.5%; Score 46; DB 2; Length 327;
Best Local Similarity 56.2%; Pred. No. 0.93;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLR 16
| | | | | | | | | | | | | | | | | | | | | |
Db 101 DRYLAIVHAVYRHR 116

RESULT 15

S28787
neuropeptide Y/peptide YY receptor Y3 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 26-Aug-1999
C;Accession: S28787
R;Rimland, J.; Xin, W.; Sweetnam, P.; Saijoh, K.; Nestler, E.J.; Duman, R.S.
Mol. Pharmacol. 40, 869-875, 1991
A;Title: Sequence and expression of a neuropeptide Y receptor cDNA.
A;Reference number: S28787; MUID:92100053
A;Accession: S28787
A;Molecule type: mRNA
A;Residues: 1-353 <RIM>
A;Cross-references: EMBL:M86739
C;Superfamily: vertebrate rhodopsin
C;Keywords: appetite; G protein-coupled receptor; transmembrane protein

Query Match 53.5%; Score 46; DB 2; Length 353;
Best Local Similarity 62.5%; Pred. No. 1;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLR 16
| | | | | | | | | | | | | | | | | | | | | |
Db 134 DRYLAIVHAVYRHR 149

Search completed: May 23, 2001, 15:32:00
Job time: 507 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:36:18 ; Search time 62.39 Seconds
(without alignments)
9.883 Million cell updates/sec

Title: US-08-887-977-10_COPY_133_150

Perfect score: 86
Sequence: 1 DRYIAIVQATKSFRLSR 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86	100.0	374	1	CCR6_HUMAN
2	83	96.5	367	1	CCR6_MOUSE
3	55	64.0	378	1	CCR7_HUMAN
4	53	61.6	378	1	CCR7_MOUSE
5	49	57.0	192	1	CCR4_SHEEP
6	49	57.0	352	1	CCR4_HUMAN
7	49	57.0	352	1	CCR4_MACFA
8	49	57.0	353	1	CCR4_PAPAN
9	49	57.0	353	1	CCR4_FELCA
10	49	57.0	359	1	CCR4_MOUSE
11	48	55.8	369	1	CCR9_MOUSE
12	48	55.8	418	1	SSR3_HUMAN
13	48	55.8	428	1	SSR3_MOUSE
14	48	55.8	428	1	SSR3_RAT
15	47	54.7	339	1	GRPH_HUMAN
16	47	54.7	360	1	CCR4_HUMAN
17	47	54.7	374	1	CCR5_MOUSE
18	47	54.7	374	1	CCR5_RAT
19	47	54.7	377	1	APJ_MOUSE
20	47	54.7	380	1	APJ_HUMAN
21	47	54.7	380	1	APJ_MACMU
22	47	54.7	381	1	V03L_CAPVK
23	46	53.5	342	1	B0NZ_CERAE
24	46	53.5	342	1	B0NZ_HUMAN
25	46	53.5	342	1	B0NZ_MACNE
26	46	53.5	343	1	B0NZ_MACMU
27	46	53.5	352	1	CCR4_CERTO
28	46	53.5	352	1	CCR4_MACMU
29	46	53.5	353	1	CCR4_BOVIN
30	46	53.5	372	1	CCR5_HUMAN
31	45	52.3	346	1	GALR_RAT
32	45	52.3	348	1	GALR_MOUSE
33	45	52.3	349	1	CCR4_RAT

RESULT 1

ID	CCR6_HUMAN	STANDARD;	PRT;	374 AA.
AC	P51684; Q92846; P78553;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CCR-6) (CC-CCR-6) (CCR-6) (IARC RECEPTOR) (GPR-CY4) (GPCY4) (CHEMOKINE RECEPTOR-LIKE 3) (CCR-L3) (DRY6).			
DE	CCR6 OR CMKBR6 OR STRL22 OR GPR29 OR CCR3.			
GN	Homo sapiens (Human).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OC	NCBI_TaxID=9606;			
OX	[1]			
RN	SEQUENCE FROM N.A., AND FUNCTION.			
RP	MEDLINE-97313465; PubMed-9169459;			
RX	Baba M., Imai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K., Nomiya H., Yoshie O.;			
RA	"Identification of CCR6, the specific receptor for a novel lymphocyte-directed CC chemokine LARC.";			
RT	J. Biol. Chem. 272:14893-14898(1997).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RP	Lautens L.L., Modi W., Bonner T.I.;			
RL	Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-97040707; PubMed-8886020;			
RA	Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G.;			
RT	"Molecular cloning and RNA expression of two new human chemokine receptor-like genes.";			
RL	Biochem. Biophys. Res. Commun. 227:846-853(1996).			
RL	[4]			
RN	SEQUENCE FROM N.A.			
RP	McCoy R., Perlmutter D.H.;			
RL	Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-97224503; PubMed-9070937;			
RA	Liao F., Lee H.-H., Farber J.M.;			
RT	"Cloning of STRL22, a new human gene encoding a G-protein-coupled receptor related to chemokine receptors and located on chromosome 6q27.";			
RL	Genomics 40:175-180(1997).			
CC	-!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.			
CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	-!- TISSUE SPECIFICITY: SPLEEN, LYMPH NODES, APPENDIX, AND FETAL LIVER. EXPRESSED IN LYMPHOCYTES, T CELLS AND B CELLS BUT NOT IN NATURAL KILLER CELLS, MONOCYTES, OR GRANULOCYTES.			
CC	-!- INDUCTION: INTERLEUKIN-2.			
CC	-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-6 IS THE INITIATOR.			

P47211 homo sapien
P32246 homo sapien
P56482 macaca mula
P51675 mus musculus
P56492 cercopithec
P51677 homo sapien
P56483 macaca mula
Q92213 cavia porce
P51678 mus musculus
O54814 rattus norv
O88410 mus musculus
P70612 rattus norv

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 CC -----

DR EMBL; U45984; AAB62714.1; -;
 DR EMBL; 279784; CAB02144.1; ALT_INIT.
 DR EMBL; U60000; AAB06949.1; -;
 DR EMBL; U68030; AAC51124.1; -;
 DR EMBL; U68032; AAC51125.1; -;
 DR HSSP; P34996; 1DDD.
 DR GCRDB; GCR_1037; -;
 DR GCRDB; GCR_1075; -;
 DR GCRDB; GCR_1906; -;
 DR GCRDB; GCR_1919; -;
 DR GCRDB; GCR_1941; -;
 DR GCRDB; GCR_2110; -;
 DR MIM; 601835; -;
 DR InterPro; IPR000276; -;
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECF1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECF2_1;
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 47
 FT TRANSMEM 48 74
 FT DOMAIN 75 83
 FT TRANSMEM 84 104
 FT DOMAIN 105 119
 FT TRANSMEM 120 141
 FT DOMAIN 142 159
 FT TRANSMEM 160 180
 FT DOMAIN 181 211
 FT TRANSMEM 212 238
 FT DOMAIN 239 259
 FT TRANSMEM 255 279
 FT DOMAIN 280 303
 FT TRANSMEM 304 321
 FT DOMAIN 322 374
 FT DISULFID 118 197
 FT CARBOHYD 7 7
 FT CONFLICT 60 60
 FT CONFLICT 74 74
 FT CONFLICT 86 86
 FT CONFLICT 164 164
 FT CONFLICT 182 182
 FT CONFLICT 192 192
 FT CONFLICT 206 206
 FT CONFLICT 225 225
 FT CONFLICT 370 374
 SQ SEQUENCE 374 AA; 42494 MW; D7F963534E990BC4 CRC64;
 SFFTM -> VVLHYVIES (IN REF. 4).
 Query Match 100.0%; Score 86; DB 1; Length 374;
 Best Local Similarity 100.0%; Pred. No. 2.9e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLRSR 18
 |||||
 DB 142 DRYIAIVQATKSFRLRSR 159

RESULT 2
 ID CKR6_MOUSE STANDARD; PRT; 367 AA.
 AC O54689;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CCR-6) (KY411).
 GN CCR6 OR CKR6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RA Yanagihara S., Komura E., Yamaguchi Y.;
 RT "Mouse G protein-coupled receptor KY411.";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=99077268; PubMed=9862452;
 RA Varona R., Zaballós A., Gutierrez J., Martin P., Roncal F.,
 RA Albar J.P., Ardavin C., Marquez G.;
 RT "Molecular cloning, functional characterization and mRNA expression
 RT analysis of the murine chemokine receptor CCR6 and its specific ligand
 RT MIP-3alpha.";
 RL FEBS Lett. 440:188-194(1998).
 CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-
 CC ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE
 CC INTRACELLULAR CALCIUM IONS LEVEL.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 DR EMBL; AB009369; BAA23776.1; -;
 DR EMBL; AJ22714; CAA10956.1; -;
 DR MGD; MGI:133397; Cmkbr6.
 DR InterPro; IPR000276; -;
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECF1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECF2_1;
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 39
 FT TRANSMEM 40 66
 FT DOMAIN 67 75
 FT TRANSMEM 76 96
 FT DOMAIN 97 111
 FT TRANSMEM 112 133
 FT DOMAIN 134 151
 FT TRANSMEM 152 172
 FT DOMAIN 173 203
 FT TRANSMEM 204 230
 FT DOMAIN 231 246
 FT TRANSMEM 247 271
 FT DOMAIN 272 295
 FT TRANSMEM 296 313
 FT DOMAIN 314 367
 FT DISULFID 110 189
 FT CARBOHYD 2 2
 FT CARBOHYD 35 35
 SQ SEQUENCE 367 AA; 42102 MW; 6A309AF83B1117E CRC64;
 Query Match 96.5%; Score 83; DB 1; Length 367;
 Best Local Similarity 94.4%; Pred. No. 9.9e-08;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLRSR 18
 |||||
 DB 134 DRYIAIVQATKSFRLRSR 151

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RESULT 3
CKR7_HUMAN
ID CKR7_HUMAN STANDARD; PRT; 378 AA.
AC P32248;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 7 PRECURSOR (C-C CKR-7) (CCR-7)
DE (MIP-3 BETA RECEPTOR) (EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 1)
DE (EBI1) (BLR2).
GN CC7 OR CMKBR7 OR EBI1 OR EVI1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1
SEQUENCE FROM N.A.
RX MEDLINE=93188173; PubMed=8383338;
RA Birkenbach M.P., Josefsen K., Yalamanchili R.R., Lenoir G.M.,
RA Elliott K.;
RT "Epstein-Barr virus-induced genes: first lymphocyte-specific G
RL protein-coupled peptide receptors.";
RL J. Virol. 67:2209-2220(1993).
RN [2]
SEQUENCE FROM N.A.
RX TISSUE=Placenta;
RL MEDLINE=95154835; PubMed=7851893;
RA Schweickart V.L., Raport C.J., Godiska R., Byers M.G., Eddy R.L. Jr.,
RA Shows T.B., Gray P.W.;
RT "Cloning of human and mouse EBI1, a lymphoid-specific
RL G-protein-coupled receptor encoded on human chromosome 17q12-q21.2.";
RL Genomics 23:643-650(1994).
CC -1- FUNCTION: RECEPTOR FOR THE MIP-3-BETA CHEMOKINE. PROBABLE MEDIATOR
CC OF EBV EFFECTS ON B LYMPHOCYTES OR OF NORMAL LYMPHOCYTE FUNCTIONS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN VARIOUS LYMPHOID TISSUES AND
CC ACTIVATED B AND T LYMPHOCYTES, STRONGLY UPREGULATED IN B CELLS
CC INFECTED WITH EPSTEIN-BARR VIRUS AND T CELLS INFECTED WITH
CC HERPESVIRUS 6 OR 7.
CC -1- INDUCTION: BY EBV.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC -----
CC EMBL; L08176; AAA58615.1; -
CC EMBL; L31584; AAA74230.1; -
CC EMBL; L31582; AAA74230.1; JOINED.
CC EMBL; L31583; AAA74230.1; JOINED.
CC EMBL; L31581; AAA74231.1; -
CC PIR; A45680; A45680.
CC HSP; P34996; 1DD0.
CC GCRDb; GCR_0492; -
CC GCRDb; GCR_0958; -
CC MIN; 600242; -
CC InterPro; IPR000276; -
CC InterPro; IPR001718; -
CC Pfam; PF00001; 7tm1.1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PRINTS; PR00641; CHEMOKINER7.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 378 C-C CHEMOKINE RECEPTOR TYPE 7.
FT DOMAIN 25 59 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 60 86 1 (POTENTIAL).

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FT DOMAIN 87 95 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 96 116 2 (POTENTIAL).
FT DOMAIN 117 130 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 131 152 3 (POTENTIAL).
FT DOMAIN 153 170 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 171 191 4 (POTENTIAL).
FT DOMAIN 192 219 5 (POTENTIAL).
FT TRANSMEM 220 247 6 (POTENTIAL).
FT DOMAIN 248 263 7 (POTENTIAL).
FT TRANSMEM 264 289 8 (POTENTIAL).
FT DOMAIN 290 313 9 (POTENTIAL).
FT TRANSMEM 314 331 10 (POTENTIAL).
FT DOMAIN 332 378 11 (POTENTIAL).
FT CARBOHYD 36 36 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 129 210 BY SIMILARITY.
FT CONFLICT 182 183 IW -> SA (IN REF. 1).
FT CONFLICT 337 337 L -> I (IN REF. 1).
SQ SEQUENCE 378 AA; 42874 MW; D4CB4213841AIBD4 CRC64;

Query Match 64.0%; Score 55; DB 1; Length 378;
Best Local Similarity 61.1%; Pred. No. 0.014;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLSR 18
   |||:||||| : ||:|
Db 153 DRYVAIVQAVSAHRHAR 170

RESULT 4
CKR7_MOUSE
ID CKR7_MOUSE STANDARD; PRT; 378 AA.
AC P47774;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 7 PRECURSOR (C-C CKR-7) (CCR-7)
DE (MIP-3 BETA RECEPTOR) (EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 1)
DE (EBI1).
GN CC7 OR CMKBR7 OR EBI1 OR EBIH.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RX STRAIN=B6/CBA; TISSUE=Thymus;
RL MEDLINE=95194835; PubMed=7851893;
RA Schweickart V.L., Raport C.J., Godiska R., Byers M.G., Eddy R.L. Jr.,
RA Shows T.B., Gray P.W.;
RT "Cloning of human and mouse EBI1, a lymphoid-specific
RL G-protein-coupled receptor encoded on human chromosome 17q12-q21.2.";
RL Genomics 23:643-650(1994).
CC -1- FUNCTION: RECEPTOR FOR THE MIP-3-BETA CHEMOKINE. PROBABLE MEDIATOR
CC OF EBV EFFECTS ON B LYMPHOCYTES OR OF NORMAL LYMPHOCYTE FUNCTIONS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC -----
CC EMBL; L31580; AAA74232.1; -
CC MGD; MGI:103011; Cmkbr7.
CC InterPro; IPR000276; -
CC InterPro; IPR001718; -
CC Pfam; PF00001; 7tm1.1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PRINTS; PR00641; CHEMOKINER7.

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DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEPTOR_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 378 C-C CHEMOKINE RECEPTOR TYPE 7.
FT DOMAIN 25 59 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 60 86 1 (POTENTIAL).
FT DOMAIN 87 95 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 96 116 2 (POTENTIAL).
FT DOMAIN 117 130 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 131 152 3 (POTENTIAL).
FT DOMAIN 153 170 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 171 191 4 (POTENTIAL).
FT DOMAIN 192 219 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 220 247 5 (POTENTIAL).
FT DOMAIN 248 263 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 264 289 6 (POTENTIAL).
FT DOMAIN 290 313 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 314 331 7 (POTENTIAL).
FT DOMAIN 332 378 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 129 210 BY SIMILARITY.
SQ SEQUENCE 378 AA; 42941 MW; ACBIA422CF54AA54 CRC64;

Query Match 61.6%; Score 53; DB 1; Length 378;
Best Local Similarity 61.1%; Pred. No. 0.032;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DRYAIVQATKSFRLSR 18
|||:||||| |:
DB 153 DRYAIVQAVSRHRRAR 170

RESULT 5
CCR4_SHEEP STANDARD; PRT; 192 AA.
ID CCR4_SHEEP
AC Q28553;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (SDF-1 RECEPTOR)
DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LEUKOCYTE-DERIVED
DE SEVEN TRANSMEMBRANE DOMAIN RECEPTOR) (LESTR) (FRAGMENT).
GN CXCR4 OR LESTR.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hypothalamus;
RA Dyer C.J., Matteri R.L., Keisler D.H.;
RT "Development of an ovine Y3 cDNA and expression of the Y3 receptor
RT mRNA in the ovine hypothalamus and pituitary.";
RL Abstr. Soc. Neurosci. 21:1890-1890(1995).
CC -!- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -!- CAUTION: WAS ORIGINALLY THOUGHT TO BE A RECEPTOR FOR NEUROPEPTIDE
CC Y, TYPE 3 (NPY3-R).

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CC EMBL; U38942; AAA81347.1; -.

DR GCRDB; GCR1581; -.
DR InterPro; IPR000276; -.
DR Pfam; PF00001; 7tm.1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEPTOR_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT NON_TER 1 1
FT DOMAIN <1 29 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 30 53 1 (POTENTIAL).
FT DOMAIN 54 69 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 70 89 2 (POTENTIAL).
FT DOMAIN 90 100 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 101 122 3 (POTENTIAL).
FT DOMAIN 123 144 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 145 165 4 (POTENTIAL).
FT DOMAIN 166 190 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 191 >192 5 (POTENTIAL).
FT DISULFID 99 176 BY SIMILARITY.
FT NON_TER 192 192
SQ SEQUENCE 192 AA; 22178 MW; A8BCFE303C52BD98 CRC64;

Query Match 57.0%; Score 49; DB 1; Length 192;
Best Local Similarity 68.8%; Pred. No. 0.081;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYAIVQATKSFRLR 16
|||:||||| |:
DB 123 DRYAIVQATNSQRP 138

RESULT 6
CCR4_HUMAN STANDARD; PRT; 352 AA.
ID CCR4_HUMAN
AC P30991; P56438;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (SDF-1 RECEPTOR)
DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LEUKOCYTE-DERIVED
DE SEVEN TRANSMEMBRANE DOMAIN RECEPTOR) (LESTR) (FB22) (NPYRL)
DE (HM89).
GN CXCR4.
OS Homo sapiens (Human), and Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606, 9598;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Human; TISSUE=Lung;
RX MEDLINE=93319629; PubMed=8329116;
RA Herzog H., Hort Y.J., Shine J., Selbie L.A.;
RT "Molecular cloning, characterization, and localization of the human
RT homolog to the reported bovine NPY Y3 receptor: lack of NPY binding
RT and activation.";
RL DNA Cell Biol. 12:465-471(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=Human; TISSUE=Brain;
RX MEDLINE=94052833; PubMed=8234909;
RA Jazin E.E., Yoo H., Blomqvist G., Yee F., Weng G., Walker M.W.,
RA Salton J., Larhammar D., Wahlestedt C.R.;
RT "A proposed bovine neurotrophin Y (NPY) receptor cDNA clone, or its
RT human homologue, confers neither NPY binding sites nor NPY
RT responsiveness on transfected cells.";
RL Regul. Pept. 47:247-258(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=Human; TISSUE=Spleen;
RX MEDLINE=93315164; PubMed=8325644;
RA Federspiel B., Delaney A.D., Clark-Lewis I., Jirik F., Duncan A.M.,
RA Schappert K.T., Melhado I.;
RT "Molecular cloning of the cDNA and chromosomal localization of the

RT gene for a putative seven-transmembrane segment (7-TMS) receptor
RL isolated from human spleen.";
RN Genomics 16:707-712(1993).
[4]
RP SEQUENCE FROM N.A.
RC SPECIES=Human; TISSUE=Leukocyte;
RX MEDLINE=94103215; PubMed=8276799;
RA Loetscher M., Geiser T., O'Reilly T., Zwahlen R., Baggiolini M.,
RA Moser B.;
RT "Cloning of a human seven-transmembrane domain receptor, LESTR, that
RT is highly expressed in leukocytes.";
RL J. Biol. Chem. 269:232-237(1994).
[5]
RN SEQUENCE FROM N.A.
RP SPECIES=Human; TISSUE=Monocytes;
RX MEDLINE=94052629; PubMed=7505609;
RA Nomura H., Nielsen B.W., Matsushima K.;
RT "Molecular cloning of cDNAs encoding a LD78 receptor and putative
RT leukocyte chemotactic peptide receptors.";
RL Int. Immunol. 5:1239-1249(1993).
[6]
RN SEQUENCE FROM N.A.
RP SPECIES=Human;
RC SPECIES=Human;
RA Wegner S.A., Ehrenberg P.K., Chang G., Dayhoff D.E., Michael N.L.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
[7]
RN SEQUENCE FROM N.A.
RP SPECIES=Human;
RX MEDLINE=98238970; PubMed=9599023;
RA Caruz A., Sansom M., Alonso J.M., Alcaml J., Baleux F.,
RA Virelizier J.L., Parmentier M., Arenzana-Seisdedos F.;
RT "Genomic organization and promoter characterization of human CXCR4
RT gene.";
RL FEBS Lett. 426:271-278(1998).
[8]
RN SEQUENCE FROM N.A.
RP SPECIES=Human;
RC SPECIES=Human;
RA Xiao L., Weiss S., Qari S., Rudolph D., Hodge T., Lal R.;
RT "Partial resistance to infection by syncytium-inducing primary HIV-1
RT in exposed uninfected individuals homozygous for CCR5 32bp
RT deletion.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
[9]
RN SEQUENCE FROM N.A.
RP SPECIES=Human; TISSUE=Blood;
RA Frodl R., Moepfs B., Gierschik P.;
RT "Genomic organization and expression pattern of the human chemokine
RT receptor CXCR4.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
[10]
RN SEQUENCE FROM N.A.
RP SPECIES=Human; TISSUE=Blood;
RX MEDLINE=98090115; PubMed=9430250;
RA Pretet J.-L., Zerbib A., Girard M., Guillet J.-G., Butor C.;
RT "Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1.";
RL AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
[11]
RN FUNCTION.
RP MEDLINE=96351077; PubMed=8752280;
RA Bleul C.C., Farzan M., Choe H., Parolin C., Clark-Lewis I.,
RA Sodroski J., Springer T.A.;
RT "The lymphocyte chemoattractant SDF-1 is a ligand for LESTR/fusin and
RT blocks HIV-1 entry.";
RL Nature 382:829-833(1996).
[12]
RN FUNCTION.
RP MEDLINE=96351078; PubMed=8752281;
RA Oberlin E., Amara A., Bachelierie F., Bessia C., Virelizier J.-L.,
RA Arenzana-Seisdedos F., Schwartz O., Heard J.-M., Clark-Lewis I.,
RA Legler D.F., Loetscher M., Baggiolini M., Moser B.;
RT "The CXCR chemokine SDF-1 is the ligand for LESTR/fusin and prevents
RT infection by T-cell-line-adapted HIV-1.";
RL Nature 382:833-835(1996).

[13]
RN ERRATUM.
RA Oberlin E., Amara A., Bachelierie F., Bessia C., Virelizier J.-L.,
RA Arenzana-Seisdedos F., Schwartz O., Heard J.-M., Clark-Lewis I.,
RA Legler D.F., Loetscher M., Baggiolini M., Moser B.;
RL Nature 384:288-289(1996).
[14]
RN CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
RX MEDLINE=96217947; PubMed=8629022;
RA Feng Y., Broder C.C., Kennedy P.E., Berger E.A.;
RT "HIV-1 entry cofactor: functional cDNA cloning of a
RT seven-transmembrane, G protein-coupled receptor.";
RL Science 272:872-877(1996).
CC -!- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. ACTS AS
CC A CO-RECEPTOR WITH CD4 FOR SYNCYTIIUM-INDUCING STRAINS (SI) (T-
CC CELL-LINE-ADAPTED) OF HIV-1 VIRUS. IT PROMOTES ENV-MEDIATED FUSION
CC OF THE VIRUS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -!- CAUTION: WAS ORIGINALLY THOUGHT TO BE A RECEPTOR FOR NEUROPEPTIDE
CC Y, TYPE 3 (NPY3-R).

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CC or send an email to license@isb-sib.ch).

DR EMBL: L01639; AAA16594.1; -
DR EMBL: M9293; AAA16617.1; -
DR EMBL: X71635; CAA50641.1; -
DR EMBL: L06797; AAA03209.1; -
DR EMBL: D10924; BAA01722.1; -
DR EMBL: AF05058; AAB93982.1; -
DR EMBL: AF052572; AAC34581.1; -
DR EMBL: AF025375; AAB81970.1; -
DR EMBL: Y14739; CAA75034.1; -
DR EMBL: U89798; AAC03718.1; -
DR PIR: S32761; S32761.
DR PIR: A45747; A45747.
DR GCRDB: GCR_0438; -
DR GCRDB: GCR_0448; -
DR GCRDB: GCR_0475; -
DR GCRDB: GCR_0529; -
DR GCRDB: GCR_0903; -
DR GCRDB: GCR_2433; -
DR GCRDB: GCR_2568; -
DR MIM: 162643; -
DR InterPro: IPR000276; -
DR InterPro: IPR001277; -
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GCRRHODOPHN.
DR PRINTS: PR00645; GCR1ORPHAN.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS00262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 40 63 1 (POTENTIAL).
FT DOMAIN 64 79 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 80 99 2 (POTENTIAL).
FT DOMAIN 100 110 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 111 132 3 (POTENTIAL).
FT DOMAIN 133 154 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 155 175 4 (POTENTIAL).
FT DOMAIN 176 200 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 201 220 5 (POTENTIAL).
FT DOMAIN 221 240 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 241 261 6 (POTENTIAL).
FT DOMAIN 262 285 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 286 305 7 (POTENTIAL).

FT DOMAIN 306 352 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 109 186 BY SIMILARITY.
 SQ SEQUENCE 352 AA; 39745 MW; 8C8476A186786B83 CRC64;

Query Match 57.0%; Score 49; DB 1; Length 352;
 Best Local Similarity 68.8%; Pred. No. 0.16;
 Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLR 16
 |||:|||||
 DB 133 DRYLAIVHATNSORPR 148

RESULT 7
 CCR4_MACFA
 ID CCR4_MACFA STANDARD; PRT; 352 AA.
 AC Q28474;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (SDF-1 RECEPTOR)
 DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LESTR).
 GN CXCR4.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tatsumi M., Takahashi H.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
 CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC
 CC EMBL; D86579; BAAL1326.1;
 CC GCRDB; GCR_1143;
 DR InterPro; IPR000276;
 DR InterPro; IPR001277;
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00645; LCR1ORPHAN.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_2; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECEPTOR_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 39
 FT TRANSMEM 40 63
 FT DOMAIN 64 79
 FT TRANSMEM 80 99
 FT DOMAIN 100 110
 FT TRANSMEM 111 132
 FT DOMAIN 133 154
 FT TRANSMEM 155 175
 FT DOMAIN 176 200
 FT TRANSMEM 201 220
 FT DOMAIN 221 240
 FT TRANSMEM 241 261
 FT DOMAIN 262 285
 FT TRANSMEM 286 305
 FT DOMAIN 306 352
 FT CARBOHYD 11 11
 FT DISULFID 109 186
 FT SEQUENCE 352 AA; 39751 MW; 468E542E1851265A CRC64;

FT DISULFID 109 186 BY SIMILARITY.
 SQ SEQUENCE 352 AA; 39753 MW; 432DA6C11859EF8A CRC64;

Query Match 57.0%; Score 49; DB 1; Length 352;
 Best Local Similarity 68.8%; Pred. No. 0.16;
 Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLR 16
 |||:|||||
 DB 133 DRYLAIVHATNSORPR 148

RESULT 8
 CCR4_PAPAN
 ID CCR4_PAPAN STANDARD; PRT; 352 AA.
 AC P56491;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (SDF-1 RECEPTOR)
 DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN).
 GN CXCR4.
 OS Papio anubis (Olive baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Papio.
 OX NCBI_TaxID=9555;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Benton P.A., Timanus D.K., Shearer M.H., Lee D.R., Kennedy R.C.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
 CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC
 CC EMBL; AF031089; AAC63831.1;
 CC GCRDB; GCR_2512;
 DR InterPro; IPR000276;
 DR InterPro; IPR001277;
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00645; LCR1ORPHAN.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_2; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECEPTOR_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 39
 FT TRANSMEM 40 63
 FT DOMAIN 64 79
 FT TRANSMEM 80 99
 FT DOMAIN 100 110
 FT TRANSMEM 111 132
 FT DOMAIN 133 154
 FT TRANSMEM 155 175
 FT DOMAIN 176 200
 FT TRANSMEM 201 220
 FT DOMAIN 221 240
 FT TRANSMEM 241 261
 FT DOMAIN 262 285
 FT TRANSMEM 286 305
 FT DOMAIN 306 352
 FT CARBOHYD 11 11
 FT DISULFID 109 186
 FT SEQUENCE 352 AA; 39751 MW; 468E542E1851265A CRC64;

Query Match 57.0%; Score 49; DB 1; Length 352;
 Best Local Similarity 68.8%; Pred. No. 0.16;
 Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYTAIVOATKSFRLR 16
 |||:|||||
 Db 133 DRYLAIVHATNSQRPR 148

RESULT 9

CCR4_FELCA STANDARD; PRT; 353 AA.
 ID CCR4_FELCA STANDARD; PRT; 353 AA.
 AC P56498; P79172; O02700;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (SDF-1 RECEPTOR)
 DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LESTR).
 GN CXCR4.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97404646; PubMed=9261358;
 RA Willett B.J., Picard L., Hosie M.J., Turner J.D., Adema K.,
 RA Clapham P.R.;
 RT "Shared usage of the chemokine receptor CXCR4 by the feline and human
 RT immunodeficiency viruses.";
 RL J. Virol. 71:6407-6415(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Willett B.J.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Lerner D.L., Elder J.H.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
 CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 DR EMBL; U63558; AAC48852.1; -;
 DR EMBL; U92795; AAB51765.1; -;
 DR GCRdb; GCR_1113; -;
 DR GCRdb; GCR_1114; -;
 DR InterPro; IPR000276; -;
 DR InterPro; IPR001277; -;
 DR Pfam; PF00001; 7tm1.1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00845; LCRIORPHAN.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 40 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 41 64 1 (POTENTIAL).
 FT DOMAIN 65 80 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 81 100 2 (POTENTIAL).
 FT DOMAIN 101 111 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 112 133 3 (POTENTIAL).
 FT DOMAIN 134 155 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 156 176 4 (POTENTIAL).
 FT DOMAIN 177 201 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 202 221 5 (POTENTIAL).
 FT DOMAIN 222 241 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 242 262 6 (POTENTIAL).
 FT DOMAIN 263 286 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 287 306 7 (POTENTIAL).
 FT DOMAIN 307 353 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 110 187 BY SIMILARITY.
 FT CONFLICT 67 Q -> H (IN REF. 3).
 FT CONFLICT 263 D -> E (IN REF. 3).
 SQ SEQUENCE 353 AA; 39935 MW; EA2BD46068A6C05B CRC64;

Query Match 57.0%; Score 49; DB 1; Length 353;
 Best Local Similarity 68.8%; Pred. No. 0.16;
 Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYTAIVOATKSFRLR 16
 |||:|||||
 Db 134 DRYLAIVHATNSQRPR 149

RESULT 10

CCR4_MOUSE STANDARD; PRT; 359 AA.
 ID CCR4_MOUSE STANDARD; PRT; 359 AA.
 AC P70658; P70346; O09062; O09059; P70233;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (SDF-1 RECEPTOR)
 DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LEUKOCYTE-DERIVED
 DE SEVEN TRANSMEMBRANE DOMAIN RECEPTOR) (LESTR).
 GN CXCR4 OR LESTR OR CMKAR4 OR SDFIR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6 X CHA; TISSUE=Thymus;
 RA Moepfs B., Prodl R., Kessler H., Gierschik P.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV;
 RA Heesen M., Berman M.A., Gerard C., Dorf M.E.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RA Heesen M., Berman M.A., Benson J.D., Gerard C., Dorf M.E.;
 RL "Cloning of the mouse fusin gene, homologue to a human HIV-1
 RT co-factor";
 RL J. Immunol. 157:5455-5460(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bone marrow;
 RX MEDLINE=97121456; PubMed=8962122;
 RA Nagasawa T., Nakajima T., Tachibana K., Iizasa H., Bleul C.C.,
 RA Yoshie O., Matsushima K., Yoshida N., Springer T.A., Kishimoto T.;
 RT "Molecular cloning and characterization of a murine pre-B-cell
 RT growth-stimulating factor/stromal cell-derived factor 1 receptor, a
 RT murine homolog of the human immunodeficiency virus 1 entry coreceptor
 RT fusin";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:14726-14729(1996).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Thymus;
 RA Suzuki G., Nakata Y., Uzawa A., Shirasawa T., Saito T., Mita K.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.

```

RN  RC  STRAIN=129/SV; TISSUE=Thymus;
RP  RA  Schubel A., Burgstahler R., Lipp M.;
RL  Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC  -!- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
CC  SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC  -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC  -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC
CC  EMBL; X99581; CAA67893.1; -
CC  EMBL; X99582; CAA67894.1; -
CC  EMBL; U59760; AAB07725.1; -
CC  EMBL; U65580; AAC52953.1; -
CC  EMBL; D87747; BAA13451.1; -
CC  EMBL; AB008003; BAA19187.1; -
CC  EMBL; Z80111; CAB02201.1; -
CC  EMBL; Z80112; CAB02202.1; -
CC  GCRDB; GCR_1138; -
CC  GCRDB; GCR_1387; -
CC  GCRDB; GCR_1646; -
CC  GCRDB; GCR_1730; -
CC  GCRDB; GCR_2592; -
CC  MGD; MGI:109563; Cmkar4.
CC  InterPro; IPR000276; -
CC  InterPro; IPR001277; -
CC  Pfam; PF00001; 7tm_1; 1.
CC  PRINTS; PR00237; GPCRHHODPSN.
CC  PRINTS; PR00645; LCRIORPHANR.
CC  PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
CC  PROSITE; PS0262; G_PROTEIN_RECEPTOR_F1_2; 1.
CC  G-protein coupled receptor; Transmembrane; Glycoprotein.
CC  DOMAIN 1 41 EXTRACELLULAR (POTENTIAL).
CC  TRANSMEM 42 65
CC  DOMAIN 66 81 CYTOPLASMIC (POTENTIAL).
CC  TRANSMEM 82 101
CC  DOMAIN 102 112 EXTRACELLULAR (POTENTIAL).
CC  TRANSMEM 113 134
CC  DOMAIN 135 156 CYTOPLASMIC (POTENTIAL).
CC  TRANSMEM 157 177
CC  DOMAIN 178 207 EXTRACELLULAR (POTENTIAL).
CC  TRANSMEM 208 227
CC  DOMAIN 228 247 CYTOPLASMIC (POTENTIAL).
CC  TRANSMEM 248 268
CC  DOMAIN 269 292 EXTRACELLULAR (POTENTIAL).
CC  TRANSMEM 293 312
CC  DOMAIN 313 359 CYTOPLASMIC (POTENTIAL).
CC  DISULFID 111 193 BY SIMILARITY.
CC  CARBOHYD 13 13 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC  CONFLICT 6 7 MISSING (IN REF. 6).
CC  CONFLICT 216 216 I -> V (IN REF. 1 AND 5).
CC  SEQUENCE 359 AA; 40426 MW; 33D1B5552A31595B CRC64;

```

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Query Match 57.0%; Score 49; DB 1; Length 359;
Best Local Similarity 68.8%; Pred. No. 0.16;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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Qy 1 DRYIAIVQATKSFRLR 16
    |||:|||||
Db 135 DRYLAIVHATNSQRP 150

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RESULT 11
CKR9_MOUSE

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ID  CKR9_MOUSE  STANDARD;  PRT;  369 AA.
AC  Q9WUT7;
DT  30-MAY-2000 (Rel. 39, Created)
DT  30-MAY-2000 (Rel. 39, Last sequence update)
DT  01-OCT-2000 (Rel. 40, Last annotation update)
DE  C-C CHEMOKINE RECEPTOR TYPE 9 (C-C CKR-9) (CCR-9)
DE  (CHEMOKINE C-C RECEPTOR 10).
GN  CCR9 OR CMKBR10.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Thymus;
RX  MEDLINE=99248139; Pubmed=10229797;
RA  Zaballio A., Gutierrez J., Varona R., Ardavin C., Marquez G.;
RT  "Cutting edge: Identification of the orphan chemokine receptor GPR-9-6
RL  as CCR9, the receptor for the chemokine TECK.";
RL  J. Immunol. 162:5671-5675(1999).
CC  -!- FUNCTION: RECEPTOR FOR CHEMOKINE SCYA25/TECK. SUBSEQUENTLY
CC  TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS
CC  LEVEL.
CC  -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC  -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE THYMUS AND LOW IN
CC  LYMPH NODES AND SPLEEN.
CC  -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC
CC  EMBL; AJ132336; CAB43480.1; -
CC  MGD; MGI:1341902; Cmkbr10.
CC  InterPro; IPR000174; -
CC  InterPro; IPR000248; -
CC  InterPro; IPR000276; -
CC  InterPro; IPR000355; -
CC  InterPro; IPR000496; -
CC  InterPro; IPR001277; -
CC  InterPro; IPR001718; -
CC  Pfam; PF00001; 7tm_1; 1.
CC  PRINTS; PR00237; GPCRHHODPSN.
CC  PRINTS; PR00241; ANGIOTENSINR.
CC  PRINTS; PR00425; BRADYKININR.
CC  PRINTS; PR00427; INTRLEUKIN8R.
CC  PRINTS; PR00641; CHEMOKINER7.
CC  PRINTS; PR00645; LCRIORPHANR.
CC  PRINTS; PR00657; CCHEMOKINER.
CC  PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
CC  PROSITE; PS0262; G_PROTEIN_RECEPTOR_F1_2; 1.
CC  G-protein coupled receptor; Transmembrane; Glycoprotein.
CC  DOMAIN 1 49 EXTRACELLULAR (POTENTIAL).
CC  TRANSMEM 50 76
CC  DOMAIN 77 85 CYTOPLASMIC (POTENTIAL).
CC  TRANSMEM 86 106
CC  DOMAIN 107 120 EXTRACELLULAR (POTENTIAL).
CC  TRANSMEM 121 142
CC  DOMAIN 143 160
CC  TRANSMEM 161 181
CC  DOMAIN 182 210 EXTRACELLULAR (POTENTIAL).
CC  TRANSMEM 211 238
CC  DOMAIN 239 254 CYTOPLASMIC (POTENTIAL).
CC  TRANSMEM 255 280
CC  DOMAIN 281 304 EXTRACELLULAR (POTENTIAL).
CC  TRANSMEM 305 322
CC  DOMAIN 323 369
CC  CARBOHYD 32 32 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC  DISULFID 119 198 BY SIMILARITY.

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SQ SEQUENCE 369 AA; 41913 MW; 6971F76F0A24B4AE CRC64;
Query Match 55.8%; Score 48; DB 1; Length 369;
Best Local Similarity 83.3%; Pred. No. 0.26;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DRYIAIVOATKS 12
    |||||
Db 143 DRYIAIVOAMKA 154

RESULT 12
SSR3_HUMAN STANDARD; PRT; 418 AA.
AC P32745;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE SOMATOSTATIN RECEPTOR TYPE 3 (SS3R) (SSR-28).
GN SSTR3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93149123; PubMed=1337145;
RA Yamada Y., Reisine T., Law S.F., Ihara Y., Kubota A., Kagimoto S.,
RA Seino M., Seino Y., Bell G.I., Seino S.;
RT "Somatostatin receptors, an expanding gene family: cloning and
RT functional characterization of human SSTR3, a protein coupled to
RT adenylyl cyclase.";
RL Mol. Endocrinol. 6:2136-2142(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93238970; PubMed=8097479;
RA Corness J.D., Demchyshyn L.L., Seeman P., van Tol H.H.M.,
RA Srikant C.B., Kent G., Patel Y.C., Niznik H.B.;
RT "A human somatostatin receptor (SSTR3), located on chromosome 22,
RT displays preferential affinity for somatostatin-14 like peptides.";
RL FEBS Lett. 321:279-284(1993).
RN [3]
RP SEQUENCE FROM N.A.
RA Connor R., Davis J.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECEPTOR FOR SOMATOSTATINS-14 AND -28. THIS RECEPTOR IS
CC COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF
CC ADENYLYL CYCLASE.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: BRAIN, PITUITARY AND PANCREAS.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M96738; AAA60592.1; -
CC EMBL; Z82188; CAB45263.1; -
CC PIR; S32501; S32501.
CC PIR; A46226; A46226.
CC HSP; P34996; 1DD0.
CC GCRdb; GCR_0452; -.
CC GCRdb; GCR_0630; -.
CC MIN; 182453; -.
CC InterPro; IPR000276; -.
CC InterPro; IPR000586; -.
CC InterPro; IPR001856; -.
CC Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PRO0237; GPCRRHODOPSN.
DR PRINTS; PRO0246; SOMATOSTATNR.
DR PRINTS; PRO0589; SOMATOSTTN3R.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family.
KW DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 44 69 1 (POTENTIAL).
FT DOMAIN 70 79 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 80 101 2 (POTENTIAL).
FT DOMAIN 102 116 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 117 138 3 (POTENTIAL).
FT DOMAIN 139 161 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 162 181 4 (POTENTIAL).
FT DOMAIN 182 205 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 206 231 5 (POTENTIAL).
FT DOMAIN 232 257 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 258 279 6 (POTENTIAL).
FT DOMAIN 280 293 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 294 316 7 (POTENTIAL).
FT DOMAIN 317 418 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 17 17 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 30 30 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 116 191 BY SIMILARITY.
FT DOMAIN 346 360 GLU-RICH (ACIDIC).
SQ SEQUENCE 418 AA; 45847 MW; 1227095F801190C4 CRC64;

Query Match 55.8%; Score 48; DB 1; Length 418;
Best Local Similarity 52.9%; Pred. No. 0.3;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYIAIVOATKSFLRS 17
    |||:|:| |:| |:
Db 140 DRYLAVVHPTRSARWT 156

RESULT 13
SSR3_MOUSE STANDARD; PRT; 428 AA.
AC P30935;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE SOMATOSTATIN RECEPTOR TYPE 3 (SS3R) (SSR-28).
GN SSTR3 OR SMSTR3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93015924; PubMed=1328199;
RA Yasuda K., Rens-Domiano S., Breder C.D., Law S.F., Saper C.B.,
RA Reisine T., Bell G.I.;
RT "Cloning of a novel somatostatin receptor, SSTR3, coupled to
RT adenylyl cyclase.";
RL J. Biol. Chem. 267:20422-20428(1992).
CC -!- FUNCTION: RECEPTOR FOR SOMATOSTATINS-14 AND -28. THIS RECEPTOR IS
CC COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF
CC ADENYLYL CYCLASE.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
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DR EMBL; M91000; AAA40144.1; -.
DR PIR; A44021; A44021.
DR HSP; P34996; 1DDD.
DR GCRDB; GCR_0470; -.
DR MGD; MGI:98329; Smstr3.
DR InterPro; IPR000276; -.
DR InterPro; IPR000586; -.
DR InterPro; IPR001856; -.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PRINTS; PR00246; SOMATOSTATNR.
DR PROSITE; PS00237; G-PROTEIN_RECP_FL_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family.
FT DOMAIN 1 45 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 46 71 1 (POTENTIAL).
FT DOMAIN 72 81 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 82 103 2 (POTENTIAL).
FT DOMAIN 104 118 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 119 140 3 (POTENTIAL).
FT DOMAIN 141 162 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 163 182 4 (POTENTIAL).
FT DOMAIN 183 206 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 207 232 5 (POTENTIAL).
FT DOMAIN 233 266 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 267 288 6 (POTENTIAL).
FT DISULFID 117 192 BY SIMILARITY.
FT DOMAIN 358 373 POLY-GLU
SQ SEQUENCE 428 AA; 47391 MW; D006E4B7BE501FAA CRC64;

Query Match 55.8%; Score 48; DB 1; Length 428;
Best Local Similarity 52.9%; Pred. No. 0.31;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYIAVQATKSFRLRS 17
| | | | | | | | | |
Db 141 DRYLAVVHPTSRWRT 157

RESULT 14
SSR3_RAT
ID SSR3_RAT STANDARD; PRT; 428 AA.
AC P30936;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE SOMATOSTATIN RECEPTOR TYPE 3 (SSR3) (SSR-28).
GN SSTR3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Brain;
RX MEDLINE=93066220; PubMed=1279674;
RA Meyerhof W., Wulfsen I., Schoenrock C., Fehr S., Richter D.;
RT "Molecular cloning of a somatostatin-28 receptor and comparison of
its expression pattern with that of a somatostatin-14 receptor in rat
brain."
RL Proc. Natl. Acad. Sci. U.S.A. 89:10267-10271(1992).
CC -!- FUNCTION: RECEPTOR FOR SOMATOSTATINS-14 AND -28. THIS RECEPTOR IS
CC COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF
CC ADENYLYL CYCLASE.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

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CC -!- TISSUE SPECIFICITY: DENSELY EXPRESSED IN CEREBELLUM AND IN MODERATE
CC LEVELS IN THE AMYGDALA, CORTEX, STRIATUM, SPLEEN, LIVER,
CC PITUITARY.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL; X63574; CAA45130.1; -.
CC PIR; S30508; S30508.
CC HSP; P34996; 1DDD.
CC GCRDB; GCR_0502; -.
CC InterPro; IPR000276; -.
CC InterPro; IPR000586; -.
CC InterPro; IPR001856; -.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRRHODOPSN.
CC PRINTS; PR00246; SOMATOSTATNR.
CC PRINTS; PR00589; SOMATOSTATNR.
CC PROSITE; PS00237; G-PROTEIN_RECP_FL_1; 1.
CC PROSITE; PS0262; G-PROTEIN_RECP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family.
FT DOMAIN 1 45 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 46 71 1 (POTENTIAL).
FT DOMAIN 72 81 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 82 103 2 (POTENTIAL).
FT DOMAIN 104 118 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 119 140 3 (POTENTIAL).
FT DOMAIN 141 162 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 163 182 4 (POTENTIAL).
FT DOMAIN 183 206 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 207 232 5 (POTENTIAL).
FT DOMAIN 233 266 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 267 288 6 (POTENTIAL).
FT DOMAIN 289 302 7 (POTENTIAL).
FT TRANSMEM 303 325 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 326 428 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 18 18 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 31 31 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 117 192 BY SIMILARITY.
FT DOMAIN 358 373 POLY-GLU
SQ SEQUENCE 428 AA; 47151 MW; BE0AA948840A9E9D CRC64;

Query Match 55.8%; Score 48; DB 1; Length 428;
Best Local Similarity 52.9%; Pred. No. 0.31;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYIAVQATKSFRLRS 17
| | | | | | | | | |
Db 141 DRYLAVVHPTSRWRT 157

RESULT 15
GPRH_HUMAN
ID GPRH_HUMAN STANDARD; PRT; 339 AA.
AC Q13304;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PUTATIVE G PROTEIN-COUPLED RECEPTOR GPR17 (R12).
GN GPR17.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=96145150; PubMed=8558062;
RA Report C.J., Schweickart V.L., Chantry D., Eddy R.L. Jr., Shows T.B.,
RT Godiska R., Gray P.W.;
RL "New members of the chemokine receptor gene family.";
RN J. Leukoc. Biol. 59:18-23(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Hippocampus;
RA MEDLINE=98181695; PubMed=9523551;
RA Blaesus R.H., Weber R.G., Lichter P., Ogilvie A.;
RT "A novel orphan G protein-coupled receptor primarily expressed in the
RL brain is localized on human chromosomal band 2q21.";
RL J. Neurochem. 70:1357-1365(1998).
CC -!- FUNCTION: ORPHAN RECEPTOR. POTENTIAL CHEMOKINE RECEPTOR.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: PRIMARILY EXPRESSED IN BRAIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; U33447; AAB16746.1; -
DR EMBL; Z94154; CAB08107.1; -
DR HSP; P34996; IDDD.
DR GCRdb; GCR_1968; -
DR GCRdb; GCR_2597; -
DR MIM; 603071; -
DR InterPro; IPR000276; -
DR Pfam; PF00001; 7cm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 36
FT TRANSMEM 37 57
FT DOMAIN 58 64
FT TRANSMEM 65 85
FT DOMAIN 86 105
FT TRANSMEM 106 126
FT DOMAIN 127 147
FT TRANSMEM 148 168
FT DOMAIN 169 195
FT TRANSMEM 196 216
FT DOMAIN 217 232
FT TRANSMEM 233 253
FT DOMAIN 254 280
FT TRANSMEM 281 301
FT DOMAIN 302 339
FT DISULFID 104 181
FT CARBOHYD 14 14
FT CARBOHYD 176 176
FT CARBOHYD 254 254
SQ SEQUENCE 339 AA; 37826 MW; BD2AEDB2FEBF15E1 CRC64;
Query Match 54.7%; Score 47; DB 1; Length 339;
Best Local Similarity 56.2%; Pred. No. 0.36;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 1 DRYTAIVQATKSFRLR 16
||:|||||:|
Db 128 DRELAIVHPVKSLKLR 143

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:35:14 ; Search time 189.03 Seconds
(without alignments)

11.161 Million cell updates/sec

Title: US-08-887-977-10_COPY_133_150

Perfect score: 86

Sequence: 1 DRYIAIVQATKSFRLRSR 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_15:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_unclassified:*
- 13: sp_vertebrate:*
- 14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	96.5	367	11 Q9R1V0	Q9R1V0 mus musculus
2	54	62.8	303	13 P70058	P70058 xenopus lae
3	54	62.8	353	13 P79960	P79960 xenopus lae
4	52	60.5	380	5 Q9NFV3	Q9NFV3 lymphnaea sta
5	52	60.5	380	5 Q9NFV2	Q9NFV2 lymphnaea sta
6	52	60.5	380	5 Q9NFV1	Q9NFV1 lymphnaea sta
7	52	60.5	380	5 Q9NFV0	Q9NFV0 lymphnaea sta
8	51	59.3	353	13 Q9PTF7	Q9PTF7 brachydanio
9	50	58.1	357	13 O42445	O42445 oncorhynch
10	49	57.0	334	6 Q9N1P4	Q9N1P4 cercopithec
11	49	57.0	334	6 Q9N1P3	Q9N1P3 hylobates l
12	49	57.0	334	6 Q9N1P2	Q9N1P2 saquinus oe
13	49	57.0	334	6 Q9N130	Q9N130 saimiri bol
14	49	57.0	337	4 O75819	O75819 homo sapien
15	49	57.0	346	6 Q9MZM4	Q9MZM4 nycticebus
16	49	57.0	346	6 Q9MZM3	Q9MZM3 nycticebus
17	49	57.0	346	6 Q9MZM2	Q9MZM2 nycticebus
18	49	57.0	347	6 Q9MZM6	Q9MZM6 hylobates c
19	49	57.0	347	6 Q9MZM5	Q9MZM5 hylobates h

ALIGNMENTS

RESULT 1

Q9R1V0
ID Q9R1V0 PRELIMINARY; PRT; 367 AA.
AC Q9R1V0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE CC CHEMOKINE LARC SPECIFIC RECEPTOR.
GN MCCR6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Tanaka Y.;
RT "Molecular Cloning of Murine Homologue of CCR6, the Specific Receptor for CC Chemokine LARC."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB016031; BAA82443.1;
DR INTERPRO; IPR000190;
DR INTERPRO; IPR000276;
DR INTERPRO; IPR000355;
DR PFAM; PF00001; 7tm.1; 1.
DR PRINTS; PR00217; GPCRHHODPSN.
DR PRINTS; PR00635; ANGIOTENSINR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 367 AA; 42082 MW; 207FD98B2F7A6DD3 CRC64;

Query Match 96.5%; Score 83; DB 11; Length 367;
Best Local Similarity 94.4%; Pred. No. 3.7e-07;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRYIAIVQATKSFRLRSR 18

Db 134 DRYIAIVQATKSFRLRSR 151

RESULT 2

Q9mzn4 hylobates l
Q9mzn3 hylobates s
Q9mzn2 pongo pygma
Q9mzn1 gorilla gor
Q9mzn0 atouatta se
Q9mzm9 ateles pani
Q9mzm7 callimico g
Q9mzm6 callicebus
Q9mzm1 eulemur mac
O77488 cercopithec
Q9ukn2 homo sapien
Q60835 homo sapien
Q9mzm5 pithecia pi
Q9pusa0 acipenser r
Q9udz6 homo sapien
Q93247 cyprinus ca
Q9jly8 rattus norv
Q9uly7 homo sapien
Q9uly6 homo sapien
Q9ue21 homo sapien
Q9wv08 mus musculu
Q9jhg3 rattus norv
O97666 macaca mula
Q9tv16 pan troglod
Q9xt45 macaca mula
Q9n0z0 cercocebus

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P70058
ID P70058 PRELIMINARY; PRT; 303 AA.
AC P70058;
DT 01-FEB-1997 (TReMBLrel. 02, Created)
DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE ANGIOTENSIN RECEPTOR RELATED PROTEIN.
GN XANGI01.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Saha M.S., Oakes J.A., Miles R.R.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; U72029; AAB17004.1; -.
DR INTERPRO; IPR000276; -.
DR PFAM; PF00001; 7tm.1; 1.
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
SQ SEQUENCE 303 AA; 34088 MW; C4E2D902DDFAF5D1 CRC64;

Query Match 62.8%; Score 54; DB 13; Length 303;
Best Local Similarity 61.1%; Pred. No. 0.067;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLRSR 18
DB 132 DRYLAIVHSLSSAKLRSR 149
|||||:|:|||||

RESULT 3
P79960
ID P79960 PRELIMINARY; PRT; 353 AA.
AC P79960;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE MESENCHYME-ASSOCIATED SERPENTINE RECEPTOR.
GN X-MSR.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-97109511; PubMed=8951791;
RA Devic E., Paquereau L., Vernier P., Knibiehler B., Audigier Y.;
RT "Expression of a new G-protein-coupled receptor X-msr is associated with an endothelial lineage in Xenopus laevis.";
RL Mech. Dev. 59:129-140(1996).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; X93045; CAA63612.1; -.
DR INTERPRO; IPR000276; -.
DR PFAM; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHDOPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
SQ SEQUENCE 353 AA; 40303 MW; 1BF757DB65057621 CRC64;

Query Match 62.8%; Score 54; DB 13; Length 353;
Best Local Similarity 61.1%; Pred. No. 0.079;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLRSR 18

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|||||:|:|||||
DB 132 DRYLAIVHSLSSAKLRSR 149

RESULT 4
Q9NFV3
ID Q9NFV3 PRELIMINARY; PRT; 380 AA.
AC Q9NFV3;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE G-PROTEIN COUPLED RECEPTOR.
GN ORPH 1.
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Basommatophora;
OC Lymnaeidae; Lymnaea.
OX NCBI_TaxID=6523;
RN [1]
RP SEQUENCE FROM N.A.
RA Saunders S.E., Burke J.F., Benjamin P.R.;
RT "Multimeric CREB binding sites in the promoter regions of a family of orphan G-protein coupled receptors related to the vertebrate galanin and nociceptin/orphanin-FQ receptor families.";
RT Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ270459; CAB77262.1; -.
DR RECEPTOR; G-protein coupled receptor.
KW RECEPTOR; G-protein coupled receptor.
SQ SEQUENCE 380 AA; 42773 MW; DFB1E56A20C72629 CRC64;

Query Match 60.5%; Score 52; DB 5; Length 380;
Best Local Similarity 58.8%; Pred. No. 0.2;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLRS 17
DB 143 DRYLAVVHAIRSMTLRS 159
|||||:|:|:|:|

RESULT 5
Q9NFV2
ID Q9NFV2 PRELIMINARY; PRT; 380 AA.
AC Q9NFV2;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE G-PROTEIN COUPLED RECEPTOR.
GN ORPH 2.
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Basommatophora;
OC Lymnaeidae; Lymnaea.
OX NCBI_TaxID=6523;
RN [1]
RP SEQUENCE FROM N.A.
RA Saunders S.E., Burke J.F., Benjamin P.R.;
RT "Multimeric CREB binding sites in the promoter regions of a family of orphan G-protein coupled receptors related to the vertebrate galanin and nociceptin/orphanin-FQ receptor families.";
RT Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ270460; CAB77263.1; -.
DR RECEPTOR; G-protein coupled receptor.
KW RECEPTOR; G-protein coupled receptor.
SQ SEQUENCE 380 AA; 42595 MW; C1CEE818CF3AF1FC CRC64;

Query Match 60.5%; Score 52; DB 5; Length 380;
Best Local Similarity 58.8%; Pred. No. 0.2;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLRS 17
DB 143 DRYLAVVHAIRSMTLRS 159
|||||:|:|:|:|

RESULT 6

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Q9NFV1
ID Q9NFV1 PRELIMINARY; PRT; 380 AA.
AC Q9NFV1;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE G-PROTEIN COUPLED RECEPTOR.
GN ORPH 3.
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Lymnaea.
OX NCBI_TaxID=6523;
RN [1]
RP SEQUENCE FROM N.A.
RA Saunders S.E., Burke J.F., Benjamin P.R.;
RT "Multimeric CREB binding sites in the promoter regions of a family of
RT orphan G-protein coupled receptors related to the vertebrate galanin
RT and nociceptin/orphanin-FQ receptor families.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ270461; CAB77264.1;
DR PRINTS; G-protein coupled receptor.
KW Receptor; G-protein coupled receptor.
SQ SEQUENCE 380 AA; 42604 MW; A072ADFCD89028D3 CRC64;

Query Match 60.5%; Score 52; DB 5; Length 380;
Best Local Similarity 58.8%; Pred. No. 0.2;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYIAIVQATKSFRLRS 17
|||:|:|:|:|:|
Db 143 DRYLAVVHAIRSMTLRS 159

RESULT 7
Q9NFV0
ID Q9NFV0 PRELIMINARY; PRT; 380 AA.
AC Q9NFV0;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE G-PROTEIN COUPLED RECEPTOR.
GN ORPH 4.
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Lymnaea.
OX NCBI_TaxID=6523;
RN [1]
RP SEQUENCE FROM N.A.
RA Saunders S.E., Burke J.F., Benjamin P.R.;
RT "Multimeric CREB binding sites in the promoter regions of a family of
RT orphan G-protein coupled receptors related to the vertebrate galanin
RT and nociceptin/orphanin-FQ receptor families.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ270462; CAB77265.1;
DR PRINTS; G-protein coupled receptor.
KW Receptor; G-protein coupled receptor.
SQ SEQUENCE 380 AA; 42723 MW; D54F5BE2BBFE4EC4 CRC64;

Query Match 60.5%; Score 52; DB 5; Length 380;
Best Local Similarity 58.8%; Pred. No. 0.2;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYIAIVQATKSFRLRS 17
|||:|:|:|:|:|
Db 143 DRYLAVVHAIRSMTLRS 159

RESULT 8
Q9PTF7
ID Q9PTF7 PRELIMINARY; PRT; 353 AA.
AC Q9PTF7;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE CHEMOKINE RECEPTOR CXCR4.
GN CXCR4.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Tseng S., Rollins B.J.;
RT "Chemokines and chemokine receptors in zebrafish.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF201451; AAF17561.1;
DR INTERPRO; IPR000276;
DR INTERPRO; IPR000355;
DR INTERPRO; IPR001277;
DR PFAM; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PRINTS; PR00645; LCR1ORPHAN.
DR PRINTS; PR00657; COCHEMOKINER.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
KW Receptor.
SQ SEQUENCE 353 AA; 39444 MW; 410F9A7F75D631BE CRC64;

Query Match 59.3%; Score 51; DB 13; Length 353;
Best Local Similarity 52.5%; Pred. No. 0.28;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DRYIAIVQATKSFRLR 16
|||:|:|:|:|:|
Db 131 DRYLAVVHAIRSMTLRS 146

RESULT 9
Q42445
ID Q42445 PRELIMINARY; PRT; 357 AA.
AC Q42445;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE CXCR4 CHEMOKINE RECEPTOR.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Daniels G.D., Charlemagne J., Secombes C.J.;
RT "Cloning and sequencing of a rainbow trout, Oncorhynchus mykiss,
RT chemokine receptor homolog.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AJ001039; CAA04493.1;
DR INTERPRO; IPR000276;
DR PFAM; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
SQ SEQUENCE 357 AA; 39817 MW; 14EC2F01DA1222C4 CRC64;

Query Match 58.1%; Score 50; DB 13; Length 357;
Best Local Similarity 58.8%; Pred. No. 0.43;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYIAIVQATKSFRLRS 17
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Db 135 DRYLAVVHAIRSMTLRS 151

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RESULT 10
Q9NIP4
ID Q9NIP4 PRELIMINARY; PRT; 334 AA.
AC Q9NIP4;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CXC CHEMOKINE RECEPTOR 4 (FRAGMENT).
GN CXCR4.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RA Zubair S., Metzberg S.;
RT "CXCR4 homologs of Gibbon ape, African green monkey, and Cotton-top
marmoset."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF178082; AAF42990.1;
KW Receptor.
FT NON_TER 1 1
FT NON_TER 334 334
SQ SEQUENCE 334 AA; 37752 MW; 8C91CED8AB54D131 CRC64;

Query Match 57.0%; Score 49; DB 6; Length 334;
Best Local Similarity 68.8%; Pred. No. 0.62;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYIAIVOATKSFRLR 16
|||:|||||
Db 120 DRYLAIVHATNSQRP 135

RESULT 11
Q9NIP3
ID Q9NIP3 PRELIMINARY; PRT; 334 AA.
AC Q9NIP3;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CXC CHEMOKINE RECEPTOR 4 (FRAGMENT).
GN CXCR4.
OS Hylobates lar (Common gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=9580;
RN [1]
RP SEQUENCE FROM N.A.
RA Zubair S., Metzberg S.;
RT "CXCR4 homologs of Gibbon ape, African green monkey, and Cotton-top
marmoset."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF178083; AAF42991.1;
KW Receptor.
FT NON_TER 1 1
FT NON_TER 334 334
SQ SEQUENCE 334 AA; 37725 MW; C8813B0CB3CF9A61 CRC64;

Query Match 57.0%; Score 49; DB 6; Length 334;
Best Local Similarity 68.8%; Pred. No. 0.62;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYIAIVOATKSFRLR 16
|||:|||||
Db 120 DRYLAIVHATNSQRP 135
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RESULT 12
Q9NIP2
ID Q9NIP2 PRELIMINARY; PRT; 334 AA.
AC Q9NIP2;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CXC CHEMOKINE RECEPTOR 4 (FRAGMENT).
GN CXCR4.
OS Saguinus oedipus (Cotton-top tamarin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
OX NCBI_TaxID=9490;
RN [1]
RP SEQUENCE FROM N.A.
RA Zubair S., Metzberg S.;
RT "CXCR4 homologs of Gibbon ape, African green monkey, and Cotton-top
marmoset."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF178084; AAF42992.1;
KW Receptor.
FT NON_TER 1 1
FT NON_TER 334 334
SQ SEQUENCE 334 AA; 37877 MW; EB2362E88D0997C5 CRC64;

Query Match 57.0%; Score 49; DB 6; Length 334;
Best Local Similarity 68.8%; Pred. No. 0.62;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYIAIVOATKSFRLR 16
|||:|||||
Db 120 DRYLAIVHATNSQRP 135

RESULT 13
Q9N130
ID Q9N130 PRELIMINARY; PRT; 334 AA.
AC Q9N130;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CXCR4 RECEPTOR (FRAGMENT).
OS Saimiri boliviensis (Bolivian squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.
OX NCBI_TaxID=27679;
RN [1]
RP SEQUENCE FROM N.A.
RA Zubair S., Metzberg S.;
RT "CXCR4 homologs of Gibbon ape, African green monkey, Cotton-top
marmoset, and Bolivian squirrel monkey."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF229128; AAF37288.1;
KW Receptor.
FT NON_TER 1 1
FT NON_TER 334 334
SQ SEQUENCE 334 AA; 37943 MW; 277227E898098DB5 CRC64;

Query Match 57.0%; Score 49; DB 6; Length 334;
Best Local Similarity 68.8%; Pred. No. 0.62;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYIAIVOATKSFRLR 16
|||:|||||
Db 120 DRYLAIVHATNSQRP 135

RESULT 14
O75819
ID O75819 PRELIMINARY; PRT; 337 AA.
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AC 075819;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DF 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE T CELL-DEATH ASSOCIATED PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98317948; PubMed=9655242;
RA Kyaw H., Zeng Z., Su K., Fan P., Shell B.K., Carter K.C., Li Y.;
RT "Cloning, characterization, and mapping of human homolog of mouse T-
RL DNA Cell Biol. 17:493-500(1998).
DR EMBL; U95218; AAC31794.1; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR000504; -
DR PFAM; PF00001; 7tm_1; 1.
DR PROSITE; PS00030; RNP_1; UNKNOWN_1.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
SQ SEQUENCE 337 AA; 39339 MW; 05DA739457B079A2 CRC64;

Query Match 57.0%; Score 49; DB 4; Length 337;
Best Local Similarity 55.6%; Pred. No. 0.63;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DRYIAIVQATKSFRLRSR 18
   |||:|:| | | | |
Db 111 DRYLAVVPLKFFFLRTR 128

RESULT 15
Q9M2M4
ID Q9M2M4 PRELIMINARY; PRT; 346 AA.
AC Q9M2M4;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DE 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE CHEMOKINE RECEPTOR CXCR4 (FRAGMENT).
GN CXCR4.
OS Nycticebus coucang (Slow loris).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirrhini; Loridae; Nycticebus.
OX NCBI_TaxID=9470;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
RT "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in
RT Primates.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF172239; AAF89359.1; -
KW Receptor.
FT NON_TER.
SQ SEQUENCE 346 AA; 39235 MW; BC176D2E634CCEE CRC64;

Query Match 57.0%; Score 49; DB 6; Length 346;
Best Local Similarity 68.8%; Pred. No. 0.64;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYIAIVQATKSFRLR 16
   |||:|:| | | | |
Db 128 DRYLAIVHATNSQRP 143

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:28:29 ; Search time 184.73 Seconds
(without alignments)
8.045 Million cell updates/sec

Title: US-08-887-977-10_COPY_151_176

Perfect score: 129

Sequence: 1 TLPRSKIICLVWGLSVIISSTFVF 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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22: /SID56/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	129	100.0	365	19	W48086 Human dendritic ce
2	129	100.0	365	21	Y97077 Primate (human) ch
3	60	46.5	354	15	R53932 Interleukin 8 (IL-
4	60	46.5	355	13	R28272 Sequence in a high
5	60	46.5	355	16	R80950 Recombinant high a
6	58	45.0	312	15	R48717 G-protein coupled
7	58	45.0	312	17	W02689 G-protein coupled
8	58	45.0	355	14	R33420 Human IL-8 recepto
9	58	45.0	355	17	B09990 Human IL-8 recepto
10	58	45.0	360	13	R28273 Sequence in a low
11	58	45.0	360	16	R80758 Interleukin 8 rece

12	58	45.0	1064	16	R70124	IL8-R type 2-GSP 1
13	57	44.2	358	13	R28274	Sequence in a lowh
14	57	44.2	358	16	R80952	Recombinant high a
15	55	42.6	342	20	W97784	African green monk
16	55	42.6	342	20	W97785	Pig-tailed macaque
17	55	42.6	368	19	W54371	Human IP-10/Mig re
18	55	42.6	368	21	Y90614	Human G protein-co
19	55	42.6	368	21	Y90648	Human mutant G-pro
20	55	42.6	378	20	Y50129	Human chemokine re
21	55	42.6	415	18	W19780	Human G-protein ch
22	54	41.9	49	21	B27602	Human secreted pro
23	54	41.9	73	19	W69998	Rodent chemokine r
24	54	41.9	350	13	R27791	Interleukin-8 rece
25	54	41.9	350	16	R68811	Interleukin-8 rece
26	54	41.9	350	16	R80756	Interleukin 8 rece
27	54	41.9	350	16	R80951	Recombinant high a
28	54	41.9	350	17	B09989	Human IL-8 recepto
29	54	41.9	367	19	W69999	Rodent chemokine r
30	54	41.9	1060	16	R70123	IL8-R type 1-GSP 1
31	53	41.1	176	22	B45701	Human 7TM clone H7
32	53	41.1	322	20	Y30164	Human dorsal root
33	53	41.1	322	21	Y87663	Human G protein-co
34	53	41.1	322	21	Y87664	Human G protein-co
35	51	39.5	395	19	W44703	Human Th2/B19. Ho
36	50	38.8	302	19	W70001	Rodent chemokine r
37	50	38.8	338	21	Y77736	Seven times membra
38	50	38.8	351	20	Y23825	A7 times membrane
39	50	38.8	372	20	W86323	Kidney injury asso
40	49	38.0	304	15	R48714	G-protein coupled
41	49	38.0	304	17	W02686	G-protein coupled
42	49	38.0	316	15	R48725	G-protein coupled
43	49	38.0	316	17	W02697	G-protein coupled
44	49	38.0	325	8	P70428	Polypeptide encode
45	49	38.0	360	16	R80953	Recombinant high a

ALIGNMENTS

RESULT	1
W48086	
ID	W48086 standard; Protein; 365 AA.
AC	
AC	W48086;
XX	
XX	
DF	11-JUN-1998 (first entry)
XX	
XX	Human dendritic cell chemokine receptor.
DE	
DE	Human; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta;
KW	receptor; dendritic cell; macrophage; inflammation; asthma.
KW	
XX	
OS	Homo sapiens.
XX	
XX	
Key	Location/Qualifiers
FT	Misc-difference 193
FT	/note= "encoded by CAN"
XX	
XX	WO9801557-A2.
PN	
PD	15-JAN-1998.
XX	
XX	
PF	02-JUL-1997; 97WO-US10819.
XX	
XX	
PR	04-JUN-1997; 97US-0048593.
PR	05-JUL-1996; 96US-0675814.
PR	11-OCT-1996; 96US-0028329.
XX	
XX	(SCHE) SCHERING CORP.
PA	
XX	
PI	Gish KC, Schall TJ, Vicari A, Wang W, Zlotnik A;
XX	
XX	WFI; 1998-101054/09.
DR	

DR N-PSDB; V15418.
 XX Novel chemokines, e.g. thymus expressed chemokine - used for
 PT treating inflammatory conditions including asthma.
 XX
 XX Claim 3; Page 94-95; 202pp; English.
 XX
 CC The present sequence represents human dendritic cell chemokine receptor.
 CC Antibodies which bind to the protein can be used in detecting or
 CC diagnosing various immunological conditions related to expression
 CC of the protein. The nucleic acid can be used for screening and
 CC isolating DNA clones for the chemokines, especially from other
 CC species. The chemokine can be used in the treatment of conditions
 CC associated with abnormal physiology or development, including
 CC inflammatory conditions such as asthma.
 XX
 XX Sequence 365 AA;
 SQ

Query Match 100.0%; Score 129; DB 19; Length 365;
 Best Local Similarity 100.0%; Pred. No. 2.1e-12;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TLPRSKIICLVWGLSVIISSTFVF 26
 DB 151 tlprskilclvwglsviisstfvf 176

RESULT 2
 Y97077
 ID Y97077 standard; Protein; 365 AA.
 XX
 XX Y97077;
 AC
 XX
 DT 04-DEC-2000 (first entry)
 XX
 DE Primate (human) chemokine receptor CCR6.
 XX
 XX MIP-3-alpha; chemokine; CCR6 receptor; ligand; cytostatic; agonist;
 KW antagonist; anti-psoriatic; dermatological; immunosuppressive;
 KW anti-inflammatory.
 XX
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 193
 FT /note= "Encoded by CAN#"
 XX
 XX WO200046248-A1.
 PN
 XX
 XX 10-AUG-2000.
 PD
 XX
 XX 02-FEB-2000; 2000WO-US00511.
 PF
 XX
 XX 03-FEB-1999; 99US-0244281.
 PR
 XX
 XX (SCHE) SCHERING CORP.
 PA
 XX
 XX Oldham ER, Horney B, Dieu-Nosjean M, Caux C, Zlotnik A;
 PI
 XX
 XX WPI; 2000-543477/49.
 DR
 XX N-PSDB; A51971.
 DR
 XX Novel methods for modulating the migration of cells within or to the
 PT skin using MIP-3-alpha or CCR6 agonists or antagonists, useful for
 PT treating skin disorders, e.g. cancer
 PT
 XX Disclosure; Page 53-54; 61pp; English.
 PS
 XX
 XX The MIP-3-alpha chemokine is expressed in inflamed skin cells. This
 CC chemokine is the ligand for the CCR6 receptor. MIP-3-alpha or CCR6
 CC agonists or antagonists can be used to modulate the migration of a cell
 CC within or to the skin of a mammal. MIP-3-alpha can be used to purify a

CC population of cells expressing a MIP-3-alpha receptor. The methods are
 CC e.g. for treating a mammalian subject with a skin disease or condition,
 CC e.g. cancer, metastasis, psoriasis, atopic or contact dermatitis,
 CC systemic lupus erythematosus and lichen ruber planus, or for treating
 CC skin transplants or grafts.
 XX
 XX Sequence 365 AA;
 SQ

Query Match 100.0%; Score 129; DB 21; Length 365;
 Best Local Similarity 100.0%; Pred. No. 2.1e-12;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TLPRSKIICLVWGLSVIISSTFVF 26
 DB 151 tlprskilclvwglsviisstfvf 176

RESULT 3
 R53932
 ID R53932 standard; Protein; 354 AA.
 XX
 XX R53932;
 AC
 XX
 DT 23-FEB-1995 (first entry)
 XX
 DE Interleukin 8 (IL-8) receptor.
 XX
 XX Interleukin; receptor; antiinflammatory; psoriasis; reperfusion;
 KW rheumatoid arthritis; allograft; graft rejection.
 KW
 XX Homo sapiens.
 OS
 XX
 XX JP06100595-A.
 PN
 XX
 XX 12-APR-1994.
 PD
 XX
 XX 27-MAY-1991; 91JP-0149245.
 PF
 XX
 XX 27-MAY-1991; 91JP-0149245.
 PR
 XX
 XX (UYBO-) UNIV BOSTON.
 PA
 XX
 XX WPI; 1994-156656/19.
 DR
 XX N-PSDB; Q63919.
 DR
 XX Recombinant interleukin-8 receptor polypeptide - having
 PT antiinflammatory properties
 PT
 XX Claim 1; Figure 1; 13pp; Japanese.
 PS
 XX Anti-inflammatory agents containing the interleukin-8 receptor
 CC polypeptide can be used for the treatment of psoriasis, rheumatoid
 CC arthritis and other acute and chronic inflammatory diseases,
 CC including reperfusion and allograft rejection.
 CC
 XX
 XX Sequence 354 AA;
 SQ

Query Match 46.5%; Score 60; DB 15; Length 354;
 Best Local Similarity 52.4%; Pred. No. 0.15;
 Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 QY 6 KIICLVWGLSVIISSTFVF 26
 DB 158 kfclgiwalsliislpfllf 178

RESULT 4
 R28272
 ID R28272 standard; Protein; 355 AA.
 XX
 XX R28272;
 AC

XX 04-APR-1993 (first entry)
 XX Sequence in a high affinity recombinant rabbit interleukin-8
 DE (IL-8) receptor polypeptide in F3R.
 XX
 XX IL-8 receptor polypeptide; G-protein-coupled receptor.
 XX
 XX Oryctolagus cuniculus.
 OS WO9218641-A.
 PN
 XX 29-OCT-1992.
 PD
 XX 10-APR-1992; 92WO-US02977.
 PF
 XX 10-APR-1991; 91US-0685101.
 PR
 PR 09-JUL-1991; 91US-0726606.
 PR
 PR 09-DEC-1991; 91US-0803842.
 XX
 XX (REP K) REPLIGEN CORP.
 PA (UYBO-) UNIV BOSTON.
 PA
 XX Navarro J, Thomas KM, Witt DP;
 PI WPI; 1992-382123/46.
 DR N-PSDB; Q30011.
 DR
 XX Recombinant mammalian interleukin-8 receptor - used for screening
 PT interleukin-8 binding antagonists, used to treat inflammation
 PT
 PS Claim 2; Fig 1; 71pp; English.
 PS
 XX Rabbit high affinity IL-8 receptor gene was isolated from rabbit
 CC peritoneal neutrophils and used as a source of poly(A)+ RNA, to
 CC produce a rabbit neutrophil cDNA library. 250,000 recombinant
 CC plaques were screened for those which hybridized to an antisense
 CC oligonucleotide (Q30015). This probe was designed based on the
 CC sequence derived from the second transmembrane domain of G-protein-
 CC coupled receptors. After tertiary screening, six plaques were
 CC isolated. The insert of one of these plaques, termed F3R was of 2.5
 CC kb in size. This insert was sequenced. The protein deduced from
 CC the F3R clone demonstrates that it belongs to the family of
 CC G-protein-coupled receptors. The deduced protein sequence
 CC indicates seven putative transmembrane segments.
 CC
 XX Sequence 355 AA;
 SQ

Query Match 46.5%; Score 60; DB 13; Length 355;
 Best Local Similarity 52.4%; Pred. NO. 0.15;
 Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 6 KIICLVWGLSVIISSTFVF 26
 Db 159 kfciigiwalisilslpfllf 179

RESULT 5
 R80950
 ID R80950 standard; Protein; 355 AA.
 XX
 XX R80950;
 AC
 XX 24-APR-1996 (first entry)
 DT
 XX Recombinant high affinity interleukin-8 receptor subtype A.
 DE
 XX IL-8A; IL-8B; receptor; monoclonal antibody; inflammatory disorder;
 KW anaphylaxis; systemic lupus erythematosus; rheumatoid arthritis;
 KW systemic necrotizing vasculitis; psoriasis; asthma; allergy; ARDS;
 KW adult respiratory distress syndrome; neutrophil detection.
 XX

Oryctolagus cuniculus.
 OS WO9525126-A1.
 PN
 XX 21-SEP-1995.
 PD
 XX 09-MAR-1995; 95WO-US03032.
 PF
 XX 02-MAY-1994; 94US-0237937.
 PR
 PR 15-MAR-1994; 94US-0210250.
 XX
 XX (REP K) REPLIGEN CORP.
 PA (UYBO-) UNIV BOSTON.
 PA
 XX Greenfield EA, Larosa GJ, Navarro J, Thomas KM;
 PI Witt DT;
 PI WPI; 1995-336945/43.
 DR N-PSDB; Q99949.
 DR
 XX Monoclonal antibody against recombinant IL-8 receptor polypeptide -
 PT useful for treating inflammatory disorders, for detecting
 PT neutrophil(s) and for isolating IL-8 receptor from liq.mixt.
 PT
 XX Claim 2; Fig 1A-B; 74pp; English.
 PS
 XX Monoclonal antibodies were raised against recombinant interleukin-8
 CC (IL-8) receptor subtypes A and B from both human and rabbit sources
 CC (R80950-53 encoded by 099949-52). The A subtype receptor (IL-8rA) is
 CC a high affinity receptor and the B subtype receptor (IL-8rB) is a
 CC low affinity receptor. The monoclonal antibody (mAb) pref. binds to
 CC the IL-8 binding domain thus blocking its activation. The mAbs are
 CC useful for treating inflammatory disorders (see key words) and for
 CC detecting the presence of neutrophils in a biological sample. The
 CC mAbs are also useful in the isolation of IL-8 receptors from a mixture.
 CC
 XX Sequence 355 AA;
 SQ

Query Match 46.5%; Score 60; DB 16; Length 355;
 Best Local Similarity 52.4%; Pred. NO. 0.15;
 Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 6 KIICLVWGLSVIISSTFVF 26
 Db 159 kfciigiwalisilslpfllf 179

RESULT 6
 R48717
 ID R48717 standard; Protein; 312 AA.
 XX
 XX R48717;
 AC
 XX 06-JUN-1996 (first entry)
 DT
 XX G-protein coupled human interleukin-8 receptor protein.
 DE
 XX G-protein coupled receptor; ligand binding assay; transmembrane domain;
 KW psychotic disorder; schizophrenia; dopamine; cAMP; adenosine; thrombin;
 KW muscarinic acetylcholine; adrenergic; endothelin; bombesin; endocrine;
 KW rhodopsin; opsin; odorant; cytomegalovirus.
 KW
 XX Homo sapiens.
 OS
 XX WO9405695-A1.
 PN
 XX 17-MAR-1994.
 PD
 XX 09-SEP-1993; 93WO-US08528.
 PF
 XX 10-SEP-1992; 92US-0943236.
 PR
 XX

PA (UUNY) UNIV NEW YORK STATE.
 XX Murphy RB, Schuster DI;
 PI
 XX WPI; 1994-101120/12.
 DR
 XX Polypeptides of G-coupled receptor proteins (GPRs) - useful for
 PT binding GPR ligands or modulating GPR binding
 PT
 XX Disclosure; Page 92; 160pp; English.
 PS
 XX Proteins R48685-R48758 represent a range of G-protein coupled receptor
 CC proteins selected from cAMP, adenosine, muscarinic acetylcholine,
 CC adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin,
 CC odorant, cytomagaloviral and other G-protein coupled receptors. The
 CC receptor proteins were used to design polypeptides, pref. based on the
 CC transmembrane domains, for use in G-protein coupled receptor ligand
 CC binding assays. The polypeptide fragments retain biological activity
 CC such as binding a GPR ligand or modulating GPR ligand binding to a GPR
 CC (see R48759-R48758, R50569-R50807 and R89189-R89195 for examples of
 CC polypeptide fragments). The polypeptide fragments can be used in
 CC compositions for treating subjects suffering from a pathology related to
 CC a GPR abnormality e.g. a psychotic disorder such as schizophrenia.
 XX
 XX SQ Sequence 312 AA;

Query Match 45.0%; Score 58; DB 15; Length 312;
 Best Local Similarity 42.9%; Pred. No. 0.27;
 Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 6 KIICLVWVGLSVIISSTFEV 26
 | | | : | | | : | | : |
 Db 115 kficlsiwglslilalpvlif 135

RESULT 7
 W02689
 ID W02689 standard; peptide; 312 AA.
 AC
 XX W02689;
 XX
 DT 12-NOV-1996 (first entry)
 XX
 DE G-protein coupled human interleukin-8 receptor.
 XX
 KW G-protein coupled receptor; ligand binding assay; transmembrane domain;
 KW schizophrenia; dopamine; cAMP; adenosine; thrombin; adrenergic; opsin;
 KW muscarinic acetylcholine; endothelin; bombesin; endocrine; rhodopsin;
 KW odorant; cytomagalovirus; serotonergic.
 XX
 OS Homo sapiens.
 XX
 PN US5508384-A.
 XX
 PD 16-APR-1996.
 XX
 PF 10-SEP-1992; 92US-0943236.
 XX
 PR 09-SEP-1993; 93US-0118270.
 PR 10-SEP-1992; 92US-0943236.
 XX
 PA (UUNY) UNIV NEW YORK STATE.
 XX
 PI Murphy RB, Schuster DI;
 XX
 DR WPI; 1996-208785/21.
 XX
 PT New dopamine receptor peptide - useful as antipsychotic agent, e.g.
 PT for treating schizophrenia
 XX
 PS Disclosure; Column 103-106; 184pp; English.
 XX

CC Proteins W02657-W02730 represent a range of G-protein coupled receptor
 CC (GPR) proteins selected from cAMP, adenosine, muscarinic acetylcholine,
 CC adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin,
 CC odorant, cytomagaloviral and other GPR proteins. The receptor proteins
 CC were used to design polypeptides, pref. based on the transmembrane
 CC domains, for use in G-protein coupled receptor ligand binding assays.
 CC The polypeptide fragments retain biological activity such as binding a
 CC GPR ligand or modulating GPR ligand binding to a GPR (see W02747-W02999
 CC for examples of polypeptide fragments). The polypeptide fragments can
 CC be used in compositions for treating subjects suffering from a pathology
 CC related to a GPR abnormality e.g. a psychotic disorder such as
 CC schizophrenia.
 XX
 XX SQ Sequence 312 AA;

Query Match 45.0%; Score 58; DB 17; Length 312;
 Best Local Similarity 42.9%; Pred. No. 0.27;
 Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 6 KIICLVWVGLSVIISSTFEV 26
 | | | : | | | : | | : |
 Db 115 kficlsiwglslilalpvlif 135

RESULT 8
 R33420
 ID R33420 standard; Protein; 355 AA.
 XX
 AC R33420;
 XX
 DT 26-JUL-1993 (first entry)
 XX
 DE Human IL-8 receptor from clone p2.
 XX
 KW Interleukin-8 receptor; probes; gene therapy; gro receptor;
 KW intracellular-calcium mobilising; ligand-binding; MIP-2 receptor.
 XX
 OS Homo sapiens.
 XX
 PN W09306229-A.
 XX
 PD 01-APR-1993.
 XX
 PF 14-SEP-1992; 92WO-US07641.
 XX
 PR 13-SEP-1991; 91US-0759568.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICE.
 XX
 PI Murphy PM;
 XX
 DR WPI; 1993-117549/14.
 DR N-PSDB; Q38747.
 XX
 PT New interleukin-8 receptor aminoacid sequence - and corresp. cdna
 PT expressed in Xenopus laevis oocytes or transfected host cells,
 PT for screening ligands of IL-8 receptor and gene therapy.
 XX
 PS Claim 1; Fig 3; 39pp; English.
 XX
 CC cDNA libraries from 2 and 3.5 kb fractions of poly(A)+ RNA from HL60
 CC neutrophils sepd. of a sucrose gradient were made in Unizap. The
 CC libraries were screened with F3R oligonucleotide probe (from rabbit
 CC IL-8 receptor) and under low stringency with a p2 cDNA probe
 CC synthesised from random primers, to isolated the clone p2, encoding
 CC human IL-8 receptor protein. The presence or absence of the DNA
 CC encoding IL-8R or related MIP-2 receptor may be detected using
 CC portions of the p2 clone as probes. P2 may also be used to screen
 CC for ligands of IL-8R and may also be used in gene therapy to treat a
 CC patient deficient in IL-8R. The IL-8R is a gro receptor and has
 CC intracellular calcium-mobilising and ligand-binding properties.
 XX

SQ Sequence 355 AA;

Query Match 45.0%; Score 58; DB 14; Length 355;
 Best Local Similarity 42.9%; Pred. No. 0.32; Length 355;
 Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 6 KIICLVWGLSVIISSTFVF 26
 | | | : | | | : | : |
 Db 158 kfclsiwglslilalpvlif 178

RESULT 9

B09990 ID B09990 standard; Protein; 355 AA.

XX AC B09990;

DT 20-OCT-2000 (first entry)

XX Human IL-8 receptor protein hIL8RB.

XX IL-8 receptor protein; hIL8RA; hIL8RB; human; interleukin-8; drug;
 KW treatment; inflammatory disease; anti-tumor.

XX OS Homo sapiens.

XX JP08103276-A.

XX 23-APR-1996.

XX 06-OCT-1994; 94JP-0242534.

XX 06-OCT-1994; 94JP-0242534.

XX (TAKE) TAKEDA CHEM IND LTD.

XX WPI; 1996-253878/26.

XX N-PSDB; A40128.

XX Recombinant human interleukin 8 receptor protein, - its prepn. and
 PT application.

XX Example 2; Fig 4; 22pp; Japanese.

XX This invention describes a novel expression vector which carries a DNA
 CC encoding human interleukin 8 receptor protein and is expressed by
 CC pAKK01.11/hIL8RA or pAKK01.11/hIL8RB. Also claimed are (I) CHO cell
 CC containing the above expression vector, (II) the preparation of a
 CC recombinant human interleukin 8 receptor protein in which the above CHO
 CC cell is cultured under a condition enabling the expression of a DNA
 CC coding human interleukin 8 receptor protein, (III) a CHO cell
 CC containing a recombinant human interleukin 8 receptor protein which can
 CC be prepared, by culturing the above CHO cell under a condition enabling
 CC the expression of a DNA coding human interleukin 8 receptor protein or
 CC its cell membrane fraction, (IV) a recombinant human interleukin 8
 CC receptor protein isolated from a CHO cell containing the above
 CC recombinant human interleukin 8 receptor protein, its partial peptide or
 CC their salt, (V) the screening of human interleukin 8 receptor agonist or
 CC antagonist in which the above CHO cell or its cell membrane fraction is
 CC used or the above recombinant human interleukin 8 receptor protein, its
 CC partial peptide or their salt is used (VI) a kit for screening the human
 CC interleukin 8 receptor agonist or antagonist containing the above CHO
 CC cell or its cell membrane fraction or the above recombinant human
 CC interleukin 8 receptor protein, its partial peptide or their salt, (VII)
 CC a human interleukin 8 receptor agonist or antagonist prepared by using
 CC the above screening method or the above screening kit or its salt, (VII)
 CC an activation promoter or a migration promoter of neutrophils containing
 CC the above agonist or its salt, and an activation inhibitor or a migration
 CC inhibitor containing the above antagonist or its salt. The agonist or the
 CC antagonist can be used in drug compositions for the prevention and
 CC treatment of inflammatory diseases and anti-tumor agents. The screening
 CC method can select an agonist or an antagonist advantageously. This

CC sequence represents the human IL-8 receptor protein hIL8RB which is
 CC described in the method of the invention.

XX SQ Sequence 355 AA;

Query Match 45.0%; Score 58; DB 17; Length 355;
 Best Local Similarity 42.9%; Pred. No. 0.32;
 Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 6 KIICLVWGLSVIISSTFVF 26
 | | | : | | | : | : |
 Db 158 kfclsiwglslilalpvlif 178

RESULT 10

R28273 ID R28273 standard; Protein; 360 AA.

XX AC R28273;

XX 04-APR-1993 (first entry)

XX Sequence in a low affinity recombinant human interleukin-8
 DE (IL-8) receptor polypeptide in 4AB.

XX KW IL-8 receptor polypeptide; G-protein-coupled receptor.

XX OS Homo sapiens.

XX PN W09218641-A.

XX 29-OCT-1992.

XX 10-APR-1992; 92WO-US02977.

XX 10-APR-1991; 91US-0685101.

XX 09-JUL-1991; 91US-0726606.

XX 09-DEC-1991; 91US-0803842.

XX (REPK) REPLIGEN CORP.

XX (UYBO-) UNIV BOSTON.

XX Navarro J, Thomas KM, Witt DP;

XX WPI; 1992-382123/46.

XX N-PSDB; Q30012.

XX Recombinant mammalian interleukin-8 receptor - used for screening
 PT interleukin-8 binding antagonists, used to treat inflammation

XX Disclosure; Fig 2; 71pp; English.

XX Rabbit high affinity IL-8 receptor gene was isolated from rabbit
 CC peritoneal neutrophils and used as a source of poly(A)+ RNA, to
 CC produce a rabbit neutrophil cDNA library. 250,000 recombinant
 CC plaques were screened for those which hybridized to an antisense
 CC oligonucleotide (Q30015). This probe was designed based on the
 CC sequence derived from the second transmembrane domain of G-protein-
 CC coupled receptors. After tertiary screening, six plaques were
 CC isolated. The insert of one of these plaques, termed F3R was of 2.5
 CC kb in size. This insert was sequenced. The protein deduced from
 CC the F3R clone demonstrates that it belongs to the family of
 CC G-protein-coupled receptors. The deduced protein sequence
 CC indicates seven putative transmembrane segments. A human
 CC peripheral blood leukocyte lambda gt10 cDNA library (5' stretch) was
 CC screened with a 652 bp EcoRI/BamHI fragment (including nucleotides
 CC -27 to 625) of the rabbit F3R clone. After tertiary screening
 CC several human clones which hybridized to the rabbit IL-8 probe
 CC were isolated. The insert of one such clone, termed 4AB was
 CC sequenced (Q30012).

XX SQ Sequence 360 AA;

XX 04-APR-1993 (first entry)
 XX Sequence in a low affinity recombinant rabbit interleukin-8
 DE (IL-8) receptor polypeptide in 5bla.
 XX IL-8 receptor polypeptide; G-protein-coupled receptor.
 KW Oryctolagus cuniculus.
 XX WO9218641-A.
 XX 29-OCT-1992.
 XX 10-APR-1992; 92WO-US02977.
 XX 10-APR-1991; 91US-0685101.
 PR 09-JUL-1991; 91US-0726606.
 PR 09-DEC-1991; 91US-0803842.
 XX (REPK) REPLIGEN CORP.
 PA (UYBO-) UNIV BOSTON.
 XX Navarro J, Thomas KM, Witt DP;
 PI WPI; 1992-382123/46.
 DR N-PSDB; Q30013.
 XX Recombinant mammalian interleukin-8 receptor - used for screening
 PT interleukin-8 binding antagonists, used to treat inflammation
 XX Claim 4; Fig 9; 71pp; English.
 XX Rabbit high affinity IL-8 receptor gene was isolated from rabbit
 CC peritoneal neutrophils and used as a source of poly(A)+ RNA, to
 CC produce a rabbit neutrophil cDNA library. 250,000 recombinant
 CC plaques were screened for those which hybridized to an antisense
 CC oligonucleotide (Q30015). This probe was designed based on the
 CC sequence derived from the second transmembrane domain of G-protein-
 CC coupled receptors. After tertiary screening, six plaques were
 CC isolated. The insert of one of these plaques, termed F3R was of 2.5
 CC kb in size. This insert was sequenced. The protein deduced from
 CC the F3R clone demonstrates that it belongs to the family of
 CC G-protein-coupled receptors. The deduced protein sequence
 CC indicates seven putative transmembrane segments. Using the methods
 CC described above, a cDNA encoding the rabbit low affinity IL-8
 CC receptor was also identified and isolated from the rabbit neutrophil
 CC library. This cDNA was subcloned into the EcoRI site of pUC19 to
 CC produce plasmid 5bla. Its nucleic acid sequence was determined by
 CC standard techniques and found to be similar, but not identical, to the
 CC high affinity receptor clone F3R.
 XX Sequence 358 AA;
 SQ

Query Match 44.2%; Score 57; DB 13; Length 358;
 Best Local Similarity 47.6%; Pred. No. 0.46;
 Matches 10; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 QY 6 KIICLVWGLSVIISSSTFFV 26
 DB 161 kfcismwgvslslp1llf 181

RESULT 14
 R80952
 ID R80952 standard; Protein; 358 AA.
 XX R80952;
 XX 24-APR-1996 (first entry)
 XX Recombinant high affinity interleukin-8 receptor subtype B.
 DE

Query Match 44.2%; Score 57; DB 16; Length 358;
 Best Local Similarity 47.6%; Pred. No. 0.46;
 Matches 10; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 QY 6 KIICLVWGLSVIISSSTFFV 26
 DB 161 kfcismwgvslslp1llf 181

RESULT 15
 W97784
 ID W97784 standard; Protein; 342 AA.
 XX W97784;
 AC W97784;
 XX 21-MAY-1999 (first entry)
 XX African green monkey HIV/SIV receptor protein Bonzo.
 XX SIV receptor; HIV receptor; Bonzo; translocation promoting agent;
 KW G protein coupled receptor; chemokine receptor; AIDS; infection;
 KW virus transmission; African green monkey.
 XX Cercopithecus aethiops.
 OS WO9903888-A1.
 XX 28-JAN-1999.
 PD

IL-8A; IL-8B; receptor; monoclonal antibody; inflammatory disorder;
 KW anaphylaxis; systemic lupus erythematosus; rheumatoid arthritis;
 KW systemic necrotizing vasculitis; psoriasis; asthma; allergy; ARDS;
 KW adult respiratory distress syndrome; neutrophil detection.
 XX Oryctolagus cuniculus.
 OS WO9525126-A1.
 XX 21-SEP-1995.
 XX 09-MAR-1995; 95WO-US03032.
 XX 02-MAY-1994; 94US-0237937.
 PR 15-MAR-1994; 94US-0210250.
 XX (REPK) REPLIGEN CORP.
 PA (UYBO-) UNIV BOSTON.
 XX Greenfield EA, Larosa GJ, Navarro J, Thomas KM,
 PI Witt DT;
 PI WPI; 1995-336945/43.
 DR N-PSDB; Q99951.
 XX Monoclonal antibody against recombinant IL-8 receptor polypeptide -
 PT useful for treating inflammatory disorders, for detecting
 PT neutrophil(s) and for isolating IL-8 receptor from liq.mixt.
 XX Claim 6; Fig 3A-B; 74pp; English.
 PS Monoclonal antibodies were raised against recombinant interleukin-8
 CC (IL-8) receptor subtypes A and B from both human and rabbit sources
 CC (R80950-53 encoded by Q99949-52). The A subtype receptor (IL-8A) is
 CC a high affinity receptor and the B subtype receptor (IL-8B) is a
 CC low affinity receptor. The monoclonal antibody (mAb) pref. binds to
 CC the IL-8 binding domain thus blocking its activation. The mAbs are
 CC useful for treating inflammatory disorders (see key words) and for
 CC detecting the presence of neutrophils in a biological sample. The
 CC mAbs are also useful in the isolation of IL-8 receptors from a mixture.
 XX Sequence 358 AA;
 SQ

```

XX 17-JUL-1998; 98WO-US14857.
XX
XX 17-JUL-1997; 97US-0896155.
XX
XX (UYNV ) UNIV NEW YORK STATE.
XX
XX Deng H, Kewalramani VN, Littman DR, Unutmaz D;
XX
XX WPI; 1999-132164/11.
XX
XX N-PSDB; X07290.
XX
XX New nucleic acid encoding the human translocation promoter Bonzo -
XX used to screen for potential agents for treating acquired immune
XX deficiency syndrome
XX
XX Disclosure; Page 80-81; 97pp; English.
XX
XX This is the amino acid sequence of African green monkey Bonzo, a
XX novel HIV/SIV translocation promoting agent that acts in conjunction
XX with CD4 to serve as a receptor for the entry into a cell of a virus
XX having a specific viral envelope glycoprotein. Bonzo is a member of
XX the 7-transmembrane G-protein coupled receptor family, is closely
XX related to the chemokine receptor family, and is expressed in
XX lymphoid tissues. The invention provides the amino acid sequences
XX (see W97783-88) and DNA sequences (see X07289-94) of human,
XX African green monkey and pig-tailed macaque Bonzo and Bob (brother
XX of Bonzo) translocation promoting agents. These novel receptors
XX were identified using an expression cloning strategy. They were
XX found to be used by particular strains of HIV-2 and M-tropic HIV-1.
XX The invention also includes: mammalian cells transfected with Bonzo
XX and/or Bob and human CD4, which can be used to screen potential
XX therapeutic agents and identify ligands; antibodies to Bonzo, which
XX can be used therapeutically, e.g. as antagonists or to target
XX toxins or radioisotopes to HIV-permissive cells; transgenic
XX animals; and antisense and ribozyme molecules, which may also be
XX used therapeutically, particularly expressed from a gene therapy
XX vector.
XX
XX Sequence 342 AA;
XX
Query Match 42.6%; Score 55; DB 20; Length 342;
Best Local Similarity 33.3%; Pred. NO. 0.9;
Matches 7; Conservative 9; Mismatches 5; Indels 0; Gaps 0;
QY 6 KIICLVWGLSVIISSTFVF 26
Db 149 kvicllwvslslvslpqiyl 169

```

Search completed: May '23, 2001, 15:28:29
Job time: 406 sec

RESULT 2
US-08-118-270-38
; Sequence 38, Application US/08118270
; Patent No. 5508384
; GENERAL INFORMATION:
; APPLICANT: Murphy, Randall B.
; APPLICANT: Schuster, David I.
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 09-SEP-1993
; APPLICATION NUMBER: US/08/118,270
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY-2A
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-118-270-38

Query Match 45.0%; Score 58; DB 1; Length 312;
Best Local Similarity 42.9%; Pred. No. 0.2;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 6 KIICLVWGLSVIISSSTFVF 26
| | | | : | | | : | | : |
Db 115 KFCILSINGLSLLALPVLFF 135

RESULT 3
PCT-US93-08528-38
; Sequence 38, Application PC/TUS9308528
; GENERAL INFORMATION:
; APPLICANT: New York University
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 19910913
; APPLICATION NUMBER: US/07/759,568
; FILING DATE: 19910913
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Scott, Watson T.
; REGISTRATION NUMBER: 26581
; REFERENCE/DOCKET NUMBER: WTS/5683/91535/WB
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 cush
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08528
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US93-08528-38

Query Match 45.0%; Score 58; DB 5; Length 312;
Best Local Similarity 42.9%; Pred. No. 0.2;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 6 KIICLVWGLSVIISSSTFVF 26
| | | | : | | | : | | : |
Db 115 KFCILSINGLSLLALPVLFF 135

RESULT 4
US-07-759-568-1
; Sequence 1, Application US/07759568
; Patent No. 5374506
; GENERAL INFORMATION:
; APPLICANT: Murphy, Philip M.
; TITLE OF INVENTION: Cloning of cDNA Encoding a Functional
; TITLE OF INVENTION: Human Interleukin-8 Receptor
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cushman, Darby & Cushman
; STREET: 1615 L Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/759,568
; FILING DATE: 19910913
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Scott, Watson T.
; REGISTRATION NUMBER: 26581
; REFERENCE/DOCKET NUMBER: WTS/5683/91535/WB
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 cush
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids

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;
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-759-568-1

Query Match 45.0%; Score 58; DB 1; Length 355;
Best Local Similarity 42.9%; Pred. No. 0.23;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 6 KIICLVWGLSVIISSTFFV 26
| ||| :||||: :|
Db 158 KFICLSIWGLSLLLALPVL 178

RESULT 5
US-08-450-393A-8
; Sequence 8, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cseri, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816COOLEYPA
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-450-393A-8

Query Match 45.0%; Score 58; DB 1; Length 355;
Best Local Similarity 42.9%; Pred. No. 0.23;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 6 KIICLVWGLSVIISSTFFV 26
| ||| :||||: :|
Db 158 KFICLSIWGLSLLLALPVL 178

RESULT 6
US-08-390-000A-5
; Sequence 5, Application US/08390000A
; Patent No. 5985583
; GENERAL INFORMATION:
; APPLICANT: Sealton, Stuart C.
; TITLE OF INVENTION: Cloning and Expression of
; TITLE OF INVENTION: Gonadotropin-Releasing Hormone Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,000A
; FILING DATE: 17-FEB-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6923-052
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-390-000A-5

Query Match 45.0%; Score 58; DB 2; Length 355;
Best Local Similarity 42.9%; Pred. No. 0.23;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 6 KIICLVWGLSVIISSTFFV 26
| ||| :||||: :|
Db 158 KFICLSIWGLSLLLALPVL 178

RESULT 7
US-08-446-669-8
; Sequence 8, Application US/08446669
; Patent No. 6132987
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,669
; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
```

ATTORNEY/AGENT INFORMATION:
NAME: Neeley, Richard
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: UCAL-237/01US
TELEPHONE: 415-843-5000
TELEFAX: 415-857-0663
TELEX: 380816CoolepA
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-446-669-8

Query Match 45.0%; Score 58; DB 4; Length 355;
Best Local Similarity 42.9%; Pred. No. 0.23;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 6 KIICLVWGLSVIISSSTFFV 26
Db 158 KFICLSIWGLSLLLALPVL 178

RESULT 8
PCT-US95-00476-8
Sequence 8, Application PC/TUS9500476
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins, Berliner & Carson
STREET: 201 N. Figueroa Street, 5th Floor
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90012-2628
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00476
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Berliner, Robert
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 5555-291
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-977-1001
TELEFAX: 310-977-1003
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
PCT-US95-00476-8

Query Match 45.0%; Score 58; DB 5; Length 355;
Best Local Similarity 42.9%; Pred. No. 0.23;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 6 KIICLVWGLSVIISSSTFFV 26
Db 158 KFICLSIWGLSLLLALPVL 178

RESULT 9
US-08-202-056-7
Sequence 7, Application US/08202056
Patent No. 5440021
GENERAL INFORMATION:
APPLICANT: Chuntharapai, Anan
APPLICANT: Hebert, Caroline
APPLICANT: Kim, Kyung Jin
APPLICANT: Lee, James
TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,056
FILING DATE: 25-FEB-1994
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-202-056-7

Query Match 45.0%; Score 58; DB 1; Length 360;
Best Local Similarity 42.9%; Pred. No. 0.24;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 6 KIICLVWGLSVIISSSTFFV 26
Db 163 KFICLSIWGLSLLLALPVL 183

RESULT 10
US-08-709-838-2
Sequence 2, Application US/08709838
Patent No. 6140064
GENERAL INFORMATION:
APPLICANT: Loetscher, Marcel
APPLICANT: Moser, Bernhard
TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
NUCLEIC ACIDS, AND METHODS OF USES THEREFOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive

;; CITY: Lexington
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02173
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/709,838
;; FILING DATE:
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Brook Esq., David E.
;; REGISTRATION NUMBER: 22,592
;; REFERENCE/DOCKET NUMBER: TK196-01
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 861-6240
;; TELEFAX: (617) 861-9540
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 368 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-709-838-2

Query Match 42.6%; Score 55; DB 4; Length 368;
Best Local Similarity 39.1%; Pred. No. 0.7;
Matches 9; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 4 RSKIIICLVVWGLSVIISSTFVF 26
| : || |||| : : ||
Db 167 RVTLTCLAVWGLCLLFPALPDFIF 189

RESULT 11
US-08-829-839-2
; Sequence 2, Application US/08829839
; Patent No. 6184358
; GENERAL INFORMATION:
; APPLICANT: Loetscher, Marcel
; APPLICANT: Moser, Bernhard
; APPLICANT: Qin, Shixin
; APPLICANT: Mackay, Charles R.
; TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
; TITLE OF INVENTION: ANTIBODIES, NUCLEIC ACIDS, AND METHODS OF USE THEREFOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,839
; FILING DATE: 31-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/709,838
; FILING DATE: 10-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook Esq., David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: TK196-01A

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 861-6240
;; TELEFAX: (617) 861-9540
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 368 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-829-839-2

Query Match 42.6%; Score 55; DB 4; Length 368;
Best Local Similarity 39.1%; Pred. No. 0.7;
Matches 9; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 4 RSKIIICLVVWGLSVIISSTFVF 26
| : || |||| : : ||
Db 167 RVTLTCLAVWGLCLLFPALPDFIF 189

RESULT 12
US-08-202-056-1
; Sequence 1, Application US/08202056
; Patent No. 5440021
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Hebert, Caroline
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Lee, James
; TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,056
FILING DATE: 25-FEB-1994
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-202-056-1

Query Match 41.9%; Score 54; DB 1; Length 350;
Best Local Similarity 47.6%; Pred. No. 0.93;
Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 6 KIICLVVWGLSVIISSTFVF 26
| : || |||| : : ||

Db 154 KVCGLGCGWGLSMNLSLPFLF 174

RESULT 13

US-08-076-093A-2 ; Sequence 2, Application US/08076093A
; Patent No. 5543503
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: Jin Kim, K.
; TITLE OF INVENTION: Antibodies to Human PF4A Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/076,093A
; FILING DATE: 11-Jun-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/677211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 706P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-076-093A-2

Query Match 41.9%; Score 54; DB 1; Length 350;
Best Local Similarity 47.6%; Pred. No. 0.93;
Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 6 KIICLVVWGLSVIISSSTFVF 26
| : || |||| : | : |
Db 154 KVCGLGCGWGLSMNLSLPFLF 174

RESULT 15

US-08-410-453A-1
; Sequence 1, Application US/08410453A
; Patent No. 5767063
; GENERAL INFORMATION:
; APPLICANT: Lee, James,
; APPLICANT: Holmes, William E.,
; APPLICANT: Woods, William I.
; TITLE OF INVENTION: Human PF4A Receptors and Their Use
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,453A
; FILING DATE: 24-Mar-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/234494
; FILING DATE: 28-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/677211

Db 154 KVCGLGCGWGLSMNLSLPFLF 174

RESULT 14

US-08-450-393A-7
; Sequence 7, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum

QY 6 KIICLVVWGLSVIISSSTFVF 26
| : || |||| : | : |
Db 154 KVCGLGCGWGLSMNLSLPFLF 174

Query Match 41.9%; Score 54; DB 1; Length 350;
Best Local Similarity 47.6%; Pred. No. 0.93;
Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 6 KIICLVVWGLSVIISSSTFVF 26
| : || |||| : | : |
Db 154 KVCGLGCGWGLSMNLSLPFLF 174

STREET: 5 Palo Alto Square
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,393A
FILING DATE: May 25, 1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: UCAL-237/020US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5165
TELEFAX: 415-8857-0663
TELEX: 380816CooLevPA
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-450-393A-7

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; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-410-453A-1

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Query Match      41.98; Score 54; DB 1; Length 350;
Best Local Similarity 47.6%; Pred. No. 0.93;
Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

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QY      6 KIICLVVWGLSVIISSSTVF 26
       1:|||||:|:|
Db     154 KVCICGCGLSMNLSPFLF 174

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Search completed: May 23, 2001, 15:30:06
Job time: 413 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 23, 2001, 15:32:00 ; Search time 110.15 seconds
(without alignments)
16.221 Million cell updates/sec

Title: US-08-887-977-10_COPY_151_176

Perfect score: 129

Sequence: 1 TLPRSKIICLVWGLSVIISSSTFEV 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_67: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	129	100.0	369	2 JC5068	G protein-coupled
2	60	46.5	354	2 A23669	interleukin-8 rece
3	60	46.5	355	2 JQ1231	interleukin-8 rece
4	58	45.0	360	2 A53611	interleukin-8 rece
5	58	45.0	371	2 G69827	conserved hypothet
6	57	44.2	358	2 A53752	interleukin-8 rece
7	55	42.6	364	2 JQ1488	bradykinin B2 rece
8	55	42.6	366	2 I49519	bradykinin B2 rece
9	54	41.9	360	2 A39445	interleukin-8 rece
10	54	41.9	357	2 JE0349	interferon-inducib
11	51	39.5	350	1 A37963	complement C5a ana
12	51	39.5	356	2 S42096	interleukin-8 rece
13	49	38.0	325	1 TVHUAS	transforming prote
14	49	38.0	366	1 OORTB2	bradykinin recepto
15	49	38.0	369	2 S48332	probable membrane
16	49	38.0	1515	2 T52081	MRP-like ABC trans
17	48	37.2	346	2 S10188	NADH dehydrogenase
18	48	37.2	483	2 A25896	beta-adrenergic re
19	47	36.4	305	2 B33465	11c-1 protein B -
20	47	36.4	324	1 TVRTAS	transforming prote
21	47	36.4	355	2 G02436	chemokine (C-C) re
22	47	36.4	357	2 S28058	serotonin receptor
23	47	36.4	357	2 B47472	5-hydroxytryptamin
24	47	36.4	359	2 S44425	angiotensin II rec
25	47	36.4	415	2 T35834	probable transcrip
26	47	36.4	425	2 A37912	thrombin receptor
27	47	36.4	427	2 S17148	alpha-thrombin rec
28	47	36.4	1027	2 T46481	hypothetical prote
29	47	36.4	1102	2 JC6316	probable protein k.

30 47 36.4 1233 2 T30989
31 46.5 36.0 315 2 S25581
32 46.5 36.0 419 2 T3272
33 46.5 36.0 905 2 T40015
34 46 35.7 279 2 B71894
35 46 35.7 334 2 JC4681
36 46 35.7 359 2 A48921
37 46 35.7 734 2 B83405
38 46 35.7 875 1 A57080
39 45.5 35.3 369 2 B41795
40 45 34.9 116 2 E71202
41 45 34.9 247 2 S42739
42 45 34.9 354 2 I58186
43 45 34.9 359 2 S15403
44 45 34.9 378 2 A39485
45 45 34.9 449 1 NBHUHS

ALIGNMENTS

RESULT 1

JC5068

G protein-coupled receptor CKR-L3 - human

C:Species: Homo sapiens (man)

C>Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000

C:Accession: JC5068

R:Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.

Biochem. Biophys. Res. Commun. 227, 846-853, 1996

A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-lik

A:Reference number: JC5067; MUID:97040707

A:Accession: JC5068

A:Molecule type: DNA

A:Residues: 1-369 <ZAB>

A:Cross-references: EMBL:279784; NID:gl668737; PIDN:CAB02144.1; PID:gl668738

C:Comment: This protein belongs to the family of alpha chemokine receptors.

C:Genetics:

A:Gene: GDB:CMKBR6; SVRL22: GPR29; CCR6: CKR-L3; GPR-CY4

A:Cross-references: GDB:5370839; OMIM:601835

A:Map position: 6q27-6q27

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

F:42-68/Domain: transmembrane #status predicted <TM1>

F:79-99/Domain: transmembrane #status predicted <TM2>

F:115-135/Domain: transmembrane #status predicted <TM3>

F:160-180/Domain: transmembrane #status predicted <TM4>

F:212-233/Domain: transmembrane #status predicted <TM5>

F:250-271/Domain: transmembrane #status predicted <TM6>

F:292-315/Domain: transmembrane #status predicted <TM7>

Query Match 100.0%; Score 129; DB 2; Length 369;
Best Local Similarity 100.0%; Pred. No. 1.9e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLPRSKIICLVWGLSVIISSSTFEV 26

DB 155 TLPRSKIICLVWGLSVIISSSTFEV 180

RESULT 2

A23669

Interleukin-8 receptor, high affinity - rabbit

N:Alternate names: fMLP receptor

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 05-Nov-1999

C:Accession: A23669

R:Thomas, K.M.; Pyun, H.Y.; Navarro, J.

J. Biol. Chem. 265, 20061-20064, 1990

A:Title: Molecular cloning of the fMet-Leu-Phe receptor from neutrophils.

A:Reference number: A23669; MUID:91056034

A:Accession: A23669

A:Molecule type: mRNA

QY 4 RSKIIICLVWGLSVIISSSTVF 26
| | | | | : : : : :
Db 96 RSLIVALLCWGLCNLTATSSRF 118

RESULT 6

A53752
Interleukin-8 receptor (clone 5Bla) - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: A53752
R:Prado, G.N.; Thomas, K.M.; Suzuki, H.; LaRosa, G.J.; Wilkinson, N.; Folco, E.; Navarro
J. Biol. Chem. 269, 12391-12394, 1994
A:Title: Molecular characterization of a novel rabbit interleukin-8 receptor isotype.
A:Reference number: A53752; MUID:94230294
A:Accession: A53752
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-358 <PRA>
A:Cross-references: GB:L24445; NID:g437661; PIDN:AAA31378.1; PID:g437662
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 44.2%; Score 57; DB 2; Length 358;
Best Local Similarity 47.6%; Pred. No. 0.66;
Matches 10; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 6 KIICLVWGLSVIISSSTVF 26
| | | | | : : : : :
Db 161 KFICLMMGVSLILSLPLLF 181

RESULT 7

JQ1488
bradykinin B2 receptor - human
C:Species: Homo sapiens (man)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 13-Aug-1999
C:Accession: JQ1488; A46022; A55559; JQ1488; JQ1400
R:Eggerickx, D.; Raspe, E.; Bertrand, D.; Vassart, G.; Parmentier, M.
Biochem. Biophys. Res. Commun. 187, 1306-1313, 1992
A:Title: Molecular cloning, functional expression and pharmacological characterization of
A:Reference number: JQ1488; MUID:93038601
A:Accession: JQ1488
A:Molecule type: DNA
A:Residues: 1-364 <EGG>
A:Cross-references: GB:S45489; NID:g256536; PIDN:AAB23467.1; PID:g256537
R:Powell, S.J.; Slyn, G.; Thomas, C.; Hopkins, B.; Briggs, I.; Graham, A.
Genomics 15, 435-438, 1993
A:Title: Human bradykinin B2 receptor: nucleotide sequence analysis and assignment to ch
A:Reference number: A46022; MUID:93194199
A:Accession: A46022
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-364 <POW>
A:Cross-references: GB:S56772; NID:g298604; PIDN:AAB25765.1; PID:g298605
A:Note: sequence extracted from NCBI backbone (NCBI:127280, NCBIP:127284)
R:Ma, J.; Wang, D.; Ward, D.C.; Chen, L.; Dessai, T.; Chao, J.; Chao, L.
Genomics 23, 362-369, 1994
A:Title: Structure and chromosomal localization of the gene (BDKRB2) encoding human brad
A:Reference number: A55559; MUID:95137582
A:Accession: A55559
A:Molecule type: DNA
A:Residues: 1-364 <MAA>
A:Cross-references: GB:L27594
R:Hess, J.F.; Borkowski, J.A.; Young, G.S.; Strader, C.D.; Ransom, R.W.
Biochem. Biophys. Res. Commun. 184, 260-268, 1992
A:Title: Cloning and pharmacological characterization of a human bradykinin (BK-2) recep
A:Reference number: JQ1488; MUID:92231936
A:Accession: JQ1488
A:Molecule type: mRNA
A:Residues: 1-364 <HES>

A:Cross-references: GB:M88714; NID:g1387999; PIDN:AAB02793.1; PID:g1388000
C:Genetics:
A:Gene: GDB:BDKRB2
A:Cross-references: GDB:135713; OMIM:113503
A:Map position: 14q32.1-14q32.2
A:Introns: #status absent
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane p
F:34-56/Domain: transmembrane #status predicted <TM1>
F:66-92/Domain: transmembrane #status predicted <TM2>
F:104-127/Domain: transmembrane #status predicted <TM3>
F:148-171/Domain: transmembrane #status predicted <TM4>
F:195-221/Domain: transmembrane #status predicted <TM5>
F:241-266/Domain: transmembrane #status predicted <TM6>
F:285-309/Domain: transmembrane #status predicted <TM7>
F:3, 12, 180/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:170, 237, 342/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status
F:242/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predi
F:316/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predi

Query Match 42.6%; Score 55; DB 2; Length 364;
Best Local Similarity 40.9%; Pred. No. 1.3;
Matches 9; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 5 SKIICLVWGLSVIISSSTVF 26
| | | | | : : : : :
Db 147 AKLYSLVWGCTLLSSPMLVF 168

RESULT 8

I49519
bradykinin B2 receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C:Accession: I49519; I49525; I48270; JC2187
R:Hess, J.F.; Borkowski, J.A.; MacNeil, T.; Stonesifer, G.Y.; Fraher, J.; Strader, C.
Mol. Pharmacol. 45, 1-8, 1994
A:Title: Differential pharmacology of cloned human and mouse B2 bradykinin receptors.
A:Reference number: I49519; MUID:94134047
A:Accession: I49519
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-366 <HES>
A:Cross-references: GB:L26047; NID:g415711; PIDN:AAA19797.1; PID:g415712
R:Ma, J.X.; Wang, D.Z.; Chao, L.; Chao, J.
Gene 149, 283-289, 1994
A:Title: Cloning, sequence analysis and expression of the gene encoding the mouse bra
A:Reference number: I49525; MUID:95047489
A:Accession: I49525
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-271, 'A', 273-366 <MAJ>
A:Cross-references: GB:L27595; NID:g508524; PIDN:AAA62616.1; PID:g691756
A:Note: in GenBank entry MUSBB2R, release 106.0, the source is designated as Mus musc
R:McIntyre, P.; Phillips, E.; Skidmore, E.; Brown, M.; Webb, M.
Mol. Pharmacol. 44, 346-355, 1993
A:Title: Cloned murine bradykinin receptor exhibits a mixed B1 and B2 pharmacological
A:Reference number: I48270; MUID:93360929
A:Accession: I48270
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-271, 'A', 273-366 <MCI>
A:Cross-references: EMBL:X69676; NID:g440551; PIDN:CAA49357.1; PID:g440552
A:Note: submitted to the EMBL/GenBank/DBJ databases December 1992; this sequence has
R:McIntyre, P.; Phillips, E.; Skidmore, E.; Brown, M.; Webb, M.
Mol. Pharmacol. 45, 561, 1994
A:Reference number: A58857
A:Contents: annotation; erratum; sequence correction
A:Note: submitted to the EMBL/GenBank/DBJ databases January 1994
R:Yokoyama, S.; Kimura, Y.; Taketo, M.; Black, J.A.; Ransom, B.R.; Higashida, H.
Biochem. Biophys. Res. Commun. 200, 634-641, 1994
A:Title: B2 bradykinin receptors in NG108-15 cells: cDNA cloning and functional expre

A:Molecule type: DNA
A:Residues: 1-325 <YOU>
A:Cross-references: GB:M13150; NID:g187388; PIDN:AAA36199.1; PID:g307158
C:Genetics:
A:Gene: GDB:MAS1
A:Cross-references: GDB:l20166; OMIM:165180
C:Map position: 6q24-6q27
C:Superfamily: mas transforming protein
C:Keywords: G protein-coupled receptor; glycoprotein; proto-oncogene; transforming pr
F:31-61/Domain: transmembrane #status predicted <TM1>
F:66-97/Domain: transmembrane #status predicted <TM2>
F:105-135/Domain: transmembrane #status predicted <TM3>
F:150-172/Domain: transmembrane #status predicted <TM4>
F:186-214/Domain: transmembrane #status predicted <TM5>
F:225-250/Domain: transmembrane #status predicted <TM6>
F:258-286/Domain: transmembrane #status predicted <TM7>
F:5,16,22,272/Binding site: carbohydrate (Asn) #status predicted

Query Match 38.0%; Score 49; DB 1; Length 325;
Best Local Similarity 27.3%; Pred. No. 9;
Matches 6; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 4 RSKIIIVVWGLSVIISSTFV 25
:|:::|:::|
Db 148 QSALVCALLWALSCLVTTMEYV 169

RESULT 14
OORTE2
bradykinin receptor type B-2 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1992 #sequence-revision 30-Sep-1992 #text_change 22-Jun-1999
C:Accession: A41283 #55079; S47529
R:McEachern, A.E.; Shelton, E.R.; Bhakta, S.; Obernolte, R.; Bach, C.; Zuppan, P.; Fu
Proc. Natl. Acad. Sci. U.S.A. 88, 7724-7728, 1991
A:Title: Expression cloning of a rat B-2 bradykinin receptor.
A:Reference number: A41283; MUID:91352062
A:Accession: A41283
A:Molecule type: mRNA
A:Residues: 1-366 <MCE>
A:Cross-references: GB:M59967
R:Pesquero, J.B.; Lindsey, C.J.; Zeh, K.; Paiva, A.C.M.; Ganten, D.; Bader, M.
J. Biol. Chem. 269, 26920-26925, 1994
A:Title: Molecular structure and expression of rat bradykinin B2 receptor gene. Evid
A:Reference number: A55079; MUID:95014558
A:Accession: A55079
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-75, 'A', 77-366 <PES>
A:Cross-references: GB:X80187; GB:X80188; GB:X80189; GB:X80190
R:Wang, D.; Ma, J.; Chao, L.; Chao, J.
Biochim. Biophys. Acta 1219, 171-174, 1994
A:Title: Molecular cloning and sequence analysis of rat bradykinin B(2) receptor gene
A:Reference number: S47529; MUID:94368850
A:Accession: S47529
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-366 <WAN>
A:Cross-references: EMBL:L26173; NID:g476749; PIDN:AAA62492.1; PID:g685244
C:Comment: This G protein-coupled receptor binds the nonapeptide bradykinin.
C:Superfamily: vertebrate rhodopsin
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; lipoprote
F:31-48/Domain: transmembrane #status predicted <TM1>
F:79-96/Domain: transmembrane #status predicted <TM2>
F:107-126/Domain: transmembrane #status predicted <TM3>
F:154-170/Domain: transmembrane #status predicted <TM4>
F:197-215/Domain: transmembrane #status predicted <TM5>
F:245-261/Domain: transmembrane #status predicted <TM6>
F:3,14,182/Binding site: carbohydrate (Asn) #status predicted
F:105-186/Disulfide bonds: #status predicted
F:326/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 38.0%; Score 49; DB 1; Length 366;
 Best Local Similarity 36.4%; Pred. No. 10;
 Matches 8; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 5 SKIICLVWGLSVIISSTFVF 26
 DB 149 AKLYSLVWISCTLLSSPMLVF 170

RESULT 15

S48332
 probable membrane protein YML066c - yeast (Saccharomyces cerevisiae)
 C:Species: Saccharomyces cerevisiae
 C:Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 04-Mar-2000
 C:Accession: S48332
 R: Bowman, S.: Church, C.
 submitted to the EMBL Data Library, August 1994
 A:Reference number: S48326
 A:Accession: S48332
 A:Molecule type: DNA
 A:Residues: 1-369 <BOW>
 A:Cross-references: EMBL:Z38114; NID:g558402; PID:g558409; GSPDB:GN00013; MIPS:YML066c
 C:Genetics:
 A:Gene: MIPS:YML066c
 A:Map position: 13L
 C:Superfamily: Saccharomyces cerevisiae probable membrane protein YML066c
 C:Keywords: transmembrane protein
 F:7-23/Domain: transmembrane #status predicted <TM1>
 F:209-225/Domain: transmembrane #status predicted <TM2>
 F:226-242/Domain: transmembrane #status predicted <TM3>
 F:267-283/Domain: transmembrane #status predicted <TM4>
 F:324-340/Domain: transmembrane #status predicted <TM5>

Query Match 38.0%; Score 49; DB 2; Length 369;
 Best Local Similarity 56.2%; Pred. No. 10;
 Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 10 LVVWGLSVIISSTFV 25
 DB 7 LIVWGVLLILSLSQFV 22

Search completed: May 23, 2001, 15:32:01
 Job time: 508 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:36:18 ; Search time 62.39 Seconds
(without alignments)
14.275 Million cell updates/sec

Title: US-08-887-977-10_COPY_151_176
Perfect score: 129
Sequence: 1 TLPKSKIIICLVVWGLSVISSTFVF 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34253486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	129	100.0	374	1	CKR6_HUMAN
2	90	69.8	367	1	CKR6_MOUSE
3	64	49.6	356	1	IL8B_CANFA
4	63	48.8	360	1	IL8B_BOVIN
5	61	47.3	350	1	IL8A_GORGO
6	60	46.5	355	1	IL8A_RABIT
7	58	45.0	353	1	IL8B_GORGO
8	58	45.0	353	1	IL8B_MACMU
9	58	45.0	353	1	IL8B_PANTR
10	58	45.0	360	1	IL8B_HUMAN
11	58	45.0	371	1	YHDY_BACSU
12	57	44.2	358	1	IL8B_RABIT
13	55	42.6	342	1	BONZ_CERAE
14	55	42.6	342	1	BONZ_MACNE
15	55	42.6	343	1	BONZ_MACMU
16	55	42.6	367	1	BRB2_RABIT
17	55	42.6	368	1	CCR3_HUMAN
18	55	42.6	372	1	BRB2_CAVPO
19	55	42.6	391	1	BRB2_HUMAN
20	54	42.6	392	1	BRB2_MOUSE
21	54	41.9	349	1	IL8A_RAT
22	54	41.9	350	1	IL8A_HUMAN
23	54	41.9	350	1	IL8A_PANTR
24	54	41.9	367	1	CCR3_MOUSE
25	51	39.5	340	1	C5AR_GORGO
26	51	39.5	340	1	C5AR_MACMU
27	51	39.5	340	1	C5AR_PANTR
28	51	39.5	340	1	C5AR_PONPY
29	51	39.5	350	1	C5AR_HUMAN
30	51	39.5	359	1	CCR3_CERAE
31	51	39.5	359	1	IL8B_RAT
32	50	38.8	371	1	CH23_HUMAN
33	50	38.8	373	1	CML1_HUMAN

34	49	38.0	325	1	MAS_HUMAN	P04201 homo sapien
35	49	38.0	369	1	YMG6_YEAST	Q04658 saccharomyc
36	49	38.0	382	1	CRH2_MOUSE	Q92316 mus musculus
37	49	38.0	396	1	BRB2_RAT	P25023 rattus norv
38	48	37.2	346	1	NU2M_CHICK	P18937 gallus gall
39	48	37.2	477	1	OAR_HELVI	Q25188 heliothis v
40	48	37.2	483	1	BIAR_MELGA	P07700 meleagris g
41	47	36.4	292	1	LICB_HAFIN	P14182 haemophilus
42	47	36.4	324	1	MAS_RAT	P12526 rattus norv
43	47	36.4	355	1	CCR3_HUMAN	P51677 homo sapien
44	47	36.4	355	1	CCR3_MACMU	P56483 macaca mula
45	47	36.4	357	1	5H5A_MOUSE	P30966 mus musculus

ALIGNMENTS

RESULT 1	
CKR6_HUMAN	
ID	CKR6_HUMAN STANDARD; PRT; 374 AA.
AC	P51684: Q92846; P78553;
DT	01-OCT-1996 (Rel. 34, Created)
DT	15-JUL-1998 (Rel. 36, Last sequence update)
DT	01-OCT-2000 (Rel. 40, Last annotation update)
DE	C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CC-CKR-6) (CCR-6) (LARC
DE	RECEPTOR) (GPR-CY4) (GPCY4) (CHEMOKINE RECEPTOR-LIKE 3) (CKR-L3)
DE	(DRY6).
GN	CCR6 OR CMKBR6 OR STRL22 OR GPR29 OR CKRL3.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A., AND FUNCTION.
RX	MEDLINE=97313465; PubMed=9169459;
RA	Baba M., Imai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K.,
RA	Nomiyama H., Yoshie O.;
RT	"Identification of CCR6, the specific receptor for a novel
RT	lymphocyte-directed CC chemokine LARC.";
RL	J. Biol. Chem. 272:14893-14898(1997).
RN	[2]
RP	SEQUENCE FROM N.A.
RA	Lautens L.L., Modi W., Bonner T.I.;
RL	Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN	[3]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=97040707; PubMed=8886020;
RA	Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G.;
RT	"Molecular cloning and RNA expression of two new human chemokine
RT	receptor-like genes.";
RL	Biochem. Biophys. Res. Commun. 227:846-853(1996).
RN	[4]
RP	SEQUENCE FROM N.A.
RA	McCoy R., Perlmutter D.H.;
RN	Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RP	SEQUENCE FROM N.A.
RX	MEDLINE=97224503; PubMed=9070937;
RA	Liao F., Lee H.-H., Farber J.M.;
RT	"Cloning of STRL22, a new human gene encoding a G-protein-coupled
RT	receptor related to chemokine receptors and located on chromosome
RT	6q27.";
RL	Genomics 40:175-180(1997).
CC	-!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-
CC	ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE
CC	INTRACELLULAR CALCIUM IONS LEVEL.
CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
CC	LIVER. EXPRESSED IN LYMPHOCYTES, T CELLS AND B CELLS BUT NOT IN
CC	NATURAL KILLER CELLS, MONOCYTES, OR GRANULOCYTES.
CC	-!- INDUCTION: INTERLEUKIN-2.
CC	-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC	-!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-6 IS THE INITIATOR.

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DR EMBL; U45984; AAB62714.1; -
 DR EMBL; 279784; CAB02144.1; ALT_INIT.
 DR EMBL; U60000; AAB06949.1; -
 DR EMBL; U68030; AAC51124.1; -
 DR EMBL; U68032; AAC51125.1; -
 DR HSSP; P34996; 1DDD.
 DR GCRDB; GCR_1037; -
 DR GCRDB; GCR_1075; -
 DR GCRDB; GCR_1906; -
 DR GCRDB; GCR_1919; -
 DR GCRDB; GCR_1941; -
 DR GCRDB; GCR_2110; -
 DR MIM; 601835; -
 DR InterPro; IPR000276; -
 DR Pfam; PF00001; 7tm1.1; -
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G-PROTEIN_RECF_F1_1; 1.
 DR PROSITE; PS0262; G-PROTEIN_RECF_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 47
 FT TRANSMEM 48 74
 FT DOMAIN 75 83
 FT TRANSMEM 84 104
 FT DOMAIN 105 119
 FT TRANSMEM 120 141
 FT DOMAIN 142 159
 FT TRANSMEM 160 180
 FT DOMAIN 181 211
 FT TRANSMEM 212 238
 FT DOMAIN 239 254
 FT TRANSMEM 255 279
 FT DOMAIN 280 303
 FT TRANSMEM 304 321
 FT DOMAIN 322 374
 FT DISULFID 118 197
 FT CARBOHYD 7 7
 FT CARBOHYD 23 23
 FT CONFLICT 60 60
 FT CONFLICT 74 74
 FT CONFLICT 86 86
 FT CONFLICT 164 164
 FT CONFLICT 182 182
 FT CONFLICT 192 192
 FT CONFLICT 206 206
 FT CONFLICT 225 225
 FT CONFLICT 370 374
 FT CONFLICT 374 374
 SQ SEQUENCE 374 AA; 42494 MW; D7F963534E990BC4 CRC64;

Query Match 100.0%; Score 129; DB 1; Length 374;
 Best Local Similarity 100.0%; Pred. No. 1.9e-11;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLPRSKIICLVWGLSVIISSTFFV 26
 |||||
 Db 160 TLPRSKIICLVWGLSVIISSTFFV 185

RESULT 2
 CCR6_MOUSE
 ID CCR6_MOUSE STANDARD: PRT; 367 AA.
 AC O54689;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CCR-6) (KY411).
 GN CCR6 OR CCKBR6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yanagihara S., Komura E., Yamaguchi Y.;
 RT "Mouse G protein-coupled receptor KY411.";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99077268; PubMed=9862452;
 RA Varona R., Zaballos A., Gutierrez J., Martin P., Roncal F.,
 RA Albar J.P., Ardavin C., Marquez G.;
 RT "Molecular cloning, functional characterization and mRNA expression
 RT analysis of the murine chemokine receptor CCR6 and its specific ligand
 RT MIP-3alpha.";
 RL FEBS Lett. 440:188-194(1998).
 CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-
 CC ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE
 CC INTRACELLULAR CALCIUM IONS LEVEL.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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DR EMBL; AB009369; BAA23776.1; -
 DR EMBL; AJ222714; CAA10956.1; -
 DR MGD; MGI:1333797; Cmkbr6.
 DR InterPro; IPR000276; -
 DR Pfam; PF00001; 7tm1.1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G-PROTEIN_RECF_F1_1; 1.
 DR PROSITE; PS0262; G-PROTEIN_RECF_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 39
 FT TRANSMEM 40 66
 FT DOMAIN 67 75
 FT TRANSMEM 76 96
 FT DOMAIN 97 111
 FT TRANSMEM 112 133
 FT DOMAIN 134 151
 FT TRANSMEM 152 172
 FT DOMAIN 173 203
 FT TRANSMEM 204 230
 FT DOMAIN 231 246
 FT TRANSMEM 247 271
 FT DOMAIN 272 295
 FT TRANSMEM 296 313
 FT DOMAIN 314 367
 FT DISULFID 110 189
 FT CARBOHYD 2 2
 FT CARBOHYD 35 35
 FT CONFLICT 367 367
 SQ SEQUENCE 367 AA; 42102 MW; 6A309AF833B1117E CRC64;

Query Match 69.8%; Score 90; DB 1; Length 367;
 Best Local Similarity 61.5%; Pred. No. 7.4e-06;
 Matches 16; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLPRSKIICLVWGLSVIISSTFFV 26
 |||||
 Db 152 TLTHSKVICVAVWFISIISSTFFIF 177

```
RESULT 3
IL8B_CANFA
ID IL8B_CANFA STANDARD; PRT; 356 AA.
AC O97571.
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GRO/MGSA
DE RECEPTOR).
GN IL8RB OR CXCR2.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BEAGLE;
RA Chang Y.F., Novosel V., Chang C.F.;
RT "The isolation and sequence of canine interleukin-8 receptor
RT homolog."
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC !- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC MESSENGER SYSTEM. THE AFFINITY OF THIS RECEPTOR IS IL-8 >> NAP-2 >
CC MGSA (GRO).
CC !- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC !- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL; AF047047; AAC98968.1; -
CC InterPro; IPR000057; -
CC InterPro; IPR000174; -
CC InterPro; IPR000276; -
CC InterPro; IPR000355; -
CC InterPro; IPR001277; -
CC Pfam; PF00001; 7tm1.1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PRINTS; PR00427; INTRLEUKIN8R.
CC PRINTS; PR00573; INTRLEUKIN8R.
CC PRINTS; PR00645; LCRIORPHANR.
CC PRINTS; PR00657; CCHEMOKINR.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Chemotaxis.
CC
CC DOMAIN 1 46 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 47 73 1 (POTENTIAL).
CC DOMAIN 74 82 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 83 103 2 (POTENTIAL).
CC DOMAIN 104 118 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 119 140 3 (POTENTIAL).
CC DOMAIN 141 161 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 162 181 4 (POTENTIAL).
CC DOMAIN 182 206 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 207 229 5 (POTENTIAL).
CC DOMAIN 230 249 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 250 269 6 (POTENTIAL).
CC DOMAIN 270 290 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 291 311 7 (POTENTIAL).
CC DOMAIN 312 356 CYTOPLASMIC (POTENTIAL).
CC CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC TRANSMEM 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC DISULFID 117 194 BY SIMILARITY.
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SQ SEQUENCE 356 AA; 40505 MW; 2B67DD4E8DD39B15 CRC64;
Query Match 49.6%; Score 64; DB 1; Length 356;
Best Local Similarity 57.1%; Pred. No. 0.039;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
OY 6 KIICLVWGLSVIISSTFVF 26
DB 161 KFCICIGWALSLLSLPIEFV 181
RESULT 4
ID IL8B_BOVIN STANDARD; PRT; 360 AA.
AC Q28003;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2).
GN IL8RB OR CXCR2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Li Y., Feng J., Templeton J.W.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
CC !- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
CC AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY (BY
CC SIMILARITY).
CC !- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC !- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL; U19947; AAA84996.1; -
CC GCRDB; GCR 1224; -
CC InterPro; IPR000174; -
CC InterPro; IPR000276; -
CC Pfam; PF00001; 7tm1.1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PRINTS; PR00427; INTRLEUKIN8R.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Chemotaxis.
CC
CC DOMAIN 1 48 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 49 75 1 (POTENTIAL).
CC DOMAIN 76 84 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 85 105 2 (POTENTIAL).
CC DOMAIN 106 120 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 121 142 3 (POTENTIAL).
CC DOMAIN 143 163 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 164 183 4 (POTENTIAL).
CC DOMAIN 184 208 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 209 231 5 (POTENTIAL).
CC DOMAIN 232 251 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 252 273 6 (POTENTIAL).
CC DOMAIN 274 294 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 295 315 7 (POTENTIAL).
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FT	TRANSMEM	112	133	3 (POTENTIAL).
FT	DOMAIN	134	154	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	155	174	4 (POTENTIAL).
FT	DOMAIN	175	199	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	200	220	5 (POTENTIAL).
FT	DOMAIN	221	242	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	243	264	6 (POTENTIAL).
FT	DOMAIN	265	285	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	286	308	7 (POTENTIAL).
FT	DOMAIN	309	350	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	3	3	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	16	16	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	110	187	BY SIMILARITY.
SEQ	SEQUENCE	350 AA;	39790 MW;	DB99591CD6C10757 CRC64;

Query Match 47.3%; Score 61; DB 1; Length 350;
 Best Local Similarity 52.4%; Pred. No. 0.1;
 Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY	6	KIICLVWGLSVIISSSTFVF	26
		:	
Db	154	KFVCLGCGWGLSMILSLPFFLF	174

RESULT 6

IL8A_RABIT	STANDARD;	PRT;	355 AA.
ID	IL8A_RABIT		
AC	P21109;		
DT	01-FEB-1991 (Rel. 17, Created)		
DT	01-MAY-1992 (Rel. 22, Last sequence update)		
DT	01-NOV-1997 (Rel. 35, Last annotation update)		
DE	HIGH AFFINITY INTERLEUKIN-8 RECEPTOR A (IL-8R A) (CXCR-1).		
GN	IL8RA OR CXCR1.		
OS	Oryctolagus cuniculus (Rabbit).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.		
NCBI_TaxID	9986;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=91378994; PubMed=1898400;		
RA	Beckmann M.P., Munger W.E., Kozlosky C., Vandenbos T., Price V.,		
RA	Lyman S., Gerard N.P., Gerard C., Cerretti D.P.;		
RT	"Molecular characterization of the interleukin-8 receptor.";		
RL	Biochem. Biophys. Res. Commun. 179:784-789(1991).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=ALBINO; TISSUE=Neutrophils;		
RX	MEDLINE=91056034; PubMed=1700779;		
RA	Thomas K.M., Pyun H.Y., Navarro J.;		
RT	"Molecular cloning of the fmet-Leu-Phe receptor from neutrophils.";		
RL	J. Biol. Chem. 265:20061-20064(1990).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RN	TISSUE=Neutrophils;		
RC	MEDLINE=92148149; PubMed=1737938;		
RX	Lee J., Kuang W.-J., Rice G.C., Wood W.I.;		
RA	"Characterization of complementary DNA clones encoding the rabbit		
RT	IL-8 receptor.";		
RL	J. Immunol. 148:1261-1264(1992).		
CC	-1- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL		
CC	NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR		
CC	CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A		
CC	G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND		
CC	MESSENGER SYSTEM.		
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.		
CC	-1- TISSUE SPECIFICITY: NEUTROPHILS.		
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.		
CC	-1- CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE THE RECEPTOR FOR		
CC	FMET-LEU-PHE (N-FORMYL PEPTIDE RECEPTOR).		

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EMBL; M74240; AAA31375.1; -;
 EMBL; M58021; AAA31377.1; -;
 EMBL; M82873; AAA31376.1; -;
 PIR; A23669; A23669.
 PIR; A46483; A46483.
 PIR; JQ1231; JQ1231.
 GCRdb; GCR_0107; -;
 GCRdb; GCR_0108; -;
 GCRdb; GCR_0298; -;
 InterPro; IPR000174; -;
 InterPro; IPR000276; -;
 InterPro; IPR001355; -;
 Pfam; PF00001; 7tm_1; 1.
 PRINTS; PR00237; GPCRHHODOPSN.
 PRINTS; PR00427; INTRLEUKIN8R.
 PRINTS; PR00572; INTRLEUKIN8R.
 PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
 PROSITE; PS0262; G-PROTEIN_RECEP_FL_2; 1.
 G-protein coupled receptor; Transmembrane; Glycoprotein; Chemotaxis.
 DOMAIN 1 40 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 41 67 1 (POTENTIAL).
 DOMAIN 68 73 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 74 92 2 (POTENTIAL).
 DOMAIN 93 114 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 115 138 3 (POTENTIAL).
 DOMAIN 139 159 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 160 184 4 (POTENTIAL).
 DOMAIN 185 204 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 205 232 5 (POTENTIAL).
 DOMAIN 233 247 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 248 270 6 (POTENTIAL).
 DOMAIN 271 290 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 291 313 7 (POTENTIAL).
 DOMAIN 314 355 CYTOPLASMIC (POTENTIAL).
 CARBOHYD 7 7 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 21 21 N-LINKED (GLCNAC. . .) (POTENTIAL).
 DISULFID 115 192 BY SIMILARITY.
 CONFLICT 90 111 DLLFALTPWIAVSKSGWIFG -> PAFCDHAYLGRLGKRLDER (IN REF. 2).
 CONFLICT 146 147 HA -> QS (IN REF. 2).
 CONFLICT 204 204 R -> C (IN REF. 2).
 CONFLICT 287 288 DI -> EL (IN REF. 2).
 SEQUENCE 355 AA; 40622 MW; EFE49ACB9D1E0F21 CRC64;

Query Match 46.5%; Score 60; DB 1; Length 355;
 Best Local Similarity 52.4%; Pred. No. 0.15;
 Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 6 KIICLVVWGLSVIISSSTFFV 26
 Db 159 KFCIGIWLSLIUSLPFFLF 179

RESULT 7
 IL8B_GORGO STANDARD; PRT; 353 AA.
 ID IL8B_GORGO
 AC Q28422;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (FRAGMENT).
 OS IL8RB OR CXCR2.
 GN Gorilla gorilla gorilla (Lowland gorilla).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.

NCBI_TaxID=9595;
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=96175151; PubMed=91110929;
 RX Alvarez V., Coto E., Setien F., Gonzalez S., Gonzalez-Roces S., Lopez-Larrea C.;
 RA "Characterization of interleukin-8 receptors in non-human primates.";
 RL Immunogenetics 43:261-267(1996).
 CC -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
 CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
 CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
 CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
 CC AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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EMBL; X91114; CAA62564.1; -;
 DR HSSP; P34996; 1DDD.
 DR InterPro; IPR000276; -;
 DR Pfam; PF00001; 7tm_1; 1.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
 DR PROSITE; PS0262; G-PROTEIN_RECEP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Chemotaxis.
 FT NON_TER 1 1
 DOMAIN <1 45 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 46 72 1 (POTENTIAL).
 DOMAIN 73 81 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 82 102 2 (POTENTIAL).
 DOMAIN 103 117 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 118 139 3 (POTENTIAL).
 DOMAIN 140 160 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 161 180 4 (POTENTIAL).
 DOMAIN 181 205 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 206 228 5 (POTENTIAL).
 DOMAIN 229 248 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 249 270 6 (POTENTIAL).
 DOMAIN 271 291 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 292 312 7 (POTENTIAL).
 DOMAIN 313 >353 CYTOPLASMIC (POTENTIAL).
 DISULFID 116 193 BY SIMILARITY.
 CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
 NON_TER 353 353
 SEQUENCE 353 AA; 39919 MW; 1FF04E31A7E825E4 CRC64;

Query Match 45.0%; Score 58; DB 1; Length 353;
 Best Local Similarity 42.9%; Pred. No. 0.28;
 Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 6 KIICLVVWGLSVIISSSTFFV 26
 Db 160 KFCISWGLSLLLALPVLFF 180

RESULT 8
 IL8B_MACMU STANDARD; PRT; 353 AA.
 ID IL8B_MACMU
 AC Q28519;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (FRAGMENT).
 GN IL8RB OR CXCR2.

OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96175151; PubMed=9110929;
 RA Alvarez V., Coto E., Setien F., Gonzalez S., Gonzalez-Roces S.,
 RA Lopez-Larrea C.;
 RT "Characterization of interleukin-8 receptors in non-human primates."
 RL Immunogenetics 43:261-267(1996).
 CC -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
 CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
 CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
 CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
 CC AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC
 DR EMBL; X91116; CAA62565.1; -
 DR HSP; P34996; IIDD.
 DR InterPro: IPR000276; -
 DR Pfam: PF00001; 7tm_1; 1.
 DR PROSITE; PS00237; G_PROTEIN_RECF1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECF1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Chemotaxis.
 FT NON_TER 1 1
 FT DOMAIN <1 45 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 46 72 1 (POTENTIAL).
 FT DOMAIN 73 81 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 82 102 2 (POTENTIAL).
 FT DOMAIN 103 117 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 118 139 3 (POTENTIAL).
 FT DOMAIN 140 160 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 161 180 4 (POTENTIAL).
 FT DOMAIN 181 205 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 206 228 5 (POTENTIAL).
 FT DOMAIN 229 248 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 249 270 6 (POTENTIAL).
 FT DOMAIN 271 291 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 292 312 7 (POTENTIAL).
 FT DOMAIN 313 >353 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 116 193 BY SIMILARITY.
 FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT NON_TER 353 353
 SQ SEQUENCE 353 AA; 39947 MW; EC8B38130657C713 CRC64;

Query Match 45.0%; Score 58; DB 1; Length 353;
 Best Local Similarity 42.9%; Pred. No. 0.28;
 Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 6 KIICLVWGLSVIISSSTFVF 26
 | ||| :||||| : :
 Db 160 KFCISIWGLSLLALPVLIF 180

RESULT 9
 IL8B_PANTR STANDARD; PRT; 353 AA.
 ID IL8B_PANTR
 AC Q28807;
 DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (FRAGMENT).
 GN IL8RB OR CXCR2.
 GN Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96175151; PubMed=9110929;
 RA Alvarez V., Coto E., Setien F., Gonzalez S., Gonzalez-Roces S.,
 RA Lopez-Larrea C.;
 RT "Characterization of interleukin-8 receptors in non-human primates."
 RL Immunogenetics 43:261-267(1996).
 CC -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
 CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
 CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
 CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
 CC AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; X91113; CAA62563.1; -
 DR HSP; P34996; IIDD.
 DR InterPro: IPR000276; -
 DR Pfam: PF00001; 7tm_1; 1.
 DR PROSITE; PS00237; G_PROTEIN_RECF1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECF1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Chemotaxis.
 FT NON_TER 1 1
 FT DOMAIN <1 45 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 46 72 1 (POTENTIAL).
 FT DOMAIN 73 81 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 82 102 2 (POTENTIAL).
 FT DOMAIN 103 117 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 118 139 3 (POTENTIAL).
 FT DOMAIN 140 160 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 161 180 4 (POTENTIAL).
 FT DOMAIN 181 205 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 206 228 5 (POTENTIAL).
 FT DOMAIN 229 248 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 249 270 6 (POTENTIAL).
 FT DOMAIN 271 291 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 292 312 7 (POTENTIAL).
 FT DOMAIN 313 >353 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 116 193 BY SIMILARITY.
 FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT NON_TER 353 353
 SQ SEQUENCE 353 AA; 39998 MW; E745ACD9EC10C1E2 CRC64;

Query Match 45.0%; Score 58; DB 1; Length 353;
 Best Local Similarity 42.9%; Pred. No. 0.28;
 Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 6 KIICLVWGLSVIISSSTFVF 26
 | ||| :||||| :
 Db 160 KFCISIWGLSLLALPVLIF 180

RESULT 10
 IL8B_HUMAN

ID IL8B_HUMAN STANDARD; PRT: 360 AA.
AC P25025;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GRO/MGSA
DE RECEPTOR) (IL-8 RECEPTOR TYPE 2) (CDW128B).
GN IL8RB OR CXCR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=91368200; PubMed=1891716;
RX Murphy P.M., Tiffany H.L.;
RA "Cloning of complementary DNA encoding a functional human
RT interleukin-8 receptor.";
RL Science 253:1280-1283(1991).
[2]
RN SEQUENCE FROM N.A., AND CHARACTERIZATION.
RP MEDLINE=93205012; PubMed=8384312;
RX Carretti D.P., Kozlosky C.J., Vanden Bos T., Nelson N., Gearing D.P.,
RA Beckmann M.P.;
RT "Molecular characterization of receptors for human interleukin-8,
RT GRO/melanoma growth-stimulatory activity and neutrophil activating
RT peptide-2.";
RL Mol. Immunol. 30:359-367(1993).
[3]
RN SEQUENCE FROM N.A.
RP MEDLINE=94209273; PubMed=7512557;
RX Sprenger H., Lloyd A.R., Lautens L.L., Bonner T.I., Kelvin D.J.;
RA "Structure, genomic organization, and expression of the human
RT interleukin-8 receptor B gene.";
RL J. Biol. Chem. 269:11065-11072(1994).
[4]
RN SEQUENCE FROM N.A.
RP TISSUE=Placenta;
RX MEDLINE=95014476; PubMed=7929358;
RA Anuja S.K., Shetty A., Tiffany H.L., Murphy P.M.;
RT "Comparison of the genomic organization and promoter function for
RT human interleukin-8 receptors A and B.";
RL J. Biol. Chem. 269:26381-26389(1994).
[5]
RN CHARACTERIZATION.
RP MEDLINE=92355587; PubMed=1379593;
RX Lee J., Horuk R., Rice G.C., Bennett G.L., Camerato T., Wood W.I.;
RT "Characterization of two high affinity human interleukin-8
RT receptors.";
RL J. Biol. Chem. 267:16283-16287(1992).
CC -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
CC AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide cdw128b entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw128b.htm".
CC
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CC
CC EMBL; M73969; AAA83148.1; -
CC EMBL; M94582; AAA36108.1; -
CC EMBL; M99412; AAC14460.1; -
CC EMBL; L19593; AAB59437.1; -

DR EMBL; U11869; AAB60656.1; -
DR PIR; A39446; A39446.
DR PIR; A53611; A53611.
DR HSSP; P34996; 1DDO.
DR GCRDB; GCR_0077; -
DR GCRDB; GCR_0610; -
DR GCRDB; GCR_1001; -
DR GCRDB; GCR_1339; -
DR GCRDB; GCR_1831; -
DR MIM; 146928; -
DR InterPro; IPR000057; -
DR InterPro; IPR000174; -
DR InterPro; IPR000276; -
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PRINTS; PR00427; INTRLEUKIN8R.
DR PRINTS; PR00573; INTRLEUKIN8BR.
DR PROSITE; PS00237; G-PROTEIN_RECF_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECF_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Chemotaxis.
FT DOMAIN 1 48 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 49 75 1 (POTENTIAL).
FT DOMAIN 76 84 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 85 105 2 (POTENTIAL).
FT DOMAIN 106 120 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 121 142 3 (POTENTIAL).
FT DOMAIN 143 163 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 164 183 4 (POTENTIAL).
FT DOMAIN 184 208 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 209 231 5 (POTENTIAL).
FT DOMAIN 232 251 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 252 273 6 (POTENTIAL).
FT DOMAIN 274 294 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 295 315 7 (POTENTIAL).
FT DOMAIN 316 360 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 22 22 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 119 196 BY SIMILARITY.
SQ SEQUENCE 360 AA; 40759 MW; 564F04A8BCC0A197 CRC64;
Query Match 45.0%; Score 58; DB 1; Length 360;
Best Local Similarity 42.9%; Pred. No. 0.29;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
Qy 6 KIICLVWGLSVIISSSTFVF 26
| | | | | : | | | | : |
Db 163 KFICLSIWGLSLLALPVLFF 183
RESULT 11
YHDY_BACSU
ID YHDY_BACSU STANDARD; PRT: 371 AA.
AC 007594;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HYPOTHETICAL 42.5 KDA PROTEIN IN CITA-SSPB INTERGENIC REGION.
GN YHDY.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Noback M.A., Terpstra P., Holsappel S., Venema G., Bron S.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE UPF0003 FAMILY.
CC
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 CC -----

DR EMBL; Y14082; CAA74509.1; -
 DR EMBL; Z99109; CAB12803.1; -
 DR Subtilist; BGI3031; yhdy.
 DR InterPro; IPR001880; -
 DR Pfam; PF00924; UPF0003; 1.
 DR PROSITE; PS01246; UPF0003; 1.
 KW Hypothetical protein; Transmembrane.
 FT TRANSMEM 9 29 POTENTIAL.
 FT TRANSMEM 58 78 POTENTIAL.
 FT TRANSMEM 98 118 POTENTIAL.
 FT TRANSMEM 133 153 POTENTIAL.
 FT TRANSMEM 159 179 POTENTIAL.
 FT TRANSMEM 183 203 POTENTIAL.
 FT TRANSMEM 330 350 POTENTIAL.
 SQ SEQUENCE 371 AA; 42537 MW; ABE76B77EBC2D9B7 CRC64;

Query Match 45.0%; Score 58; DB 1; Length 371;
 Best Local Similarity 43.5%; Pred. No. 0.29;
 Matches 10; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 4 RSKICLVVWGLSVIISSTFVF 26

DB 96 RSLIVALLCWGLNLTATSSFF 118

RESULT 12

IL8B_RABIT STANDARD; PRT; 358 AA.
 AC P35344;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GRO/MGSA
 DE RECEPTOR)
 GN IL8RB OR CXCR2.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ALBINO; TISSUE=Blood;
 RX MEDLINE=94230294; PubMed=8175642;
 RA Prado G.N., Thomas K.M., Suzuki H., Larosa G.J., Wilkinson N.C.,
 RA Folco E., Navarro J.;
 RT "Molecular characterization of a novel rabbit interleukin-8 receptor
 RT isotype."
 RL J. Biol. Chem. 269:12391-12394(1994).
 CC -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
 CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
 CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
 CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER SYSTEM. THE AFFINITY OF THIS RECEPTOR IS IL-8 >> NAP-2 >
 CC MSGA (GRO).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: EXPRESSED PREFERENTIALLY IN NEUTROPHILS.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----

DR EMBL; L24445; AAA31378.1; -
 DR PIR; A53752; A53752.
 DR GCRDb; GCR 0861; -
 DR InterPro; IPR000057; -
 DR InterPro; IPR000174; -
 DR InterPro; IPR000276; -
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00427; INTRLEUKIN8R.
 DR PRINTS; PR00573; INTRLEUKIN8R.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS00262; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Chemotaxis.
 FT DOMAIN 1 46 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 47 73 1 (POTENTIAL).
 FT DOMAIN 74 82 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 83 103 2 (POTENTIAL).
 FT DOMAIN 104 118 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 119 140 3 (POTENTIAL).
 FT DOMAIN 141 161 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 162 181 4 (POTENTIAL).
 FT DOMAIN 182 206 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 207 229 5 (POTENTIAL).
 FT DOMAIN 230 249 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 250 271 6 (POTENTIAL).
 FT DOMAIN 272 292 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 293 313 7 (POTENTIAL).
 FT DOMAIN 314 358 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 20 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 117 BY SIMILARITY.
 SQ SEQUENCE 358 AA; 40632 MW; 6899716944D6126A CRC64;

Query Match 44.2%; Score 57; DB 1; Length 358;
 Best Local Similarity 47.6%; Pred. No. 0.4;
 Matches 10; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 6 KIIICLVVWGLSVIISSTFVF 26

DB 161 KPICLSMWGVSLILSLPILLF 181

RESULT 13

BONZ_CERAE STANDARD; PRT; 342 AA.
 ID BONZ_CERAE
 AC O18983;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE G PROTEIN-COUPLED RECEPTOR BONZO.
 GN BONZO.
 OS Cercopithecus aethiops (Green monkey) (Grivet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Cercopithecus.
 OX NCBI_TaxID=9534;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97373958; PubMed=9230441;
 RA Deng H.K., Unutmaz D., Kewalramani V.N., Littman D.R.;
 RT "Expression cloning of new receptors used by simian and human
 RT immunodeficiency viruses."
 RL Nature 388:296-300(1997).
 CC -!- FUNCTION: ORPHAN RECEPTOR. COULD BE A CHEMOKINE RECEPTOR. USED AS
 CC A CORCEPTOR BY SIYS AND BY STRAINS OF HIV-2 AND M-TROPIC HIV-1.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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EMBL; AF124380; AAD31419.1; -	
InterPro; IPR000276; -	
InterPro; IPR002235; -	
Pfam; PF00001; 7tm_1; 1.	
PRINTS; PR00237; GPCRRHODOPSIN.	
PRINTS; PR01105; BONZOORPHANR.	
PROSITE; PS00233; G_PROTEIN_RECEP_FL_1; 1.	
PROSITE; PS02623; G_PROTEIN_RECEP_FL_2; 1.	
G-protein coupled receptor; Transmembrane; Glycoprotein.	
EXTRACELLULAR (POTENTIAL).	
DOMAIN 1 33	
TRANSMEM 34 60	1 (POTENTIAL).
DOMAIN 61 69	CYTOPLASMIC (POTENTIAL).
TRANSMEM 70 90	2 (POTENTIAL).
DOMAIN 91 104	EXTRACELLULAR (POTENTIAL).
TRANSMEM 105 126	3 (POTENTIAL).
DOMAIN 127 144	CYTOPLASMIC (POTENTIAL).
TRANSMEM 145 165	4 (POTENTIAL).
DOMAIN 166 188	EXTRACELLULAR (POTENTIAL).
TRANSMEM 189 216	5 (POTENTIAL).
DOMAIN 217 232	CYTOPLASMIC (POTENTIAL).
TRANSMEM 233 260	6 (POTENTIAL).
DOMAIN 261 276	EXTRACELLULAR (POTENTIAL).
TRANSMEM 277 294	7 (POTENTIAL).
DOMAIN 295 343	CYTOPLASMIC (POTENTIAL).
CARBOHYD 17 17	N-LINKED (GLCNAC...) (POTENTIAL).
DISULFIDE 103 181	BY SIMILARITY.
SEQUENCE 343 AA; 39423.MW; 48B2544949EB83F CRC64;	

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Query Match      42.68; Score 55; DB 1; Length 343;
Local Similarity 33.3%; Pred. No. 0.74;
Matches 7; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

        6 KIICLVWGLSVIISSSTFFV 26
          :|::|::||::|::|::|
150 KVICLLIWIISLVLSPQIII 170
```

Run completed: May 23, 2001, 15:36:18
Time: 649 sec


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Q9TU48      Q9TU48      PRELIMINARY;      PRT;      174 AA.
AC Q9TU48;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE INTERLEUKIN 8 RECEPTOR-LIKE PROTEIN (FRAGMENT).
GN IL8R.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Grosse W.M., Kappes S.M., Laegreid W.W., Keele J.W.,
RA Chitko-Mckown C.G., Heaton M.P.;
RT "Single Nucleotide Polymorphism (SNP) Discovery and Linkage Mapping of
RT Bovine Nucleotide Polymorphism (SNP) Discovery and Linkage Mapping of
RL Mamm. Genome 10:1062-1069(1999).
DR EMBL; AF140650; AAF07867.1; -
DR INTERPRO; IPR000174; -
DR INTERPRO; IPR000276; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR00427; INTRLEUKIN8R.
KW Receptor.
FT NON_TER      1      174
FT NON_TER      174      174
SQ SEQUENCE      174 AA; 20107 MW; D20E223B0EFE836 CRC64;

Query Match      48.8%; Score 63; DB 6; Length 174;
Best Local Similarity 52.4%; Pred. No. 0.13;
Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY      6 KIICLVWGLSVIISSSTVF 26
Db      11 KFCIGIWALSVALPIF 31

RESULT      3
Q9TOS7      Q9TOS7      PRELIMINARY;      PRT;      174 AA.
AC Q9TOS7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE INTERLEUKIN 8 RECEPTOR-LIKE PROTEIN (FRAGMENT).
GN IL8R.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Grosse W.M., Kappes S.M., Laegreid W.W., Keele J.W.,
RA Chitko-Mckown C.G., Heaton M.P.;
RT "Single Nucleotide Polymorphism (SNP) Discovery and Linkage Mapping of
RT Bovine Nucleotide Polymorphism (SNP) Discovery and Linkage Mapping of
RL Mamm. Genome 10:1062-1069(1999).
DR EMBL; AF140652; AAF07869.1; -
DR EMBL; AF140648; AAF07865.1; -
DR EMBL; AF140649; AAF07866.1; -
DR EMBL; AF140651; AAF07868.1; -
DR INTERPRO; IPR000174; -
DR INTERPRO; IPR000276; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR00427; INTRLEUKIN8R.
KW Receptor.
FT NON_TER      1      174
FT NON_TER      174      174
SQ SEQUENCE      174 AA; 20107 MW; D20E223B0EFE836 CRC64;

Query Match      48.8%; Score 63; DB 6; Length 174;
Best Local Similarity 52.4%; Pred. No. 0.13;
Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY      6 KIICLVWGLSVIISSSTVF 26
Db      11 KFCIGIWALSVALPIF 31

RESULT      3
Q9TOS7      Q9TOS7      PRELIMINARY;      PRT;      174 AA.
AC Q9TOS7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE INTERLEUKIN 8 RECEPTOR-LIKE PROTEIN (FRAGMENT).
GN IL8R.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Grosse W.M., Kappes S.M., Laegreid W.W., Keele J.W.,
RA Chitko-Mckown C.G., Heaton M.P.;
RT "Single Nucleotide Polymorphism (SNP) Discovery and Linkage Mapping of
RT Bovine Nucleotide Polymorphism (SNP) Discovery and Linkage Mapping of
RL Mamm. Genome 10:1062-1069(1999).
DR EMBL; AF140652; AAF07869.1; -
DR EMBL; AF140648; AAF07865.1; -
DR EMBL; AF140649; AAF07866.1; -
DR EMBL; AF140651; AAF07868.1; -
DR INTERPRO; IPR000174; -
DR INTERPRO; IPR000276; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR00427; INTRLEUKIN8R.
KW Receptor.
FT NON_TER      1      174
FT NON_TER      174      174
SQ SEQUENCE      174 AA; 20107 MW; D20E223B0EFE836 CRC64;

Query Match      48.8%; Score 63; DB 6; Length 174;
Best Local Similarity 52.4%; Pred. No. 0.13;
Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY      6 KIICLVWGLSVIISSSTVF 26
Db      11 KFCIGIWALSVALPIF 31

RESULT      3
Q9TOS7      Q9TOS7      PRELIMINARY;      PRT;      174 AA.
AC Q9TOS7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE INTERLEUKIN 8 RECEPTOR-LIKE PROTEIN (FRAGMENT).
GN IL8R.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Grosse W.M., Kappes S.M., Laegreid W.W., Keele J.W.,
RA Chitko-Mckown C.G., Heaton M.P.;
RT "Single Nucleotide Polymorphism (SNP) Discovery and Linkage Mapping of
RT Bovine Nucleotide Polymorphism (SNP) Discovery and Linkage Mapping of
RL Mamm. Genome 10:1062-1069(1999).
DR EMBL; AF140652; AAF07869.1; -
DR EMBL; AF140648; AAF07865.1; -
DR EMBL; AF140649; AAF07866.1; -
DR EMBL; AF140651; AAF07868.1; -
DR INTERPRO; IPR000174; -
DR INTERPRO; IPR000276; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR00427; INTRLEUKIN8R.
KW Receptor.
FT NON_TER      1      174
FT NON_TER      174      174
SQ SEQUENCE      174 AA; 20107 MW; D20E223B0EFE836 CRC64;
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FT NON_TER      174      174
SQ SEQUENCE      174 AA; 20116 MW; D21C877CEC5BAFC6 CRC64;

Query Match      48.8%; Score 63; DB 6; Length 174;
Best Local Similarity 52.4%; Pred. No. 0.13;
Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY      6 KIICLVWGLSVIISSSTVF 26
Db      11 KFCIGIWALSVALPIF 31

RESULT      4
Q9JIU9      Q9JIU9      PRELIMINARY;      PRT;      367 AA.
AC Q9JIU9;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CHEMOKINE RECEPTOR CXCR3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang X., Li X., Schmidt D.B., Foley J.J., Barone F.C., Ames R.S.,
RA Sarau H.M.;
RT "Identification and molecular characterization of rat CXCR3: receptor
RT expression and interferon-inducible protein-10 binding are increased
RL in focal stroke";
RL Mol. Pharmacol. 57:1190-1198(2000).
DR EMBL; AF223642; AAF76982.1; -
KW Receptor.
SQ SEQUENCE      367 AA; 40934 MW; F67C0362EDDBFCB7 CRC64;

Query Match      46.5%; Score 60; DB 11; Length 367;
Best Local Similarity 43.5%; Pred. No. 0.65;
Matches 10; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY      4 RSKICLVWGLSVIISSSTVF 26
Db      166 RVALTCIVWGLCVLFPDFIF 188

RESULT      5
Q9TS32      Q9TS32      PRELIMINARY;      PRT;      148 AA.
AC Q9TS32;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE C5A RECEPTOR.
OS Bos sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=29061;
RN [1]
RP SEQUENCE FROM N.A.
RA Perret J.J., Raspe E., Vassart G., Parmentier M.;
RT "Cloning and functional expression of the canine anaphylatoxin C5a
RT receptor. Evidence for high interspecies variability.";
RL Biochem. J. 288:911-917(1992).
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR000496; -
DR INTERPRO; IPR000826; -
DR INTERPRO; IPR001274; -
DR INTERPRO; IPR002234; -
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DR PFAM; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00425; BRADYKININR.
 DR PRINTS; PR00426; C5ANPHYLTXNR.
 DR PRINTS; PR00526; FMETLEUPHER.
 DR PRINTS; PR01104; ANPHYLATONXR.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 SQ SEQUENCE 148 AA; 16542 MW; 5EC5457F246562CE CRC64;

Query Match 43.4%; Score 56; DB 6; Length 148;
 Best Local Similarity 40.0%; Pred. No. 1.1;
 Matches 8; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

OY 7 IICLVVWGLSVIISSTFFV 26
 : | | | | : : : : :
 Db 73 VACAVAGLALLLTIPSFV 92

RESULT 6
 O9XT45
 ID O9XT45 PRELIMINARY; PRT; 343 AA.
 AC O9XT45;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE CHEMOKINE RECEPTOR BONZO.
 GN STRL33.

OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Margulies B.J., Hauer D.A., Clements J.E.;
 RT "Identification of Thirteen Rhesus Macaque Chemokine Receptors."
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF124380; AAD31419.1; -

DR INTERPRO; IPR000248; -
 DR INTERPRO; IPR000276; -
 DR INTERPRO; IPR000355; -
 DR INTERPRO; IPR001277; -
 DR INTERPRO; IPR002235; -
 DR PFAM; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00241; ANGIOTENSINR.
 DR PRINTS; PR00645; LCRIORPHANR.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01105; BONZOORPHANR.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 KW Receptor.
 SQ SEQUENCE 343 AA; 39423 MW; 48DB2544949EB83F CRC64;

Query Match 42.6%; Score 55; DB 6; Length 343;
 Best Local Similarity 33.3%; Pred. No. 3.2;
 Matches 7; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

OY 6 KIICLVVWGLSVIISSTFFV 26
 : | | | | : : : : :
 Db 150 KVICLLIWISLVSLPQIIY 170

RESULT 7
 O9N0Z0
 ID O9N0Z0 PRELIMINARY; PRT; 343 AA.
 AC O9N0Z0;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE STRL33.
 OS Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Cercocebus.
 OX NCBI_TaxID=9531;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20261727; PubMed-10799581;
 RA Pohlmann S., Lee B., Meister S., Krumbiegel M., Leslie G., Doms R.W.,
 RA Kirchhoff F.;
 RT "Simian immunodeficiency virus utilizes human and sooty mangabey but
 RT not rhesus macaque STRL33 for efficient entry."
 RL J. Virol. 74:5075-5082(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Pohlmann S., Lee B., Meister S., Krumbiegel M., Leslie G., Doms R.W.,
 RA Kirchhoff F.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF237559; AAF68392.1; -
 SQ SEQUENCE 343 AA; 39588 MW; A75B7A0751C13455 CRC64;

Query Match 42.6%; Score 55; DB 6; Length 343;
 Best Local Similarity 33.3%; Pred. No. 3.2;
 Matches 7; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

OY 6 KIICLVVWGLSVIISSTFFV 26
 : | | | | : : : : :
 Db 150 KVICLLIWISLVSLPQIIY 170

RESULT 8
 O15185
 ID O15185 PRELIMINARY; PRT; 415 AA.
 AC O15185;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE G PROTEIN-COUPLED RECEPTOR CKR-L2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gutierrez J., Varona R., Zaballeros A., Lind P., Marquez G.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z79783; CAB02143.1; -
 DR INTERPRO; IPR000276; -
 DR PFAM; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 SQ SEQUENCE 415 AA; 45608 MW; DE474B2084BC299B CRC64;

Query Match 42.6%; Score 55; DB 4; Length 415;
 Best Local Similarity 39.1%; Pred. No. 3.8;
 Matches 9; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

OY 4 RSKICLVVWGLSVIISSTFFV 26
 : | | | | : : : : :
 Db 214 RVTLCVWGLCLLFPDFIF 236

RESULT 9
 O88410
 ID O88410 PRELIMINARY; PRT; 367 AA.
 AC O88410;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE CHEMOKINE RECEPTOR CXCR3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=98318636; PubMed=9653165;
 RA Soto H., Wang W., Strieter R.M., Copeland N.G., Gilbert D.J.,
 RA Jenkins N.A., Hedrick J., Zlotnik A.;
 RT "The CC chemokine 6CKine binds the CXC chemokine receptor CXCR3.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:8205-8210(1998).
 DR EMBL: AF045146; AAC40163.1; -;
 DR INTERPRO: IPR000276; -;
 DR PFAM: PF000001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHHODOPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 SQ SEQUENCE 367 AA; 41016 MW; 029FBB778E3CD4EA CRC64;

Query Match 41.9%; Score 54; DB 11; Length 367;

Best Local Similarity 34.8%; Pred. No. 4.7;
 Matches 8; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 4 RSKIIICLVVWGLSVIISSTFFV 26

DB 166 RVALTCIVVWGLCLLFPDFIY 188

RESULT 10

Q9QWN6 PRELIMINARY; PRT; 367 AA.

AC Q9QWN6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE INTERFERON-INDUCIBLE PROTEIN 10 RECEPTOR.
 GN MCXCR3.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=BLOOD;
 RA Tanami M., Tominaga Y., Yatsunami K., Narumi S.;
 RT "Cloning of the murine interferon-inducible protein 10 (IP-10)
 RT receptor and its specific expression in lymphoid organs.";
 RL Biochem. Biophys. Res. Commun. 251:41-48(1998).
 DR EMBL: AB003174; BAA34045.1; -;
 DR INTERPRO: IPR000174; -;
 DR INTERPRO: IPR000248; -;
 DR INTERPRO: IPR000276; -;
 DR INTERPRO: IPR000355; -;
 DR INTERPRO: IPR001277; -;
 DR PFAM: PF000001; 7tm_1; 1.

DR PRINTS: PR00237; GPCRHHODOPSN.
 DR PRINTS: PR00241; ANGIOTENSINR.
 DR PRINTS: PR00427; INTRLEUKIN8R.
 DR PRINTS: PR00645; LCRIORPHANR.
 DR PRINTS: PR00657; CCHEMOKINER.
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 KW Receptor.
 SQ SEQUENCE 367 AA; 41017 MW; EF0348A8358AD951 CRC64;

Query Match 41.9%; Score 54; DB 11; Length 367;

Best Local Similarity 34.8%; Pred. No. 4.7;
 Matches 8; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 4 RSKIIICLVVWGLSVIISSTFFV 26

DB 166 RVALTCIVVWGLCLLFPDFIY 188

RESULT 11

042444

ID O42444 PRELIMINARY; PRT; 368 AA.

AC O42444;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE INTERLEUKIN-8-LIKE RECEPTOR.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zou J., Daniels G.D., Cunningham C., Secombes C.J.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ003159; CAA05917.1; -;
 DR INTERPRO: IPR000276; -;
 DR PFAM: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHHODOPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 SQ SEQUENCE 368 AA; 41523 MW; BE28E2D4C47E821A CRC64;

Query Match 41.1%; Score 53; DB 13; Length 368;

Best Local Similarity 40.9%; Pred. No. 6.6;
 Matches 9; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 5 SKIIICLVVWGLSVIISSTFFV 26

DB 165 SKFVCACVWLLAVLLALPEFMF 186

RESULT 12

O94765

ID O94765 PRELIMINARY; PRT; 395 AA.

AC O94765;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE CRTH2.
 GN DLIR.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=B19; TISSUE=BLOOD;
 RX MEDLINE=99138803; PubMed=9973380;
 RA Nagata K., Tanaka K., Ogawa K., Kemmotsu K., Imai T., Yoshie O.,
 RA Abe H., Tada K., Nakamura M., Sugamura K., Takano S.;
 RT "Selective expression of a novel surface molecule by human Th2 cells
 RT in vivo.";
 RL J. Immunol. 162:1278-1286(1999).
 RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=PLACENTA;

RA Methner A., Schroeder S.;

RT "Tissue expression and chromosomal organization of a novel G protein-
 RT coupled receptor.";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AB008535; CAB17235.1; -;

DR EMBL: AF144308; AAD34539.1; -;

DR INTERPRO: IPR000276; -;

DR INTERPRO: IPR000826; -;

DR INTERPRO: IPR001179; -;

DR INTERPRO: IPR002234; -;

DR PFAM: PF00001; 7tm_1; 1.

DR PRINTS: PR00237; GPCRHHODOPSN.

DR PRINTS: PR00526; FMETLEUPHER.

DR PRINTS: PR01104; ANPHYLATOXNR.

DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.

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DR PROSITE; PS00453; FKBP_PPIASE_1; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 395 AA; 43239 MW; 9DBB53B2008C1D1 CRC64;

Query Match
Best Local Similarity 41.1%; Score 53; DB 4; Length 395;
Matches 10; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 TLPRSKIICLVVWGLSVIISSSTFFV 26
   : : |||:| :|: : |||
Db 144 TVAAAHKVCVLWALVAVLNTVPYFVF 169

RESULT 13
QY5Y4
ID QY5Y4 PRELIMINARY; PRT; 502 AA.
AC QY5Y4;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
DE ORPHAN G PROTEIN-COUPLED RECEPTOR GPR44.
GN GPR44.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99156852; PubMed-10036181;
RA Marchese A., Sawadargo M., Nguyen T., Cheng R., Heng H.H., Nowak T.,
RA Im D.S., Lynch K.R., George S.R., O'dowd B.F.;
RT "Discovery of three novel orphan G-protein-coupled receptors.";
RL Genomics 56:12-21(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA O'dowd B.F.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AF118265; AAD21055.1; -
DR INTERPRO; IPRO00276; -
DR INTERPRO; IPRO00826; -
DR INTERPRO; IPRO01179; -
DR INTERPRO; IPRO02234; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOODPSN.
DR PRINTS; PR00526; FMETLEUPHER.
DR PRINTS; PR01104; ANPHYLATOXNR.
DR PROSITE; PS00237; G-PROTEIN-RECEPTOR; UNKNOWN_1.
DR PROSITE; PS00453; FKBP_PPIASE_1; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 502 AA; 54759 MW; 841F8A5A16CD9BAC CRC64;

Query Match
Best Local Similarity 41.1%; Score 53; DB 4; Length 502;
Matches 10; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 TLPRSKIICLVVWGLSVIISSSTFFV 26
   : : |||:| :|: : |||
Db 221 TVAAAHKVCVLWALVAVLNTVPYFVF 246

RESULT 14
Q9P491
ID Q9P491 PRELIMINARY; PRT; 770 AA.
AC Q9P491;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TRENBLrel. 15, Last annotation update)
DE GLUCAN 1,3-BETA-GLUCOSIDASE GLUC78 PRECURSOR (EC 3.2.1.58).
OS Trichoderma atroviride.
OC Eukaryota; Fungi; Ascomycota; anamorphic Ascomycota; Trichoderma.
OX NCBI_TaxID=63577;
```

```
[1]
SEQUENCE FROM N.A.
RC STRAIN=P1;
RA Donzelli B.G.G., Lorito M., Scala F., Harman G.E.;
RT "Cloning, sequence and structure of a gene encoding an antifungal
glucan 1,3-beta-glucosidase from Trichoderma atroviride (T. harzianum)
with a spliced regulatory sequence.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AF253421; AAF80600.1; -
KW Signal; Hydrolase; Glycosidase.
FT SIGNAL 1 40 POTENTIAL.
SQ SEQUENCE 770 AA; 81896 MW; 85148BB3B0A33D78 CRC64;

Query Match
Best Local Similarity 41.1%; Score 53; DB 3; Length 770;
Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 9 CLVVWGLSVIISSSTFFV 26
   : ||:| :|:|:|
Db 679 CAGTGWIRVVNSNTFIY 696

RESULT 15
O88860
ID O88860 PRELIMINARY; PRT; 901 AA.
AC O88860;
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
DE CHLORIDE CHANNEL CACC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Romio L., Musante L., Cinti R., Moran O., Seri M., Galletta L.J.V.;
RT "Characterization of a murine gene homologous to the bovine CaCC
chloride channel.";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AF052746; AAC35003.1; -
DR INTERPRO; IPRO02035; -
SQ SEQUENCE 901 AA; 100038 MW; 13DF068BF3337AAB CRC64;

Query Match
Best Local Similarity 41.1%; Score 53; DB 11; Length 901;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 8 ICLVVWGLSVIISS 21
   ||: |||:| :|
Db 885 ICMTIWGLTVIFNS 898

Search completed: May 23, 2001, 15:35:15
Job time: 621 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:28:29 ; Search time 184.73 Seconds
(without alignments)
9.283 Million cell updates/sec

Title: US-08-887-977-10_COPY_177_206

Perfect score: 164

Sequence: 1 NQKYNTQGSVCBPKYQTVSEPIRWKLML 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq_0401.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	164	100.0	365	19 W48086	Human dendritic ce
2	158	96.3	365	21 Y97077	Primate (human) ch
3	57	34.8	1757	20 W84351	Murine ubiquitin-p
4	50	30.5	547	21 Y79188	Haematopoietic ste
5	49	29.9	260	21 G42023	Arabidopsis thalia
6	49	28.9	395	21 G42022	Arabidopsis thalia
7	46.5	28.4	68	7 P60749	Sequence encoded b
8	46.5	28.4	353	12 R12365	HTLV-1 P40x antige
9	46.5	28.4	353	18 W25225	Tax mutant m319 pr
10	46	28.0	2050	20 W90117	Human mature von W
11	46	28.0	2050	20 W73499	Von Willebrand fac

12	46	28.0	2050	21 Y67241	Human von Willebra
13	46	28.0	2813	7 P60462	Sequence of human
14	45	27.4	52	19 W48752	T-cell surface ant
15	45	27.4	136	21 Y92363	G protein-coupled
16	45	27.4	406	20 Y32757	Endo-xylogalacturo
17	45	27.4	831	21 B01248	Human CD97 recepto
18	45	27.4	835	19 W48756	T-cell surface ant
19	45	27.4	835	20 Y41090	Human CD97 protein
20	45	27.4	835	21 B15728	Human CD97 protein
21	45	27.4	1621	18 W31228	Human immunodefici
22	44.5	27.1	88	21 G02929	Human secreted pro
23	44.5	27.1	361	20 Y28810	nn296.2 secreted p
24	44.5	27.1	450	20 Y30788	Guinea pig HKNG1 o
25	44.5	27.1	466	20 Y30787	Protein encoded by
26	44	26.8	84	20 Y30432	Mature nematode ex
27	44	26.8	84	21 B15317	A. caninum nematod
28	44	26.8	91	17 R91701	AcanAPC2. Ancylos
29	44	26.8	91	20 Y30393	Nematode extracted
30	44	26.8	91	20 Y30454	Nematode extracted
31	44	26.8	91	21 B15346	A. caninum nematod
32	44	26.8	151	20 Y07016	Breast cancer asso
33	44	26.8	217	20 Y01087	Mammalian disabled
34	44	26.8	482	17 W08085	Macrophage membran
35	44	26.8	505	14 R41941	prk gene LptK-2 pr
36	44	26.8	505	16 R85929	Protein tyrosine-k
37	44	26.8	1148	20 Y07087	Renal cancer assoc
38	43.5	26.5	1438	21 B18270	Plasmodium falcipa
39	43	26.2	131	21 G10847	Arabidopsis thalia
40	43	26.2	131	21 G45068	Arabidopsis thalia
41	43	26.2	143	18 Y11243	Streptococcus pneu
42	43	26.2	143	19 W38644	Streptococcus pneu
43	43	26.2	193	21 G33614	Arabidopsis thalia
44	43	26.2	199	21 G33613	Arabidopsis thalia
45	43	26.2	246	21 G10846	Arabidopsis thalia

ALIGNMENTS

RESULT 1
W48086
ID W48086 standard; Protein; 365 AA.
AC W48086;
XX
XX
XX 11-JUN-1998 (first entry)
DT Human dendritic cell chemokine receptor.
XX
XX Human; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta;
KW receptor; dendritic cell; macrophage; inflammation; asthma.
XX Homo sapiens.
OS
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 193 /note= "encoded by CAN"
FT
XX
XX WO9801557-A2.
XX
XX 15-JAN-1998.
XX
XX 02-JUL-1997; 97WO-US10819.
XX
XX 04-JUN-1997; 97US-0048593.
PR 05-JUL-1996; 96US-0675814.
PR 11-OCT-1996; 96US-0028329.
XX
XX (SCHE) SCHERING CORP.
XX
XX Gish KC, Schall TJ, Vicari A, Wang W, Zlotnik A;
XX WPI; 1998-101054/09.
DR

DR N-PSDB; V15418.
 XX Novel chemokines, e.g. thymus expressed chemokine - used for
 PT treating inflammatory conditions including asthma.
 PS Claim 3; Page 94-95; 202pp; English.
 XX The present sequence represents human dendritic cell chemokine receptor.
 CC Antibodies which bind to the protein can be used in detecting or
 CC diagnosing various immunological conditions related to expression
 CC of the protein. The nucleic acid can be used for screening and
 CC isolating DNA clones for the chemokines, especially from other
 CC species. The chemokine can be used in the treatment of conditions
 CC associated with abnormal physiology or development, including
 CC inflammatory conditions such as asthma.
 XX Sequence 365 AA;
 SQ

Query Match 100.0%; Score 164; DB 19; Length 365;
 Best Local Similarity 100.0%; Pred. No. 5.1e-17;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NQYNTQGSVDCEPKYQTVSEPIRWKLLML 30
 DB 177 nqyntggsdvcepkqyxtvsepirwklml 206

RESULT 2
 Y97077
 ID Y97077 standard; Protein; 365 AA.
 XX AC Y97077;
 XX AC
 DT 04-DEC-2000 (first entry)
 XX DE Primate (human) chemokine receptor CCR6.
 XX KW MIP-3-alpha; chemokine; CCR6 receptor; ligand; cytostatic; agonist;
 KW antagonist; anti-psoriatic; dermatological; immunosuppressive;
 KW anti-inflammatory.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Misc-difference 193 /note= "Encoded by CAN#"
 FT
 XX WO200046248-A1.
 XX PN
 XX PD 10-AUG-2000.
 XX PF 02-FEB-2000; 2000WO-US00511.
 XX PR 03-FEB-1999; 99US-0244281.
 XX PA (SCHE) SCHERING CORP.
 XX PI Oldham ER, Honey B, Dieu-Nosjean M, Caux C, Zlotnik A;
 XX WPI; 2000-543477/49.
 XX DR N-PSDB; A51971.
 XX Novel methods for modulating the migration of cells within or to the
 PT skin using MIP-3-alpha or CCR6 agonists or antagonists, useful for
 PT treating skin disorders, e.g. cancer
 XX Disclosure; Page 53-54; 61pp; English.
 PS The MIP-3-alpha chemokine is expressed in inflamed skin cells. This
 XX chemokine is the ligand for the CCR6 receptor. MIP-3-alpha or CCR6
 CC agonists or antagonists can be used to modulate the migration of a cell
 CC within or to the skin of a mammal. MIP-3-alpha can be used to purify a

CC population of cells expressing a MIP-3-alpha receptor. The methods are
 CC useful for treating a mammalian subject with a skin disease or condition,
 CC e.g. cancer, metastasis, psoriasis, atopic or contact dermatitis,
 CC systemic lupus erythematosus and lichen ruber planus, or for treating
 CC skin transplants or grafts.
 XX Sequence 365 AA;
 SQ

Query Match 96.3%; Score 158; DB 21; Length 365;
 Best Local Similarity 96.7%; Pred. No. 4.2e-16;
 Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NQYNTQGSVDCEPKYQTVSEPIRWKLLML 30
 DB 177 nqyntggsdvcepkqyxtvsepirwklml 206

RESULT 3
 W84351
 ID W84351 standard; Protein; 1757 AA.
 XX AC W84351;
 XX AC
 DT 25-MAR-1999 (first entry)
 XX DE Murine ubiquitin-protein ligase Ubr1.
 XX KW Ubiquitin-protein ligase; Ubr1; mouse; ubiquitinylation; degradation;
 KW N-end rule pathway; stress-related muscle wasting; inhibitor; screen.
 XX OS Mus sp.
 XX PN US5861312-A.
 XX PD 19-JAN-1999.
 XX PF 02-DEC-1997; 97US-0982956.
 XX PR 02-DEC-1997; 97US-0982956.
 XX PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
 XX PI Kwon YT, Varshavsky A;
 XX WPI; 1999-130395/11.
 DR N-PSDB; Y99308.
 XX Mouse and human Ubr1 cDNA - useful for producing recombinant Ubr1
 PT polypeptides
 XX Disclosure; Columns 15-28; 18pp; English.
 PS The present sequence represents a ubiquitin-protein ligase called Ubr1.
 CC The Ubr1 enzymes are involved in protein ubiquitinylation and
 CC ultimate degradation through the N-end rule pathway and have been
 CC linked to stress-related muscle wasting. Recombinant Ubr1 polypeptides
 CC can be used to screen for inhibitors of muscle wasting when this is
 CC associated with the N-end rule pathway.
 XX Sequence 1757 AA;
 SQ

Query Match 34.8%; Score 57; DB 20; Length 1757;
 Best Local Similarity 31.4%; Pred. No. 7.6;
 Matches 11; Conservative 7; Mismatches 7; Indels 10; Gaps 1;

QY 1 NQYNTQGSVDCEPKYQTVSEPIRW 25
 DB 456 mnkfngqsgdklgrvavacdtkylliskpviw 490

RESULT 4

Y79188
ID Y79188 standard; Protein; 547 AA.
XX
AC Y79188;
XX
DT 19-JUN-2000 (first entry)
XX
DE Haematopoietic stem cell specific protein.
XX
KW Haematopoietic stem cell; immune system disorder;
KW leukaemia; antileukaemic; immunomodulator; therapy; mouse.
XX
OS Mus musculus.
XX
PN WO200011168-A2.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US19052.
XX
PR 21-AUG-1998; 98US-0138132.
XX
PA (UYPR-) UNIV PRINCETON.
XX
PI Lemischka I, Moore K;
XX
DR WPI; 2000-237650/20.
DR N-PSDB; 294129.
XX
PT Hematopoietic stem cell signaling proteins modulating replication and
PT differentiation for treating immune system disorders and leukaemia -
XX
PS Claim 21; Page 240-242; 256pp; English.
XX
CC The present sequence is that of a mouse haematopoietic stem cell
CC (HSC) specific protein. It is an example of claimed HSC-specific
CC proteins (see Y79176-93) predicted from novel isolated HSC-specific
CC nucleic acids (see Z94077-131). The HSCs are especially primitive
CC HSCs (PHSCs) such as umbilical cord cells, bone marrow cells and
CC foetal liver cells. The encoded proteins are growth factors,
CC transcription factors, splicing factors, capping factors, transport
CC proteins, translation factors or replication factors that modulate
CC HSC activity, especially differentiation or replication. The
CC invention provides claimed methods: for identifying PHSC-specific
CC nucleic acids; for generating a stem cell/progenitor cell from
CC PHSCs; for identifying the presence of a PHSC in a sample; for
CC identifying the presence in a sample of a compound that modulates
CC HSC activity; for using such a compound to treat an immune system
CC condition, especially leukaemia; for introducing exogenous nucleic
CC acid into a HSC; and for ex vivo expansion of HSCs. Also claimed
CC are vectors, host cells, and an antibody that specifically binds a
CC an HSC-specific protein.
XX
SQ Sequence 547 AA;

Query Match 30.5%; Score 50; DB 21; Length 547;
Best Local Similarity 50.0%; Pred. No. 22;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Oy 3 KYNTQGSVDCEPKY 16
:l |:: |::|l|l|
Db 312 eyeaggaekcqpky 325

RESULT 5
ID G42023
XX G42023 standard; Protein; 260 AA.
AC G42023;
XX
DT 18-OCT-2000 (first entry)
XX

DE Arabidopsis thaliana protein fragment SEQ ID NO: 52357.
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
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PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
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PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
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PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.

PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
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PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
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PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
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PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
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PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.

PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 29.9%; Score 49; DB 21; Length 260;

Best Local Similarity 41.7%; Pred No. 13; Mismatches 11; Indels 0; Gaps 0;

Matches 10; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

Qy 1 NOKYNTQGSVDCEPKRYQTVSEPIR 24
| | | | | : | : | | |
Db 228 nnnvqqgsgmqgqyqnnppnr 251

RESULT 6

G42022

ID G42022 standard; Protein; 395 AA.

XX

AC G42022;

XX

XX 18-OCT-2000 (first entry)

XX

XX Arabidopsis thaliana protein fragment SEQ ID NO: 52356.

XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX

OS Arabidopsis thaliana.

XX PN EP1033405-A2.
XX XX
PD PD
XX XX
PF PF 25-FEB-2000; 2000EP-0301439.
XX XX 25-FEB-1999; 99US-0121825.
PR PR 05-MAR-1999; 99US-0123180.
PR PR 09-MAR-1999; 99US-0123548.
PR PR 23-MAR-1999; 99US-0125788.
PR PR 25-MAR-1999; 99US-0126264.
PR PR 29-MAR-1999; 99US-0126785.
PR PR 01-APR-1999; 99US-0127462.
PR PR 06-APR-1999; 99US-0128234.
PR PR 08-APR-1999; 99US-0128714.
PR PR 16-APR-1999; 99US-0129845.
PR PR 19-APR-1999; 99US-0130077.
PR PR 21-APR-1999; 99US-0130449.
PR PR 23-APR-1999; 99US-0130510.
PR PR 28-APR-1999; 99US-0130891.
PR PR 28-APR-1999; 99US-0131449.
PR PR 30-APR-1999; 99US-0132048.
PR PR 30-APR-1999; 99US-0132407.
PR PR 04-MAY-1999; 99US-0132484.
PR PR 05-MAY-1999; 99US-0132485.
PR PR 06-MAY-1999; 99US-0132486.
PR PR 07-MAY-1999; 99US-0132487.
PR PR 11-MAY-1999; 99US-0132486.
PR PR 14-MAY-1999; 99US-0134218.
PR PR 14-MAY-1999; 99US-0134219.
PR PR 14-MAY-1999; 99US-0134221.
PR PR 14-MAY-1999; 99US-0134370.
PR PR 18-MAY-1999; 99US-0134768.
PR PR 19-MAY-1999; 99US-0134941.
PR PR 20-MAY-1999; 99US-0135124.
PR PR 21-MAY-1999; 99US-0135353.
PR PR 24-MAY-1999; 99US-0135629.
PR PR 25-MAY-1999; 99US-0136021.
PR PR 27-MAY-1999; 99US-0136392.
PR PR 28-MAY-1999; 99US-0136782.
PR PR 01-JUN-1999; 99US-0137222.
PR PR 03-JUN-1999; 99US-0137528.
PR PR 04-JUN-1999; 99US-0137502.
PR PR 07-JUN-1999; 99US-0137724.
PR PR 08-JUN-1999; 99US-0138094.
PR PR 10-JUN-1999; 99US-0138540.
PR PR 10-JUN-1999; 99US-0138847.
PR PR 14-JUN-1999; 99US-0139119.
PR PR 16-JUN-1999; 99US-0139452.
PR PR 16-JUN-1999; 99US-0139453.
PR PR 17-JUN-1999; 99US-0139492.
PR PR 18-JUN-1999; 99US-0139454.
PR PR 18-JUN-1999; 99US-0139455.
PR PR 18-JUN-1999; 99US-0139456.
PR PR 18-JUN-1999; 99US-0139457.
PR PR 18-JUN-1999; 99US-0139458.
PR PR 18-JUN-1999; 99US-0139459.
PR PR 18-JUN-1999; 99US-0139460.
PR PR 18-JUN-1999; 99US-0139461.
PR PR 18-JUN-1999; 99US-0139462.
PR PR 18-JUN-1999; 99US-0139463.
PR PR 18-JUN-1999; 99US-0139750.
PR PR 18-JUN-1999; 99US-0139763.
PR PR 21-JUN-1999; 99US-0139817.
PR PR 22-JUN-1999; 99US-0139899.
PR PR 23-JUN-1999; 99US-0140353.
PR PR 23-JUN-1999; 99US-0140354.
PR PR 24-JUN-1999; 99US-0140695.
PR PR 28-JUN-1999; 99US-0140823.
PR PR 29-JUN-1999; 99US-0140991.
PR PR 30-JUN-1999; 99US-0141287.
PR PR 01-JUL-1999; 99US-0141842.
PR PR 01-JUL-1999; 99US-0142154.
PR PR 02-JUL-1999; 99US-0142055.
PR PR 06-JUL-1999; 99US-0142390.
PR PR 08-JUL-1999; 99US-0142803.
PR PR 09-JUL-1999; 99US-0142920.
PR PR 12-JUL-1999; 99US-0142977.
PR PR 13-JUL-1999; 99US-0143542.
PR PR 14-JUL-1999; 99US-0143624.
PR PR 15-JUL-1999; 99US-0144005.
PR PR 16-JUL-1999; 99US-0144085.
PR PR 16-JUL-1999; 99US-0144086.
PR PR 19-JUL-1999; 99US-0144325.
PR PR 19-JUL-1999; 99US-0144331.
PR PR 19-JUL-1999; 99US-0144332.
PR PR 19-JUL-1999; 99US-0144333.
PR PR 19-JUL-1999; 99US-0144334.
PR PR 19-JUL-1999; 99US-0144335.
PR PR 20-JUL-1999; 99US-0144352.
PR PR 20-JUL-1999; 99US-0144632.
PR PR 21-JUL-1999; 99US-0144884.
PR PR 21-JUL-1999; 99US-0144814.
PR PR 21-JUL-1999; 99US-0145086.
PR PR 21-JUL-1999; 99US-0145088.
PR PR 22-JUL-1999; 99US-0145085.
PR PR 22-JUL-1999; 99US-0145087.
PR PR 22-JUL-1999; 99US-0145089.
PR PR 22-JUL-1999; 99US-0145192.
PR PR 23-JUL-1999; 99US-0145145.
PR PR 23-JUL-1999; 99US-0145218.
PR PR 26-JUL-1999; 99US-0145224.
PR PR 27-JUL-1999; 99US-0145913.
PR PR 27-JUL-1999; 99US-0145918.
PR PR 27-JUL-1999; 99US-0145919.
PR PR 28-JUL-1999; 99US-0145951.
PR PR 02-AUG-1999; 99US-0146386.
PR PR 02-AUG-1999; 99US-0146388.
PR PR 02-AUG-1999; 99US-0146389.
PR PR 03-AUG-1999; 99US-0147038.
PR PR 04-AUG-1999; 99US-0147204.
PR PR 04-AUG-1999; 99US-0147302.
PR PR 05-AUG-1999; 99US-0147192.
PR PR 05-AUG-1999; 99US-0147260.
PR PR 06-AUG-1999; 99US-0147303.
PR PR 06-AUG-1999; 99US-0147416.
PR PR 09-AUG-1999; 99US-0147493.
PR PR 09-AUG-1999; 99US-0147935.
PR PR 10-AUG-1999; 99US-0148171.
PR PR 11-AUG-1999; 99US-0148319.
PR PR 12-AUG-1999; 99US-0148341.
PR PR 13-AUG-1999; 99US-0148565.
PR PR 13-AUG-1999; 99US-0148684.
PR PR 16-AUG-1999; 99US-0149368.
PR PR 17-AUG-1999; 99US-0149175.
PR PR 18-AUG-1999; 99US-0149426.
PR PR 20-AUG-1999; 99US-0149722.
PR PR 20-AUG-1999; 99US-0149723.
PR PR 20-AUG-1999; 99US-0149929.
PR PR 23-AUG-1999; 99US-0149902.
PR PR 23-AUG-1999; 99US-0149930.
PR PR 25-AUG-1999; 99US-0150566.
PR PR 26-AUG-1999; 99US-0150884.
PR PR 27-AUG-1999; 99US-0151065.
PR PR 27-AUG-1999; 99US-0151066.
PR PR 27-AUG-1999; 99US-0151080.
PR PR 30-AUG-1999; 99US-0151303.
PR PR 31-AUG-1999; 99US-0151438.
PR PR 01-SEP-1999; 99US-0151930.
PR PR 07-SEP-1999; 99US-0152363.
PR PR 10-SEP-1999; 99US-0153070.
PR PR 13-SEP-1999; 99US-0153758.
PR PR 15-SEP-1999; 99US-0154018.

PR 16-SEP-1999; 99US-0154039.
 PR 20-SEP-1999; 99US-0154779.
 PR 22-SEP-1999; 99US-0155139.
 PR 23-SEP-1999; 99US-0155486.
 PR 24-SEP-1999; 99US-0155659.
 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
 PR 05-OCT-1999; 99US-0157753.
 PR 06-OCT-1999; 99US-0157865.
 PR 07-OCT-1999; 99US-0158029.
 PR 08-OCT-1999; 99US-0158232.
 PR 12-OCT-1999; 99US-0158369.
 PR 13-OCT-1999; 99US-0159293.
 PR 13-OCT-1999; 99US-0159294.
 PR 13-OCT-1999; 99US-0159295.
 PR 14-OCT-1999; 99US-0159329.
 PR 14-OCT-1999; 99US-0159330.
 PR 14-OCT-1999; 99US-0159331.
 PR 14-OCT-1999; 99US-0159637.
 PR 14-OCT-1999; 99US-0159638.
 PR 18-OCT-1999; 99US-0159584.
 PR 21-OCT-1999; 99US-0160741.
 PR 21-OCT-1999; 99US-0160767.
 PR 21-OCT-1999; 99US-0160768.
 PR 21-OCT-1999; 99US-0160770.
 PR 21-OCT-1999; 99US-0160814.
 PR 21-OCT-1999; 99US-0160815.
 PR 22-OCT-1999; 99US-0160980.
 PR 22-OCT-1999; 99US-0160981.
 PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-0161404.
 PR 25-OCT-1999; 99US-0161405.
 PR 25-OCT-1999; 99US-0161406.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 29.9%; Score 49; DB 21; Length 395;
 Best Local Similarity 41.7%; Pred. No. 21;
 Matches 10; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 NQKYNQSGSDVCEPKYQTVSEPIR 24
 | | | | | : : | : | | |
 Db 363 nnnqqgsgmqgpgyqnnppnr 386

RESULT 7
 P60749
 ID P60749 standard; Protein: 68 AA.
 AC P60749;

DT 23-AUG-1991 (first entry)

DE Sequence encoded by the X-region of viruses in the HTLV family, esp.
 DE HTLV-I and HTLV-II.

KW Adult T-cell leukaemia; X region; immunoassay; HTLV; retrovirus;
 KW epitope; anti-X region protein antibody.

OS Human T-lymphotropic viruses.

PN WO8601834-A.

PD 27-MAR-1986.

XX 19-SEP-1985; 85WO-0904763.

XX

PR 19-SEP-1984; 84US-0652775.
 XX
 PA (REGC) UNIV OF CALIFORNIA.
 PA (SLAM/) SLAMON D J.
 XX
 PI Slamon DJ, Chen IS, Cline MJ;
 XX
 DR WPI; 1986-094087/14.
 XX
 XX New retroviral polypeptide(s), fragments antisera and antibodies
 PT - useful for detection of retro:viruses in HTLV family, e.g.
 PT causing adult T-cell leukaemia
 XX
 PS Claim 22; Page 27; 33pp; English.

CC The inventors claim a polypeptide having a mol. wt. of about 35kd-
 CC 42kd and having at least one of the SQ in P60743-P60746. In
 CC P60743-P60746, X in the SQ corresp. to an AA such that the SQ is
 CC substantially the same as a polypeptide expressed by an HTLV, esp.
 CC HTLV-I or HTLV-II (see P60747-P60749). Also claimed is a
 CC polypeptide having a mol. wt. of not greater than about 42kd and
 CC having an AA SQ of at least 12 AAs found within at least one of
 CC the polypeptide SQ in P60743-P60746. Polypeptides encoded for in
 CC the region described as PX-IV in the X SQ of HTLV-I and the region
 CC described as PX-C in the X SQ of HTLV-II are characterized by being
 CC respectively about 40kd and 37kd. Detection of antibodies to these
 CC proteins in serum may be used to determine whether exposure to an HTLV
 CC virus has occurred.

XX Sequence 68 AA;

Query Match 28.4%; Score 46.5; DB 7; Length 68;

Best Local Similarity 57.1%; Pred. No. 6.4;

Matches 12; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

QY 8 GSDVCEPKYQTVSEPIRWKLL 28
 | | | | | : | : | | |
 Db 39 gsvvcmylyq-lspptwpll 58

RESULT 8

R12365
 ID R12365 standard; Protein: 353 AA.

XX AC R12365;

XX DT 19-AUG-1991 (first entry)

XX DE HTLV-1 P40x antigenic polypeptide.

XX KW Adult T-cell leukaemia; tropical spastic paraparesis.

XX OS Human t-cell leukaemia virus.

XX PN WO9107510-A.

XX PD 30-MAY-1991.

XX PF 14-NOV-1990; 90WO-US06647.

XX PR 17-NOV-1989; 89US-0438666.

XX PA (AMGE-) AMGEN INC.

XX PI Hare DL, Kieft GL, Lau EP, Renick MA, Yancik SA;

XX DR WPI; 1991-178118/24.

XX DR N-PSDB; Q12066.

XX PT DNA encoding HTLV-1 antigenic polypeptide(s) - used in immunoassay
 XX to detect HTLV-1 virus in serum or plasma.

PS Claim 24; Fig 3; 64pp; English.

CC The gene product may be used to raise Abs, useful in immunoassay for
 CC HTLV-1. Using Abs raised to env, tax and gag genes together
 CC maximises sensitivity to the virus. The antigens may be expressed
 CC from a transformed esp. E.coli.

XX Sequence 353 AA;

Query Match 28.4%; Score 46.5; DB 12; Length 353;
 Best Local Similarity 57.1%; Pred. No. 45;
 Matches 12; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

QY 8 GSDVCEPKYQTVSEPIRWKLL 28
 ||||| ||:|||||
 Db 149 gsvvcmylyq-lspptwpll 168

RESULT 9

ID W25225 standard; protein; 353 AA.

XX AC W25225;

XX DT 13-MAR-1998 (first entry)

XX DE Tax mutant m319 protein.

XX KW Tax mutant m319; NFkappaB; NFkB2 precursor; inhibition; cancer;
 XX inflammation; rheumatism; Immunoglobulin.

XX OS Synthetic.

XX PN JP09187283-A.

XX PD 22-JUL-1997.

XX PF 12-JAN-1996; 96JP-0021891.

XX PR 12-JAN-1996; 96JP-0021891.

XX PA (SHIO) SHIONOGI & CO LTD.

XX DR WPI; 1997-419401/39.

XX PT A cell constitutionally expressing NFkappaB - used to screen for
 PT agents inhibiting NFkappaB or the NFkB2 precursor

XX PS Claim 4; Fig 1; 22pp; Japanese.

XX CC A transfected cell strain has been developed which constitutively
 CC expresses NFkappaB. A method has been developed for screening a
 CC substance specifically inhibiting the activity of NFkappaB protein or
 CC of NFkB2 precursor by using the above cell strain. The present sequence
 CC represents a Tax mutant m319 protein sequence. The cells are used for
 CC screening for agents that can inhibit the gene activating effect of
 CC NFkappaB. This may be useful in the treatment of such conditions as
 CC cancer, inflammation and rheumatism.

XX Sequence 353 AA;

Query Match 28.4%; Score 46.5; DB 18; Length 353;
 Best Local Similarity 57.1%; Pred. No. 45;
 Matches 12; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

QY 8 GSDVCEPKYQTVSEPIRWKLL 28
 ||||| ||:|||||
 Db 149 gsvvcmylyq-lspptwpll 168

RESULT 10

W90117
 ID W90117 standard; Protein; 2050 AA.

XX AC W90117;

XX DT 12-APR-1999 (first entry)

XX DE Human mature von Willebrand Factor.

XX KW von Willebrand Factor; vWF; human; GPIb binding domain;
 KW antiagregant; platelet aggregation; cerebrovascular disorder;
 KW cardiovascular disorder; myocardial infarction; angina;
 KW thrombolytic; platelet adhesion; therapy.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 FT Domain 504..728

FT Disulfide-bond /note= "GPIb binding domain"
 FT 509..695

XX PN US5849702-A.

XX PD 15-DEC-1998.

XX PF 05-JUN-1995; 95US-0464962.

XX PR 03-SEP-1991; 91US-0753815.

XX PR 02-MAR-1990; 90US-0487767.

XX PR 01-MAR-1991; 91WO-US01416.

XX PR 22-JUN-1993; 93US-0080690.

XX PR 30-NOV-1994; 94US-0347594.

XX PR 05-JUN-1995; 95US-0464962.

XX PA (BIOT-) BIO-TECHNOLOGY GENERAL CORP.

XX PI Garfinkel L, Richter T;

XX DR WPI; 1999-069781/06.

XX DR N-PSDB; V74156.

XX PT Composition for inhibiting blood platelet aggregation - containing
 PT polypeptide comprising von Willebrand factor GPIb binding domain

XX PS Example 1; Fig 12A-H; 50pp; English.

XX CC This is the translated sequence of mature human von Willebrand
 CC Factor (vWF), as encoded by an isolated endothelial cDNA clone
 CC (see V74156). The invention provides non-glycosylated, biologically
 CC active polypeptides (see W90119-20) which comprise the vWF GPIb
 CC binding domain. Expression plasmids encoding these polypeptides
 CC and methods of production using transformed bacterial cells are
 CC also provided. The polypeptides are used in claimed methods for
 CC inhibiting platelet aggregation, for treating cerebrovascular
 CC disorders, for treating cardiovascular disorders, especially acute
 CC myocardial infarction or angina, for inhibiting platelet aggregation
 CC before, during or after angioplasty, thrombolytic treatment or
 CC coronary bypass surgery, for maintaining blood vessel patency
 CC before, during or after coronary bypass surgery, for inhibiting
 CC thrombosis, optionally associated with an inflammatory response,
 CC for inhibiting platelet adhesion to damaged vascular surfaces, for
 CC preventing platelet adhesion to prosthetic materials or devices,
 CC for inhibiting re-occlusion after angioplasty or thrombolysis, for
 CC preventing vaso-occlusive crises in sickle-cell anaemia, for
 CC thrombolytic treatment of thrombi-containing platelet-rich
 CC aggregates, for preventing platelet activation and thrombus
 CC formation due to high shear forces in a subject with stenosed or
 CC partially obstructed arteries, or for preventing thrombin-induced
 CC platelet activation.

XX Sequence 2050 AA;

Query Match 28.0%; Score 46; DB 20; Length 2050;
Best Local Similarity 41.2%; Pred. No. 4.4e+02;
Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 7 QGSDVCEPKYQTVSEPI 23

Db 1551 qnadqccpeycvcdpv 1567

RESULT 11

ID W73499 standard; Protein; 2050 AA.

XX AC W73499;

DT 26-FEB-1999 (first entry)

XX Von Willebrand factor.

XX Von Willebrand factor; GPIb binding domain; inhibitor; re-occlusion;
KW platelet aggregation; cerebrovascular disorder; cardiovascular disorder;
KW angioplasty; thrombi-containing platelet-rich aggregate; thrombosis;
KW therapy.

XX Homo sapiens.

XX US5849536-A.

XX 15-DEC-1998.

XX 30-NOV-1994; 94US-0347594.

XX 01-MAR-1991; 91WO-US01416.

XX 02-MAR-1990; 90US-0487767.

XX 03-SEP-1991; 91US-0753815.

XX 22-JUN-1993; 93US-0080690.

XX 30-NOV-1994; 94US-0347594.

XX (BIOT-) BIO-TECHNOLOGY GENERAL CORP.

XX Garfinkel L, Richter T;

XX WPI; 1999-069733/06.

XX N-PSDB; V08901.

XX Polypeptide comprising von Willebrand factor GPIb binding domain -
useful as platelet aggregation inhibitor

XX Disclosure; Fig 12; 62pp; English.

XX This sequence represents the mature human Von Willebrand factor protein.
CC GPIb binding domain of this sequence represents the protein of the
CC invention. The protein is used for inhibiting platelet aggregation,
CC especially for treating cerebrovascular disorders. It is also used for
CC treating cardiovascular disorders, especially acute myocardial infarction
CC or angina. The protein is also used for inhibiting platelet aggregation
CC before, during or after angioplasty, thrombolytic treatment or coronary
CC bypass surgery, for maintaining blood vessel potency before, during or
CC after coronary bypass surgery. It can also be used for inhibiting
CC thrombosis, optionally associated with an inflammatory response, for
CC inhibiting platelet adhesion to damaged vascular surfaces, for preventing
CC platelet adhesion to prosthetic materials or devices, for inhibiting
CC re-occlusion after angioplasty or thrombolysis, or for thrombolytic
CC treatment of thrombi-containing platelet-rich aggregates.

XX Sequence 2050 AA;

Query Match 28.0%; Score 46; DB 20; Length 2050;

Best Local Similarity 41.2%; Pred. No. 4.4e+02;

Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 7 QGSDVCEPKYQTVSEPI 23

Db 1551 qnadqccpeycvcdpv 1567

RESULT 12

Y67241
ID Y67241 standard; Protein; 2050 AA.

XX AC Y67241;

XX 27-MAR-2000 (first entry)

XX Human von Willebrand Factor (vWF) amino acid sequence.

XX Von Willebrand Factor; vWF; GPIb binding domain; arteriosclerosis;
KW platelet adhesion inhibitor; stenosis; cerebrovascular injury; human;
KW thrombosis; cardiovascular injury.

XX Homo sapiens.

XX US6008193-A.

XX 28-DEC-1999.

XX 05-JUN-1995; 95US-0463682.

XX 30-NOV-1994; 94US-0347594.

XX 03-SEP-1991; 91US-0753815.

XX 22-JUN-1993; 93US-0080690.

XX 02-MAR-1990; 90US-0487767.

XX 01-MAR-1991; 91WO-US01416.

XX (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX Richter T, Garfinkel L;

XX WPI; 2000-096379/08.

XX N-PSDB; Z56177.

XX Preventing arteriosclerosis and stenosis using polypeptides derived
from the human von Willebrand factor GPIb binding domain -

XX Claim 1; Fig 12; 65pp; English.

XX This is the amino acid sequence of human von Willebrand factor (vWF).
CC The invention relates to methods of treating arteriosclerosis and
CC stenosis using polypeptides derived from the human vWF GPIb binding
CC domain. vWF is a large plasma protein which is synthesised in the
CC endothelial cells of the blood vessels, and also by megakaryocytes which
CC are the precursors of platelets. The treatment methods involve the
CC administration of a polypeptide (see Y67242 or Y67243). These
CC polypeptides contain a fragment of the vWF GPIb binding domain amino acid
CC sequence. The polypeptides inhibit platelet adhesion and aggregation,
CC therefore the methods may be used for preventing arteriosclerosis and
CC stenosis (as a result of smooth muscle proliferation following vascular
CC injury). The polypeptides may also be used for treating other
CC cerebrovascular and cardiovascular injuries and thrombosis.

XX Sequence 2050 AA;

Query Match 28.0%; Score 46; DB 21; Length 2050;

Best Local Similarity 41.2%; Pred. No. 4.4e+02;

Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 7 QGSDVCEPKYQTVSEPI 23

Db 1551 qnadqccpeycvcdpv 1567

RESULT 13

P60462

ID P60462 standard; Protein; 2813 AA.

XX AC P60462;
 XX 25-JUN-1991 (first entry)
 XX DE Sequence of human von Willebrand Factor (VWF) precursor.
 XX KW Chronic renal failure; therapy; factor VIII C.
 XX OS Homo sapiens.
 XX PN W08606096-A.
 XX PD 23-OCT-1986.
 XX PF 10-APR-1986; 86WO-US00760.
 XX PR 11-APR-1985; 85US-0722108.
 XX PA (CHIL-) CHILDRENS MED CENT.
 XX PA (GINS/) GINSBURG D.
 XX PI Ginsburg D, Orkin SH, Kaufman RJ;
 XX DR WPI; 1986-291663/44.
 XX DR N-PSDB; N60404.
 XX PT Pure Von Willebrand Factor - produced using an expression vector
 XX PT including a DNA sequence encoding functional VWF protein
 XX PS Disclosure; Table 2, Pages 18-36A; 54pp; English.
 XX CC cDNA clones pVWH33, pVWH5 and pVWH6 which span 9 kb pairs of DNA and
 XX CC encompass the entire protein coding region of VWF, were selected to
 XX CC construct full length cDNA (N60404). The pure VWF produced is useful
 XX CC in the treatment of von Willebrand's disease (VWD) and the patients
 XX CC with chronic renal failure whose abnormal bleeding times are
 XX CC corrected by crude cryoprecipitate. Pure VWF can also be used to
 XX CC carry, stabilise and improve the therapeutic efficacy of factor
 XX CC VIII:C.
 XX SQ Sequence 2813 AA;
 Query Match 28.08; Score 46; DB 7; Length 2813;
 Best Local Similarity 41.28; Pred. No. 6.3e+02;
 Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 QY 7 QGSDVCEPKYQTVSEPI 23
 | : | : | : | : | :
 Db 2314 qnadqccpeycvcdpv 2330
 RESULT 14
 W48752
 ID W48752 standard; Peptide; 52 AA.
 XX AC W48752;
 XX 14-SEP-1998 (first entry)
 XX DE T-cell surface antigen CD97 EGF-like repeat 2.
 XX KW T-cell surface antigen; CD97; human; inflammation; angiogenesis;
 XX KW atherosclerosis; antagonist; antibody; human.
 XX OS Homo sapiens.
 XX PN W09817796-A2.
 XX PD 30-APR-1998.
 XX PF 24-OCT-1997; 97WO-US19772.

XX 25-OCT-1996; 96US-0027871.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Kelly K;
 XX WP1; 1998-261492/23.
 XX PT New soluble CD97 alpha subunit isoform(s) - used to develop
 XX PT products for the detection and treatment of inflammation,
 XX PT atherosclerosis and angiogenesis
 XX PS Claim 1; Page 88; 101pp; English.
 XX CC This peptide comprises EGF-like repeat 2 found in alpha subunits
 XX CC of human T-cell surface antigen CD97 (see W48756). Novel soluble
 XX CC CD97 alpha subunits of the invention contain different combinations
 XX CC of 5 EGF-like repeats (see W48751-55). They are selected from:
 XX CC alpha1, which contains EGF-like repeats 1-5; alpha2, which contains
 XX CC EGF-like repeats 1, 2, 3 and 5; and alpha3, which contains EGF-like
 XX CC repeats 1, 2 and 5. The alpha subunit of CD97 is localised
 XX CC extracellularly on T-cells. Upon activation, expression of the
 XX CC alpha subunit is dramatically increased and shed into the external
 XX CC medium. The alpha subunit plays a role in angiogenesis,
 XX CC inflammation and atherosclerosis. Detection and inhibition of the
 XX CC alpha subunit using CD97 alpha polypeptides, nucleic acids,
 XX CC antibodies and antagonists provides diagnostic and therapeutic
 XX CC methods for these disease states.
 XX SQ Sequence 52 AA;
 Query Match 27.48; Score 45; DB 19; Length 52;
 Best Local Similarity 52.68; Pred. No. 7.9;
 Matches 10; Conservative 3; Mismatches 4; Indels 2; Gaps 1;
 QY 4 YNTQGS--DVCEPKYQTVS 20
 | : | : | : | : | : | :
 Db 20 wntegsydcvcsppgpeps 38
 RESULT 15
 Y92363
 ID Y92363 standard; Protein; 136 AA.
 XX AC Y92363;
 XX 10-AUG-2000 (first entry)
 XX DE G protein-coupled receptor protein 3.
 XX KW GCRP-3; G protein-coupled receptor protein; antipsoriatic; antirheumatic;
 XX KW CD97; immunosuppressive; antiasthmatic; antianemic; antiarteriosclerotic;
 XX KW antithyroid; cytostatic; hepatotropic; dermatological; anti-inflammatory;
 XX KW antigout; thyromimetic; haemostatic; virucide; hepatotropic; osteopathic;
 XX KW antiparasitic; immunostimulant.
 XX OS Homo sapiens.
 XX FH Key
 XX FT Peptide 1..25 Location/Qualifiers
 FT Domain /label= signal_peptide
 FT Domain /label= EGF-like
 FT Domain /label= EGF-like
 FT Modified-site /label= EGF-like
 FT Modified-site /note= "Asx hydroxylation site"
 FT Modified-site 64
 FT Modified-site /note= "potential phosphorylation site"
 FT Modified-site 67
 FT Modified-site /note= "potential glycosylation site"

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FT Modified-site 80 /note= "potential phosphorylation site"
FT Modified-site 86 /note= "potential phosphorylation site"
FT Modified-site 124 /note= "potential phosphorylation site"
FT Modified-site 124 /note= "potential phosphorylation site"
XX
PN W0200020590-A2.
XX
XX 13-APR-2000.
XX
XX 06-OCT-1999; 99WO-US23317.
XX
XX 06-OCT-1998; 98US-0167219.
PR 06-OCT-1998; 98US-0172211.
PR 11-MAY-1999; 99US-0133585.
XX
PA (INCY-) INCYTE PHARM INC.
XX
XX Tang YT, Yue H, Lal P, Bandman O, Au-Oung J, Reddy R, Corley NC;
PI Guegler KJ, Gorgone GA, Baughn MR, Azimzai Y;
XX
DR WPI: 2000-328934/28.
DR N-PSDB; A09349.
XX
XX Novel human G-protein coupled receptor proteins used in the diagnosis,
PT treatment and prevention of nervous system disorders,
PT autoimmune/inflammatory disorders, and cell proliferative disorders
PT such as cancer
XX
XX Claim 1; Page 70; 84pp; English.
XX
XX This sequence shows human G-protein coupled receptor protein (GCRP) 3,
CC which has similarity with human CD97. The GCRP polypeptides,
CC polynucleotides, antibodies, antagonists and agonists may be administered
CC to human patients for the diagnosis, treatment and prevention of nervous
CC system disorders (e.g. epilepsy, stroke, neoplasms, Alzheimer's disease),
CC autoimmune or inflammatory disorders, complications of cancer,
CC haemodialysis and extracorporeal circulation, and cell proliferative
CC disorders. They are also used to treat or prevent disorders associated
CC with decreased or increased expression or activity of GCRP.
XX
SQ Sequence 136 AA;

Query Match 27.4%; Score 45; DB 21; Length 136;
Best Local Similarity 52.6%; Pred. No. 25;
Matches 10; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

QY 4 YNTQGS--DVCEPKYQTVS 20
Db :||:| | | | | | | |
42 wntegsydcvcspgypvs 60

Search completed: May 23, 2001, 15:28:31
Job time: 408 sec

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Db 1551 QNADCCPEYECVDPV 1567

RESULT 2

US-08-242-677-2
; Sequence 2, Application US/08242677
; Patent No. 5677143
; GENERAL INFORMATION:
; APPLICANT: Gaynor, Richard B
; APPLICANT: Wu, Foon W.
; TITLE OF INVENTION: Cellular Nucleic Acid Binding Protein
; TITLE OF INVENTION: and Uses Thereof in regulating Gene Expression and in the
; TITLE OF INVENTION: Treatment of AIDS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/242,677
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mayfield, Denise L.
; REGISTRATION NUMBER: 33,732
; REFERENCE/DOCKET NUMBER: UTSD:401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-787-1400
; TELEFAX: 713-789-2679
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1621 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-242-677-2

Query Match 27.4%; Score 45; DB 1; Length 1621;
Best Local Similarity 40.7%; Pred. No. 1.7e+02;
Matches 11; Conservative 4; Mismatches 8; Indels 4; Gaps 1;

QY 2 QKYN----TQSDVCEPKYQTVSEPIR 24
:||: |||: || | |||
Db 901 KKYHPLIPTGSEILLEPLPAVQMPIR 927

RESULT 3

US-08-465-380-59
; Sequence 59, Application US/08465380
; Patent No. 5863894
; GENERAL INFORMATION:
; APPLICANT: George P. Vlasuk, Patric H. Stanssens,
; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
; APPLICANT: Yves R. Laroche, Laurent S. Jespers,
; APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
; APPLICANT: Peter W. Bergum
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles

; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,380
; FILING DATE: June 5, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 213/268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Ancylostoma caninum
US-08-465-380-59

Query Match 26.8%; Score 44; DB 2; Length 84;
Best Local Similarity 43.5%; Pred. No. 6.6;
Matches 10; Conservative 4; Mismatches 7; Indels 2; Gaps 1;

QY 1 NOKYNTQGSVDVCEP--KYQTVSE 21
:|||: || | || | || |
Db 9 NEKYDCGSKCKKCKYDGVVEE 31

RESULT 4

US-08-486-397-59
; Sequence 59, Application US/08486397
; Patent No. 5866542
; GENERAL INFORMATION:
; APPLICANT: George P. Vlasuk, Patric H. Stanssens,
; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
; APPLICANT: Yves R. Laroche, Laurent S. Jespers,
; APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
; APPLICANT: Peter W. Bergum
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 357
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,397

; FILING DATE: June 5, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 213/269
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Ancylostoma caninum
; US-08-486-397-59

Query Match 26.8%; Score 44; DB 2; Length 84;
Best Local Similarity 43.5%; Pred. No. 6.6;
Matches 10; Conservative 4; Mismatches 7; Indels 1;

Oy 1 NQKNTQGSVDCEP--KYQTVSE 21
I::: || |
Db 9 NEKYDSCGSKCKKCKYDGVVEE 31

RESULT 5

US-08-486-399-59
; Sequence 59, Application US/08486399
; Patent No. 5866543
; GENERAL INFORMATION:
; APPLICANT: George P. Vlasuk, Patric H. Stanssens,
; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
; APPLICANT: Yves R. Laroche, Laurent S. Jespers,
; APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
; APPLICANT: Peter W. Bergum
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,399
; FILING DATE: June 5, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 213/270
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Ancylostoma caninum
; US-08-486-399-59

Query Match 26.8%; Score 44; DB 2; Length 84;
Best Local Similarity 43.5%; Pred. No. 6.6;
Matches 10; Conservative 4; Mismatches 7; Indels 1;

Oy 1 NQKNTQGSVDCEP--KYQTVSE 21
I::: || |
Db 9 NEKYDSCGSKCKKCKYDGVVEE 31

RESULT 6

US-08-461-965-59
; Sequence 59, Application US/08461965
; Patent No. 5872098
; GENERAL INFORMATION:
; APPLICANT: George P. Vlasuk, Patric H. Stanssens,
; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
; APPLICANT: Yves R. Laroche, Laurent S. Jespers,
; APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
; APPLICANT: Peter W. Bergum
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,965
; FILING DATE: June 5, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 210/243
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Ancylostoma caninum
; US-08-461-965-59

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; ORGANISM: Ancylostoma caninum
US-08-634-641-59

Query Match          26.8%; Score 44; DB 2; Length 84;
Best Local Similarity 43.5%; Pred. No. 6.6;
Matches 10; Conservative 4; Mismatches 7; Indels 2; Gaps 1;

QY 1 NOKYNTQSDVCEP--KYQTVSE 21
   I::: I I I I
Db 9 NEKYDSGSKCEDKCKYDGVSE 31

RESULT 8
US-09-249-471-59
; Sequence 59, Application US/09249471
; Patent No. 6040441
; GENERAL INFORMATION:
; APPLICANT: Vlasuk, George Phillip
; APPLICANT: Stanssens, Patrick Eric Hugo
; APPLICANT: Messens, Joris Hilda Lieven
; APPLICANT: Lauwereys, Marc Josef
; APPLICANT: Laroche, Yves Rene
; APPLICANT: Jespers, Laurent Stephane
; APPLICANT: Ganssemans, Yannick Georges Jozef
; APPLICANT: Moyle, Matthew
; APPLICANT: Beirum, Peter W.
; TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US/09/249,471
; FILING DATE:
; APPLICATION DATA:
; APPLICATION NUMBER: 08/809,455
; FILING DATE: April 17, 1997
; APPLICATION NUMBER: PCT/US95/13231
; FILING DATE: October 17, 1995
; APPLICATION NUMBER: 08/486,399
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/486,397
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/465,380
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/461,965
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 216/270
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:

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; ORGANISM: Ancylostoma caninum
US-08-634-641-59

Query Match          26.8%; Score 44; DB 2; Length 84;
Best Local Similarity 43.5%; Pred. No. 6.6;
Matches 10; Conservative 4; Mismatches 7; Indels 2; Gaps 1;

QY 1 NOKYNTQSDVCEP--KYQTVSE 21
   I::: I I I I
Db 9 NEKYDSGSKCEDKCKYDGVSE 31

RESULT 7
US-08-634-641-59
; Sequence 59, Application US/08634641
; Patent No. 5955294
; GENERAL INFORMATION:
; APPLICANT: Vlasuk, George P. Vlasuk
; APPLICANT: Stanssens, Patrick Eric Hugo
; APPLICANT: Messens, Joris Hilda Lieven
; APPLICANT: Lauwereys, Marc Josef
; APPLICANT: Laroche, Yves Rene
; APPLICANT: Jespers, Laurent Stephane
; APPLICANT: Ganssemans, Yannick Georges Jozef
; APPLICANT: Moyle, Matthew
; APPLICANT: Beirum, Peter W.
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/634,641
; FILING DATE: April 19, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13231
; FILING DATE: October 17, 1995
; APPLICATION NUMBER: 08/486,399
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/486,397
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/465,380
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/461,965
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 219/136
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:

```

; LENGTH: 84 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Ancylostoma caninum
US-09-249-471-59

Query Match 26.8%; Score 44; DB 3; Length 84;
Best Local Similarity 43.5%; Pred. No. 6.6;
Matches 10; Conservative 4; Mismatches 7; Indels 2; Gaps 1;

QY 1 NOKYNTQSDVCEP--KYQTVSE 21
I::: || |:
Db 9 NEKYDSGSKCEDKCKRYDGVVE 31

RESULT 9
US-09-249-472-59
; Sequence 59, Application US/09249472
; Patent No. 6046318
; GENERAL INFORMATION:
; APPLICANT: Vlasuk, George Phillip
; APPLICANT: Stanssens, Patrick Eric Hugo
; APPLICANT: Messens, Joris Hilda Lieven
; APPLICANT: Lauwereys, Marc Josef
; APPLICANT: Laroche, Yves Rene
; APPLICANT: Jespers, Laurent Stephane
; APPLICANT: Ganssemans, Yannick Georges Jozef
; APPLICANT: Moyle, Matthew
; APPLICANT: Bergum, Peter W.
; TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
; TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/249,472
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/809,455
; FILING DATE: April 17, 1997
; APPLICATION NUMBER: PCT/US95/13231
; FILING DATE: October 17, 1995
; APPLICATION NUMBER: 08/486,399
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/486,397
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/465,380
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/461,965
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 216/270
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Ancylostoma caninum
US-09-249-472-59

Query Match 26.8%; Score 44; DB 3; Length 84;
Best Local Similarity 43.5%; Pred. No. 6.6;
Matches 10; Conservative 4; Mismatches 7; Indels 2; Gaps 1;

QY 1 NOKYNTQSDVCEP--KYQTVSE 21
I::: || |:
Db 9 NEKYDSGSKCEDKCKRYDGVVE 31

RESULT 10
US-09-249-451-59
; Sequence 59, Application US/09249451
; Patent No. 6087487
; GENERAL INFORMATION:
; APPLICANT: Vlasuk, George Phillip
; APPLICANT: Stanssens, Patrick Eric Hugo
; APPLICANT: Messens, Joris Hilda Lieven
; APPLICANT: Lauwereys, Marc Josef
; APPLICANT: Laroche, Yves Rene
; APPLICANT: Jespers, Laurent Stephane
; APPLICANT: Ganssemans, Yannick Georges Jozef
; APPLICANT: Moyle, Matthew
; APPLICANT: Bergum, Peter W.
; TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
; TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/249,451
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/809,455
; FILING DATE: April 17, 1997
; APPLICATION NUMBER: PCT/US95/13231
; FILING DATE: October 17, 1995
; APPLICATION NUMBER: 08/486,399
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/486,397
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/465,380
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/461,965
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994

APPLICATION NUMBER: 08/326,110
 FILING DATE: October 18, 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: BIGGS, SUZANNE L.
 REGISTRATION NUMBER: 30,158
 REFERENCE/DOCKET NUMBER: 213/268
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 128:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 91 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 ORIGINAL SOURCE:
 ORGANISM: Ancylostoma caninum
 US-08-485-380-128

Query Match 26.8%; Score 44; DB 2; Length 91;
 Best Local Similarity 43.5%; Pred. No. 7.3;
 Matches 10; Conservative 4; Mismatches 7; Indels 2; Gaps 1;

QY 1 NOKYNTQGSVDVCEP--KYQTVSE 21
 I::I::I I I I I
 Db 16 NEKYDSCGSKCKCKYDGVVEE 38

RESULT 15
 US-08-480-478-50
 Sequence 50, Application US/08480478
 Patent No. 5864009
 GENERAL INFORMATION:
 APPLICANT: GEORGE P. VLASUK; PATRICK ERIC
 APPLICANT: HUGO STANSSENS; JORIS HILDA
 APPLICANT: LIEVEN MESSENS; MARC JOZEF
 APPLICANT: LAUMEREYS; YVES RENE LAROCHE;
 APPLICANT: LAURENT STEPHANE JESPEERS; and
 APPLICANT: YANNICK GEORGES JOZEF
 APPLICANT: GANSEMAN
 TITLE OF INVENTION: NEMATODE-EXTRACTED ANTI-
 TITLE OF INVENTION: COAGULANT PROTEIN
 NUMBER OF SEQUENCES: 86
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FastSeq Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/480,478
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/326,110
 FILING DATE: 18 OCTOBER 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: BIGGS, SUZANNE L.
 REGISTRATION NUMBER: 30,158
 REFERENCE/DOCKET NUMBER: 208/290
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440

TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 50:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 91 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-480-478-50
 Query Match 26.8%; Score 44; DB 2; Length 91;
 Best Local Similarity 43.5%; Pred. No. 7.3;
 Matches 10; Conservative 4; Mismatches 7; Indels 2; Gaps 1;
 QY 1 NOKYNTQGSVDVCEP--KYQTVSE 21
 I::I::I I I I I
 Db 16 NEKYDSCGSKCKCKYDGVVEE 38
 Search completed: May 23, 2001, 15:30:07
 Job time: 414 sec



GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 23, 2001, 15:32:01 ; Search time 110.15 seconds
(without alignments)
18.717 Million cell updates/sec

Title: US-08-887-977-10_COPY_177_206

Perfect score: 164
Sequence: 1 NOKYNTQSDVCEPKYQTVSEPIRWKLLML 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_67: *
1: piri: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	164	100.0	369	JC5068	G protein-coupled
2	57	34.8	1737	T14318	ubiquitin-protein
3	52	31.7	98	B64360	hypothetical prote
4	50	30.5	453	T21528	hypothetical prote
5	48	29.3	357	A72220	conserved hypotet
6	48	29.3	500	S61591	hypothetical prote
7	48	29.3	1257	I58383	retinoblastoma bin
8	47	28.7	424	T08979	hypothetical prote
9	47	28.7	1116	T07213	DNA-directed DNA p
10	46.5	28.4	263	T02227	NBS-LRR type resis
11	46.5	28.4	353	G61547	trans-activating t
12	46.5	28.4	358	TNLCJH1	trans-activating t
13	46.5	28.4	358	TNLCJCN	trans-activating t
14	46.5	28.4	633	S49788	probable membrane
15	46	28.0	443	D64477	cobyrinic acid a,c
16	46	28.0	678	T05821	hypothetical prote
17	46	28.0	1139	T05821	sterol regulatory
18	46	28.0	2813	VWBU	von Willebrand fac
19	45.5	27.7	338	JGECT	thiosulfate-bindin
20	45	27.4	387	S64082	probable membrane
21	45	27.4	742	I37225	leucocyte antigen
22	45	27.4	867	GNLJMP	pol polyprotein (c
23	45	27.4	1621	S62356	TRP-185 protein -
24	44.5	27.1	196	T47140	hypothetical prote
25	44.5	27.1	239	T20255	hypothetical prote
26	44.5	27.1	950	T23975	hypothetical prote
27	44	26.8	316	A57356	lacyl-carrier-prot
28	44	26.8	372	S74859	hypothetical prote
29	44	26.8	373	T35452	probable solute bi

30	44	26.8	492	2	T43859	uroporphyrinogen I
31	44	26.8	505	2	I38396	protein-tyrosine k
32	44	26.8	510	2	F82523	hypothetical prote
33	44	26.8	687	2	A41905	ferric vibriobacti
34	44	26.8	747	2	B47093	cellulase (EC 3.2.
35	44	26.8	1009	2	T18533	CryIAC toxin-bindi
36	44	26.8	1148	2	T09073	splicing factor Si
37	44	26.8	3051	2	S42373	hypothetical prote
38	43.5	26.5	437	2	S60957	transcription modu
39	43.5	26.5	721	2	A44133	phenylalanine ammo
40	43.5	26.5	1438	2	B71610	WD40 WEB-1 homolog
41	43	26.2	80	2	H82194	conserved hypotet
42	43	26.2	200	2	T42678	hypothetical prote
43	43	26.2	241	2	H81536	hypothetical prote
44	43	26.2	246	2	T48338	arabinosylactan pr
45	43	26.2	254	2	T12688	hypothetical prote

ALIGNMENTS

RESULT 1

JC5068
G protein-coupled receptor CKR-L3 - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
C:Accession: JC5068
R:Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
Biochem. Biophys. Res. Commun. 227, 846-853, 1996
A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-lik
A:Reference number: JC5067; MUID:97040707
A:Accession: JC5068
A:Molecule type: DNA
A:Residues: 1-369 <ZAB>
A:Cross-references: EMBL:Z79784; NID:G1668737; PIDN:CAB02144.1; PID:G1668738
C:Comment: This protein belongs to the family of alpha chemokine receptors.
C:Genetics:
A:Gene: GDB:CMKBR6; SFRSL22: GPR29; CCR6: CKR-L3; GPR-CY4
A:Cross-references: GDB:5370639; OMIM:601835
A:Map position: 6q27-6q27
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein
F:42-68/Domain: transmembrane #status predicted <TM1>
F:79-99/Domain: transmembrane #status predicted <TM2>
F:115-136/Domain: transmembrane #status predicted <TM3>
F:160-180/Domain: transmembrane #status predicted <TM4>
F:212-233/Domain: transmembrane #status predicted <TM5>
F:250-271/Domain: transmembrane #status predicted <TM6>
F:292-315/Domain: transmembrane #status predicted <TM7>

Query Match 100.0%; Score 164; DB 2; Length 369;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NOKYNTQSDVCEPKYQTVSEPIRWKLLML 30
|||||
Db 181 NOKYNTQSDVCEPKYQTVSEPIRWKLLML 210

RESULT 2

T14318
ubiquitin-protein ligase E3-alpha - mouse
N:Alternate names: N-recogin E3-alpha
C:Species: Mus musculus (house mouse)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T14318
R:Kwon, Y.T.; Reiss, Y.; Fried, V.A.; Hershko, A.; Yoon, J.K.; Gonda, D.K.; Sangan, P
Proc. Natl. Acad. Sci. U.S.A. 95, 7898-7903, 1998
A:Title: The mouse and human genes encoding the recognition component of the N-end ru
A:Reference number: 217977; MUID:98318583
A:Accession: T14318
A:Status: preliminary; translated from GB/EMBL/DBJ

Qy 2 QKYNTQGSVDCEPKYQTVSEPIRW 25
pb 20 EOVRLOVSDVIDPRYDTKWNMLRW 43

C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21
C:Accession: A72220

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, C.M.

A:Accession number: A72200, M016.33207310
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <ARN>
A:Cross-references: GB:AE001810; GB:AE000512; NID:G498271; PID:G498272.1; PID:G498273.1
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM1695
C:Superfamily: unassigned tetratricontide repeat proteins: tetratricontide repeat

	Matches	10;	Conservative	2;	Mismatches	5;	Indels	2;	Gaps	1;
Qy	12	CEPKYQTVSEPIRWKLLML	30							
		↑ : ↑ ↑ ↑ ↑		↑ : ↑ ↑						
Db	262	CKPKYTELEP--WARVML	278							

hypothetical protein YDR036c - yeast (Saccharomyces cerevisiae)
 N;Alternate names: hypothetical protein D3455; hypothetical protein YD9673.08c
 C;Species: Saccharomyces cerevisiae
 C;Date: 09-Mar-1996 #sequence_revision 12-Apr-1996 #text_change 29-Oct-1999

A;Accession: S01951
A;Molecule type: DNA
A;Residues: 1-500 <CNU>
A;Cross-references: EMBL:Z68196; NID:gl301809; PIDN:CAA92375.1; PID:e2i3848; PID:gl112
A;Experimental source: strain AB972
R;Mirande, M.; Waller, J.P.
J. Biol. Chem. 263, 18443-18451, 1988
A;Title: The yeast lysyl-tRNA synthetase gene. Evidence for general amino acid control
A;Reference number: A92695; MUID:89054027
A;Accession: B31899
A;Molecule type: DNA
A;Residues: 1-265 <MIR>
A;Cross-references: GB:J04186; PIDN:g171798; PIDN:AAA66915.1; PID:g808839
R;Arnold, W.; Becker, A.; Jaeger, W.; Kuester, H.; Nussbaumer, B.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67842
A;Accession: S67850
A;Molecule type: DNA
A;Residues: 1-500 <ARN>
A;Cross-references: EMBL:Z74332; NID:gl431481; PIDN:CAA98862.1; PID:e253306; PID:gl434
A;Experimental source: strain S288C

A:Map position: 4R
C:Superfamily: enoyl-CoA hydratase homology
F:59-222/Domain: enoyl-CoA hydratase homology <ECH>

Query Match 29.3%; Score 48; DB 2; Length 500;
 Best Local Similarity 50.0%; Pred. No. 28;
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 11 VCEPKYQTVSEPIRWK 26
 ||| | : : : |||
 Db 485 VCEKCEVNDGLRWK 500

RESULT 7
 I58383
 retinoblastoma binding protein 1, splice form I - human
 N:Alternate names: retinoblastoma-associated protein 2 (mismomer)
 N:Contains: retinoblastoma binding protein 1, splice form II
 C:Species: Homo sapiens (man)
 C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
 C:Accession: I58383; S16953; B42997
 R:Fattaey, A.R.; Helin, K.; Dembski, M.S.; Dyson, N.; Harlow, E.; Vuocolo, G.A.; Hanobik
 -Oncogene 8, 3149-3156, 1993
 A:Title: Characterization of the retinoblastoma binding proteins RBP1 and RBP2.
 A:Reference number: I58383; MUID:94020841
 A:Accession: I58383
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1257 <FAT>
 A:Cross-references: GB:S66427; NID:g435775; PIDN:RAB28543.1; PID:g435776
 R:Otterson, G.A.; Kratzke, R.A.; Lin, A.Y.; Johnston, P.G.; Kaye, F.J.
 Oncogene 8, 949-957, 1993
 A:Title: Alternative splicing of the RBP1 gene clusters in an internal exon that encodes
 A:Reference number: I58390; MUID:93205410
 A:Accession: I58390
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 338-384, 'V', 386-617, 'R', 619-652, 'V', 654-778, 'T', 780-1257 <OTT1>
 A:Cross-references: GB:S57153; NID:g298681; PIDN:RAB25833.1; PID:g298682
 A:Accession: I78883
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 338-384, 'V', 386-617, 'R', 619-652, 'V', 654-778, 'T', 780-1120, 1175-1257 <OTT2>
 A:Cross-references: GB:S57160; NID:g298683; PIDN:RAB25834.1; PID:g298684
 R:DeFeo-Jones, D.; Huang, P.S.; Jones, R.E.; Haskell, K.M.; Vuocolo, G.A.; Hanobik, M.G.
 Nature 352, 251-254, 1991
 A:Title: Cloning of cDNAs for cellular proteins that bind to the retinoblastoma gene pro
 A:Reference number: S16953; MUID:91312450
 A:Accession: S16953
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 855-1177, 'S', 1179-1195, 'SENIICL' <DEF>
 R:Kaelin Jr., W.G.; Krek, W.; Sellers, W.R.; DeCaprio, J.A.; Ajchenbaum, F.; Fuchs, C.S.
 Cell 70, 351-364, 1992
 A:Title: Expression cloning of a cDNA encoding a retinoblastoma-binding protein with E2F
 A:Reference number: A42997; MUID:92346721
 A:Accession: B42997
 A:Molecule type: mRNA
 A:Residues: 'MTFWKL', 510-617, 'R', 619-1257 <KAE>
 A:Experimental source: Akata cells
 A:Note: the cited GenBank accession number, M96577, is apparently a misprint and does no
 A:Note: sequence extracted from NCBI backbone (NCBIN:110020, NCBI:110022)
 C:Genetics:
 A:Gene: GDB:RBP1
 A:Cross-references: GDB:120340; OMIM:180260
 A:Map position: 3q21-3q22
 C:Superfamily: human retinoblastoma binding protein 1
 C:Keywords: alternative splicing
 F:1-1257/Product: retinoblastoma binding protein 1, splice form I #status predicted <SFI
 F:1-1120,1175-1257/Product: retinoblastoma binding protein 1, splice form II #status pre

Query Match 29.3%; Score 48; DB 1; Length 1257;
 Best Local Similarity 35.3%; Pred. No. 74;
 Matches 12; Conservative 6; Mismatches 8; Indels 8; Gaps 1;

QY 4 YNTQGSDV-----CEPKYQTVSEPIRWKLLM 29
 | | | | | | | | | | | | | | : | | |
 Db 9 YLTGTDVSAKYRGAFCEAKIKTKVRLVKVKVLL 42

RESULT 8
 T08979
 hypothetical protein F6G3.60 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 22-Oct-1999
 C:Accession: T08979
 R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.
 submitted to the Protein Sequence Database, May 1999
 A:Reference number: Z16520
 A:Accession: T08979
 A:Molecule type: DNA
 A:Residues: 1-424 <BEV>
 A:Cross-references: EMBL:AL078464; GSPDB:GN0062; ATSP:F6G3.60
 A:Experimental source: cultivar Columbia; BAC clone F6G3
 C:Genetics:
 A:Gene: ATSP:F6G3.60
 A:Map position: 4

Query Match 28.7%; Score 47; DB 2; Length 424;
 Best Local Similarity 36.1%; Pred. No. 33;
 Matches 13; Conservative 5; Mismatches 8; Indels 10; Gaps 2;

QY 2 QKYNTOGSDV-----CEP-----KYQTVSEPIRWKL 27
 | : | | | | | | | | | | | | | | : | | |
 Db 284 QRYRSOGGTVIDTGCSTILAREAYFTLSEIDFLL 319

RESULT 9
 S77213
 DNA-directed DNA polymerase (EC 2.7.7.7) III chain dnaX - Synecchocystis sp. (strain P
 N:Alternate names: protein sll1360
 C:Species: Synecchocystis sp.
 A:Variety: PCC 6803
 C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,
 O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas
 DNA Res. 3, 109-136, 1996
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecchocys
 s.
 A:Reference number: S74322; MUID:97061201
 A:Accession: S77213
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-1116 <KAN>
 A:Cross-references: EMBL:D90907; GB:AB001339; NID:g1652618; PIDN:BAAL17547.1; PID:d101
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C:Genetics:
 A:Gene: dnaX
 C:Keywords: nucleotidyltransferase

Query Match 28.7%; Score 47; DB 2; Length 1116;
 Best Local Similarity 55.6%; Pred. No. 92;
 Matches 10; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 7 QGSDVCEPKYQTVSEPIR 24
 | | | | | | | | | | : | | |
 Db 375.QDWDVCHPKYD--SQPIK 390

RESULT 10
 T0227
 NBS-LRR type resistance protein - rice (fragment)
 C:Species: Oryza sativa (rice)
 C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 03-Nov-2000
 C:Accession: T0227

C;Comment: By in vitro mutagenesis of the tat gene, it was demonstrated that the presend

Matches 9; Conservative 4; Mismatches 2; Indels 3; Gaps 1;

Qy 1 NQKY---NTQGSVDCEPK 15
: : : : :
Db 242 HKKYRYKNTKTRSDICTPK 259

RESULT 15

D64477
cobyrrinic acid a,c-diamide synthase homolog - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: D64477
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999
A:Accession: D64477
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-443 <BUL>
A:Cross-references: GB:U67583; GB:L77117; NID:g2826409; PIDN:AAB99432.1; PID:g1592071; T
C:Genetics:
A:Map position: REV1387339-1386008
C:Superfamily: coxyrrinic acid a,c-diamide synthase

Query Match 28.0%; Score 46; DB 2; Length 443;

Best Local Similarity 37.5%; Pred. No. 48;

Matches 9; Conservative 5; Mismatches 6; Indels 4; Gaps 1;

Qy 1 NQKYNTO-----GSDVCEPKYQTVS 20
: : : : :
Db 29 SKKYNVQGYKVGPDYIDPTYHTIA 52

Search completed: May 23, 2001, 15:32:01
Job time: 508 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:36:18 ; Search time 62.39 Seconds
(without alignments)
16.472 Million cell updates/sec

Title: US-08-887-977-10_COPY_177_206
Perfect score: 164
Sequence: 1 NQYNTQGSVDCEPKYQTVSEPIRWKLLML 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	164	100.0	374	1	CRK6_HUMAN
2	110	67.1	367	1	CRK6_MOUSE
3	52	31.7	98	1	Y481_METJA
4	51.5	31.4	815	1	RPCR_HUMAN
5	50	30.5	453	1	YUQP_CAEEL
6	49	29.9	1277	1	NPCL_FIG
7	48	29.3	500	1	YDAK_YEAST
8	46.5	28.4	358	1	RBBL_HUMAN
9	46.5	28.4	358	1	TAT_HTLIA
10	46.5	28.4	358	1	TAT_HTLIC
11	46.5	28.4	633	1	YIJ2_YEAST
12	46	28.0	443	1	COBB_METJA
13	46	28.0	1139	1	SRE2_CRIGR
14	46	28.0	2813	1	VWF_HUMAN
15	45.5	27.7	122	1	IFSG_MUSLU
16	45.5	27.7	168	1	ARPL_CAEEL
17	45.5	27.7	338	1	CYSP_ECOLI
18	45.5	27.7	338	1	CYSP_SALTY
19	45	27.4	835	1	YGH5_YEAST
20	45	27.4	867	1	CD97_HUMAN
21	45	27.4	867	1	POL_MPMV
22	44.5	27.1	950	1	YRM2_CAEEL
23	44	26.8	505	1	FRK_HUMAN
24	44	26.8	687	1	VIUA_VIBCH
25	44	26.8	747	1	GUND_CELFI
26	44	26.8	1009	1	AMPM_HELVI
27	44	26.8	3051	1	YXN3_CAEEL
28	43.5	26.5	437	1	WTM1_YEAST
29	43.5	26.5	721	1	PAL5_LYCES
30	43	26.2	285	1	GVC2_HALNI
31	43	26.2	285	1	GVC2_HALN2
32	43	26.2	566	1	XYLR_PSEPU
33	43	26.2	681	1	TRE_MANSE

34	43	26.2	867	1	POL_SRV1
35	43	26.2	901	1	SVV_LACCA
36	43	26.2	1691	1	POLN_HEVME
37	43	26.2	2183	1	RRPL_RINDR
38	42.5	25.9	453	1	GP39_HUMAN
39	42.5	25.9	1092	1	DPDQ_DRONE
40	42.5	25.9	1827	1	MAP2_HUMAN
41	42	25.6	116	1	MCS_HUMAN
42	42	25.6	513	1	COX1_HUMAN
43	42	25.6	514	1	COX1_PONPA
44	42	25.6	514	1	COX1_RHIUN
45	42	25.6	522	1	FBX7_HUMAN

ALIGNMENTS

RESULT	1
CKR6_HUMAN	
ID	CKR6_HUMAN
STANDARD:	PRT; 374 AA.
AC	P51684; Q92846; P78553;
DT	01-OCT-1996 (Rel. 34, Created)
DT	15-JUL-1998 (Rel. 36, Last sequence update)
DT	01-OCT-2000 (Rel. 40, Last annotation update)
DE	C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CCR-6) (LARC
DE	RECEPTOR) (GPR-CY4) (GPRCY4) (CHEMOKINE RECEPTOR-LIKE 3) (CKR-L3)
DE	(DRY6).
GN	CCR6 OR CMKR6 OR STRL22 OR GPR29 OR CKRL3.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A., AND FUNCTION.
RX	MEDLINE=97313465; PubMed=9169459;
RA	Baba M., Imai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K.,
RA	Nomiyama H., Yoshie O.
RT	"Identification of CCR6, the specific receptor for a novel
RT	lymphocyte-directed CC chemokine LARC."
RL	J. Biol. Chem. 272:14893-14898(1997).
RN	[2]
RP	SEQUENCE FROM N.A.
RA	Lautens L.L., Modi W., Bonner T.I.;
RL	Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN	[3]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=97040707; PubMed=8886020;
RA	Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G.;
RT	"Molecular cloning and RNA expression of two new human chemokine
RT	receptor-like genes."
RL	Biochem. Biophys. Res. Commun. 227:846-853(1996).
RN	[4]
RP	SEQUENCE FROM N.A.
RA	McCoy R., Perlmuter D.H.;
RL	Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN	[5]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=97224503; PubMed=9070937;
RA	Liao F., Lee H.-H., Farber J.M.;
RT	"Cloning of STRL22, a new human gene encoding a G-protein-coupled
RT	receptor related to chemokine receptors and located on chromosome
RT	6q27."
RL	Genomics 40:175-180(1997).
CC	-!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-
CC	ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE
CC	INTRACELLULAR CALCIUM IONS LEVEL.
CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC	-!- TISSUE SPECIFICITY: SPLEEN, LYMPH NODES, APPENDIX, AND FETAL
CC	LIVER. EXPRESSED IN LYMPHOCYTES, T CELLS AND B CELLS BUT NOT IN
CC	NATURAL KILLER CELLS, MONOCYTES, OR GRANULOCYTES.
CC	-!- INDUCTION: INTERLEUKIN-2.
CC	-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC	-!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-6 IS THE INITIATOR.


```
RESULT 3
Y481_METJA STANDARD; PRT; 98 AA.
AC Q57906;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL PROTEIN MJ0481.
GN MJ0481.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii".
RN Science 273:1058-1073(1996).
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CC -----
CC EMBL: U67498; AAB98472.1; --
CC TIGR: MJ0481; --
CC KW Hypothetical protein.
SQ SEQUENCE 98 AA; 11218 MW; 6F31A08240C3CB3 CRC64;

Query Match 31.7%; Score 52; DB 1; Length 98;
Best Local Similarity 52.6%; Pred. No. 0.64; 7; Indels 0; Gaps 0;
Matches 10; Conservative 2; Mismatches 7;

QY 3 KYNTQGSVDCEPKYQTVSE 21
II :|||: ||||
Db 29 KYQKNGSDITFEKYPTVGE 47

RESULT 4
RPCR_HUMAN STANDARD; PRT; 815 AA.
AC Q2834; Q93039; O00737; O00702;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE X-LINKED RETINITIS PIGMENTOSA GTPASE REGULATOR.
GN RPCR OR RP3 OR XLRP3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96241570; PubMed=8673101;
RA Meindl A., Dry K., Herrmann K., Manson F., Ciccodicola A.,
RA Edgar A., Carvalho M.R.S., Achatz H., Hellebrand H., Lennon A.,
RA Migliaccio C., Porter K., Zrenner E., Bird A., Jay M., Lorenz B.,
RA Wittwer B., D'Urso M., Meitinger T., Wright A.;
RT "A gene (RPCR) with homology to the RCC1 guanine nucleotide exchange
RT factor is mutated in X-linked retinitis pigmentosa (RP3).";
RN Nat. Genet. 13:35-42(1996).
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RA Berger W.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 1-509 FROM N.A., AND VARIANTS RP3 C-130; S-235 AND S-275.
RC TISSUE=Retina;
RX MEDLINE=96414315; PubMed=8817343;
RA Roepman R., van Duijnhoven G., Rosenberg T., Pinckers A.J.L.G.,
RA Bleeker-Wagemakers L.M., Bergen A.A.B., Post J., Beck A.,
RA Reinhardt R., Ropers H.-H., Cremers F., Berger W.;
RT "Positional cloning of the gene for X-linked retinitis pigmentosa 3:
RT homology with the guanine-nucleotide-exchange factor RCC1.";
RL Hum. Mol. Genet. 5:1035-1041(1996).
RN [4]
RP VARIANTS RP3.
RX MEDLINE=98153625; PubMed=9399904;
RA Buraczynska M., Wu W., Fujita R., Buraczynska K., Phelps E.,
RA Andreasson S., Bennett J., Birch D.G., Fishman G.A., Hoffman D.R.,
RA Inana G., Jacobson S.G., Musarella M.A., Sieving P.A., Swaroop A.;
RT "Spectrum of mutations in the RPCR gene that are identified in 20% of
RT families with X-linked retinitis pigmentosa.";
RL Am. J. Hum. Genet. 61:1287-1292(1997).
RN [5]
RP VARIANT RP3 VAL-60.
RX MEDLINE=99070804; PubMed=9855162;
RA Fishman G.A., Grover S., Jacobson S.G., Alexander K.R., Derlacki D.J.,
RA Wu W., Buraczynska M., Swaroop A.;
RT "X-linked retinitis pigmentosa in two families with a missense
RT mutation in the RPCR gene and putative change of glycine to valine at
RT codon 60.";
RL Ophthalmology 105:2286-2296(1998).
CC -!- FUNCTION: COULD BE GUANINE-NUCLEOTIDE RELEASING FACTOR.
CC -!- SUBCELLULAR LOCATION: POSSIBLY MEMBRANE-ANCHORED.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. THE SMALL FORM
CC LACKS PART OF REPEAT 7.
CC -!- TISSUE SPECIFICITY: HEART, BRAIN, PLACENTA, LUNG, LIVER, MUSCLE,
CC KIDNEY, PANCREAS AND FETAL RETINAL PIGMENT EPITHELIUM.
CC -!- DISEASE: DEFECTS IN RPCR ARE RESPONSIBLE FOR X-LINKED RETINITIS
CC PIGMENTOSA-3 (XLRP-3 OR RP3), A FORM OF CHOROIDO-RETINAL
CC DEGENERATION WHICH IS DISTINGUISHED FROM OTHER TYPES BY THE
CC PRESENCE IN HETEROZYGOUS WOMEN OF A TAPETAL-LIKE RETINAL REFLEX (A
CC BRILLIANT, SCINTILLATING, GOLDEN-HUED, PATCHY APPEARANCE MOST
CC STRIKING AROUND THE MACULA) BUT NO VISUAL DEFECT.
CC -!- SIMILARITY: CONTAINS 7 RCC1 REPEATS.
CC -!- DATABASE: NAME-Mutations of the RPCR gene;
CC NOTE=Retina International's Scientific Newsletter;
CC WWW="http://www.irpa.org/sci-news/rp3mut.htm".
CC -----
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CC -----
CC EMBL: U57629; AAC50481.1; --
CC DR EMBL: X97668; CAA66258.1; --
CC MIM: 312610; --
CC InterPro: IPR000408; --
CC Pfam: PF00415; RCC1_7.
CC PROSITE: PS00626; RCC1_2; 4.
CC PROSITE: PS00112; RCC1_3; 6.
CC Guanine-nucleotide releasing factor; Alternative splicing; Repeat;
KW Vision; Retinitis pigmentosa; Disease mutation.
FT REPEAT 11 52
FT REPEAT 53 104
FT RCC1 2.
```

FT REPEAT 106 157 RCC1 3.
FT REPEAT 158 207 RCC1 4.
FT REPEAT 208 260 RCC1 5.
FT REPEAT 262 312 RCC1 6.
FT REPEAT 314 366 RCC1 7.
FT VARSPLIC 354 415 MISSING (IN SHORT ISOFORM).
FT VARIANT 60 60 G -> V (IN RP3).
FT VARIANT 60 60 G -> N (IN RP3).
FT VARIANT 60 60 /FTId=VAR_008501.
FT VARIANT 60 60 /FTId=VAR_008502.
FT VARIANT 75 75 I -> V (IN RP3).
FT VARIANT 75 75 /FTId=VAR_008503.
FT VARIANT 98 98 H -> Q (IN RP3).
FT VARIANT 98 98 /FTId=VAR_008504.
FT VARIANT 130 130 F -> C (IN RP3).
FT VARIANT 130 130 /FTId=VAR_008505.
FT VARIANT 215 215 G -> V (IN RP3).
FT VARIANT 215 215 /FTId=VAR_008506.
FT VARIANT 235 235 P -> S (IN RP3).
FT VARIANT 235 235 /FTId=VAR_008507.
FT VARIANT 250 250 C -> R (IN RP3).
FT VARIANT 250 250 /FTId=VAR_008508.
FT VARIANT 262 262 A -> G (IN RP3).
FT VARIANT 262 262 /FTId=VAR_008509.
FT VARIANT 275 275 G -> S (IN RP3).
FT VARIANT 275 275 /FTId=VAR_008510.
FT VARIANT 425 425 R -> K (IN RP3).
FT VARIANT 425 425 /FTId=VAR_008511.
FT VARIANT 431 431 I -> V (IN RP3).
FT VARIANT 436 436 /FTId=VAR_008512.
FT VARIANT 566 566 G -> E (IN RP3).
FT VARIANT 566 566 /FTId=VAR_008513.
FT CONFLICT 1 3 MRE -> MAKLRSTTAL (IN REF. 3).
SQ SEQUENCE 815 AA; 90244 MW; 70D84EAD988348D1 CRC64;

Query Match 31.4%; Score 51.5; DB 1; Length 815;
Best Local Similarity 32.1%; Pred. No. 7;
Matches 9; Conservative 7; Mismatches 5; Indels 7; Gaps 1;

Qy 5 NTOQ-----SDVCEPKYQTVSEPIRW 25
I::I I::I I::I I::I I::I I::I I::I I::I I::I I::I
Db 167 NSEQIGLKNSVNCVPOQVTGKPVSW 194

RESULT 5
YUQP_CAEEL STANDARD; PRT; 453 AA.
AC Q19895;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL 52.9 KDA PROTEIN F28H7.8 IN CHROMOSOME V.
GN F28H7.8.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Berks M.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SEC14 CYTOSOLIC FACTOR FAMILY.
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CC -----
DR EMBL; 272508; CAA96639.1; -
DR WormPep; F28H7.8; CE05757.
DR InterPro; IPR001251; -
DR Pfam; PF00650; CRAL_TRIO; 1.
DR Hypothetical protein.
SQ SEQUENCE 453 AA; 52926 MW; CC07AF08D50FDE79 CRC64;

Query Match 30.5%; Score 50; DB 1; Length 453;
Best Local Similarity 37.5%; Pred. No. 6.3;
Matches 9; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy 2 QKYNTOGSDVCEPKYQTVSEPIRW 25
I::I I::I I::I I::I I::I I::I I::I I::I I::I I::I
Db 20 EQVRLQVSDVIDPRYDTKNMLRW 43

RESULT 6

NPCL_PIG STANDARD; PRT; 1277 AA.
AC P56941.
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE NIEMANN-PICK C1 PROTEIN PRECURSOR.
GN NPCL.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Gevry N.Y., Lacroix D.A., Song J.H., Murphy B.D.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INVOLVED IN THE INTRACELLULAR TRAFFICKING OF CHOLESTEROL
CC MAY BE CRUCIAL FOR MAINTAINING THE STRUCTURAL AND FUNCTIONAL
CC INTEGRITY OF NERVE TERMINALS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. FOUND IN LATE
CC ENDOSOMES AND LYOSOMES (BY SIMILARITY).
CC -!- DOMAIN: A CYSTEINE-RICH N-TERMINAL DOMAIN AND A C-TERMINAL DOMAIN
CC CONTAINING A DI-LEUCINE MOTIF NECESSARY FOR LYOSOMAL TARGETING
CC ARE CRITICAL FOR MOBILIZATION OF CHOLESTEROL FROM LYOSOMES (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE PATCHED FAMILY.
CC -----
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DR EMBL; AF169635; RAD47090.1; -
DR PROSITE; PS50156; SSD; 1.
KW Signal; Glycoprotein; Transmembrane; Lysosome.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 1277 NIEMANN-PICK C1 PROTEIN.
FT DOMAIN 249 259 POLY-PRO.
FT DOMAIN 1274 1277 DI-LEUCINE MOTIF.
FT TRANSMEM 271 291 POTENTIAL.
FT TRANSMEM 352 372 POTENTIAL.
FT TRANSMEM 623 643 POTENTIAL.
FT TRANSMEM 655 675 POTENTIAL.
FT TRANSMEM 685 705 POTENTIAL.
FT TRANSMEM 761 781 POTENTIAL.
FT TRANSMEM 834 854 POTENTIAL.
FT TRANSMEM 1099 1119 POTENTIAL.
FT TRANSMEM 1125 1145 POTENTIAL.
FT TRANSMEM 1196 1216 POTENTIAL.

[illegible]

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RESULT 9
TAT_HTLIA
ID TAT_HTLIA STANDARD; PRT; 358 AA.
AC P03409;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 01-JAN-1990 (Rel. 13, Last annotation update)
DE TRANS-ACTIVATING TRANSCRIPTIONAL REGULATORY PROTEIN (X-LOR PROTEIN)
DE (PX PROTEIN).
GN TAT.
OS Human T-cell leukemia virus type I (strain ATK) (HTLV-I).
OC Viruses; Retroviridae; BLV-HTLV retroviruses.
OX NCBI_TaxID=11926;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83221647; PubMed=6304725;
RA Seiki M., Hattori S., Hirayama Y., Yoshida M.;
RT "Human adult T-cell leukemia virus: complete nucleotide sequence of
the provirus genome integrated in leukemia cell DNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:3618-3622(1983).
RN [2]
RP EXPERIMENTAL DETAILS.
RX MEDLINE=85244620; PubMed=2990037;
RA Chen I.S.Y., Slamon D.J., Rosenblatt J.D., Shah N.P., Quan S.G.,
RA Wachsmann W.;
RT "The x gene is essential for HTLV replication.";
RL Science 229:54-58(1985).
CC -!- MISCELLANEOUS: BY IN VITRO MUTAGENESIS OF THE TAT-I GENE, IT WAS
CC DEMONSTRATED THAT THE PRESENCE OF A FUNCTIONAL TAT-I GENE PRODUCT
CC WAS NECESSARY FOR EFFICIENT HTLV TRANSCRIPTION.
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CC -----
DR EMBL; J02029; -: NOT_ANNOTATED_CDS.
DR PIR; A04011; TNLJH1.
KW Transcription regulation.
SQ SEQUENCE 358 AA; 39984 MW; EFA172B360542E41 CRC64;

Query Match 28.4%; Score 46.5; DB 1; Length 358;
Best Local Similarity 57.1%; Pred. No. 16;
Matches 12; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

QY 8 GSDVCEPKYQTVSEPIRWKLL 28
|| || || || || || || ||
Db 154 GSVVCMYLYQ-LSPPTWPLL 173

RESULT 10
TAT_HTLIC
ID TAT_HTLIC STANDARD; PRT; 358 AA.
AC P14079;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-AUG-1990 (Rel. 15, Last annotation update)
DE TRANS-ACTIVATING TRANSCRIPTIONAL REGULATORY PROTEIN (X-LOR PROTEIN)
DE (PX PROTEIN).
GN TAT.
OS Human T-cell leukemia virus type I (Caribbean isolate) (HTLV-I).
OC Viruses; Retroviridae; BLV-HTLV retroviruses.
OX NCBI_TaxID=11927;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88274338; PubMed=2899128;
RA Malik K.T.A., Even J., Karpas A.;
RT "Molecular cloning and complete nucleotide sequence of an adult T
cell leukaemia virus/human T cell leukaemia virus type I
--
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RT (ATLV/HTLV-I) isolate of Caribbean origin: relationship to other
RT members of the ATLV/HTLV-I subgroup.";
RL J. Gen. Virol. 69:1695-1710(1988).
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CC -----
DR EMBL; D13784; -: NOT_ANNOTATED_CDS.
DR PIR; E28136; TNLJCN.
KW Transcription regulation.
SQ SEQUENCE 358 AA; 40026 MW; 3CACDB50934426E3 CRC64;

Query Match 28.4%; Score 46.5; DB 1; Length 358;
Best Local Similarity 57.1%; Pred. No. 16;
Matches 12; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

QY 8 GSDVCEPKYQTVSEPIRWKLL 28
|| || || || || || || ||
Db 154 GSVVCMYLYQ-LSPPTWPLL 173

RESULT 11
YIJ2_YEAST
ID YIJ2_YEAST STANDARD; PRT; 633 AA.
AC F40497;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHEICAL 71.0 KDA PROTEIN IN SGAI-KTR7 INTERGENIC REGION.
GN YIL052W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,
RA Churcher C.M., Connor R., Copsey T., Hunt S., Devlin K., Fraser A.,
RA Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M.,
RA Louis E., Lyle G., Moule S., Moule T., Odell C., Pearson D.,
RA Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
RA Walsh S.V., Whitehead S.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; Z46728; CAA86702.1; -.
DR SGD; S0001354; YIL092W.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 99 118 POTENTIAL.
FT TRANSMEM 217 233 POTENTIAL.
SQ SEQUENCE 633 AA; 71006 MW; 7B9279E345D4F656 CRC64;

Query Match 28.4%; Score 46.5; DB 1; Length 633;
Best Local Similarity 50.0%; Pred. No. 29;
Matches 9; Conservative 4; Mismatches 2; Indels 3; Gaps 1;

QY 1 NQKY---NTQSGDVCEPK 15
::|| || || || || || || ||
```


FT DNA_BIND 328 341 BASIC DOMAIN.
 FT DOMAIN 342 379 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
 FT DOMAIN 378 399 LEUCINE-ZIPPER (POTENTIAL).
 FT DOMAIN 589 593 POLY-ALA.
 FT DOMAIN 857 860 POLY-SER.
 FT SITE 460 461 BREAKPOINT FOR TRANSLLOCATION TO FORM
 FT SREBP-2 FUSION PROTEINS IN SRD
 FT PHENOTYPES.
 FT SITE 466 467 CLEAVAGE: (BY APOPAIN AND CASPASE-7) (BY
 FT VARIANT 493 493 S -> N (IN 50% OF THE MOLECULES)).
 FT SEQUENCE 1139 AA; 123655 MW; E81C2778EBF02653 CRC64;
 SQ

Query Match 28.0%; Score 46; DB 1; Length 1139;
 Best Local Similarity 31.6%; Pred. No. 64;
 Matches 6; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 7 QGSDVCEPKYQTVSEPIRW 25
 : : | : : | : : | :
 Db 740 RAQSLCGPEHSTVPSLRW 758

RESULT 14
 VWF_HUMAN
 ID VWF_HUMAN STANDARD; PRT; 2813 AA.
 AC P04275;
 DT 20-MAR-1987 (Rel. 04; Created)
 DT 01-JUL-1993 (Rel. 26; Last sequence update)
 DT 01-OCT-2000 (Rel. 40; Last annotation update)
 DE VON WILLEBRAND FACTOR PRECURSOR (VWF).
 GN FBWV OR VWF.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90062044; PubMed=2584182;
 RA Mancuso D.J., Tuley E.A., Westfield L.A., Worrall N.K.,
 RA Shelton-Inloes B.B., Sorace J.M., Alevy Y.G., Sadler J.E.;
 RT "Structure of the gene for human von Willebrand factor.";
 RL J. Biol. Chem. 264:19514-19527(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87016349; PubMed=3489923;
 RA Bonthron D., Orr E.C., Mitsock L.M., Ginsburg D., Handin R.I.,
 RA Orkin S.H.;
 RT "Nucleotide sequence of pre-pro-von Willebrand factor cDNA.";
 RL Nucleic Acids Res. 14:7125-7128(1986).
 RN [3]
 RP SEQUENCE OF 1-120 FROM N.A. AND SEQUENCE OF 23-56.
 RC TISSUE-Umbilical vein endothelial cells;
 RX MEDLINE=87213253; PubMed=3495266;
 RA Shelton-Inloes B.B., Broze G.J. Jr., Millett J.P., Sadler J.E.;
 RT "Evolution of human von Willebrand factor: cDNA sequence
 RT polymorphisms, repeated domains, and relationship to von Willebrand
 RT antigen II.";
 RL Biochem. Biophys. Res. Commun. 144:657-665(1987).
 RN [4]
 RP SEQUENCE OF 1-1400 FROM N.A.
 RX MEDLINE=87004550; PubMed=3019665;
 RA Verweij C.L., Diergaarde P.J., Hart M., Pannekoek H.;
 RT "Full-length von Willebrand factor (vWF) cDNA encodes a highly
 RT repetitive protein considerably larger than the mature vWF subunit.";
 RL EMBO J. 5:1839-1847(1986).
 RN [5]
 RP ERRATUM.
 RA Verweij C.L., Diergaarde P.J., Hart M., Pannekoek H.;
 RL EMBO J. 5:3074-3074(1986).
 RN [6]
 RP SEQUENCE OF 764-2813.
 RX MEDLINE=86269895; PubMed=3524673;

RA Titani K., Kumar S., Takio K., Ericsson L.H., Wade R.D., Ashida K.,
 RA Walsh K.A., Chopek M.W., Sadler J.E., Fujikawa K.;
 RT "Amino acid sequence of human von Willebrand factor.";
 RL Biochemistry 25:3171-3184(1986).
 RN [7]
 RP SEQUENCE OF 781-1424 FROM N.A.
 RX MEDLINE=86269894; PubMed=3488076;
 RA Shelton-Inloes B.B., Titani K., Sadler J.E.;
 RT "cDNA sequences for human von Willebrand factor reveal five types of
 RT repeated domains and five possible protein sequence polymorphisms.";
 RL Biochemistry 25:3164-3171(1986).
 RN [8]
 RP SEQUENCE OF 764-873 AND 1289-2813 FROM N.A.
 RX MEDLINE=86016708; PubMed=2864688;
 RA Sadler J.E., Shelton-Inloes B.B., Sorace J.M., Harlan J.M.,
 RA Titani K., Davie E.W.;
 RT "Cloning and characterization of two cDNAs coding for human von
 RT Willebrand factor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:6394-6398(1985).
 RN [9]
 RP SEQUENCE OF 990-1947 FROM N.A.
 RX MEDLINE=91105089; PubMed=1988024;
 RA Mancuso D.J., Tuley E.A., Westfield L.A., Lester-Mancuso T.L.,
 RA Le Beau M.M., Sorace J.M., Sadler J.E.;
 RT "Human von Willebrand factor gene and pseudogene: structural analysis
 RT and differentiation by polymerase chain reaction.";
 RL Biochemistry 30:253-269(1991).
 RN [10]
 RP SEQUENCE OF 2731-2813 FROM N.A.
 RX MEDLINE=85269603; PubMed=3875078;
 RA Verweij C.L., de Vries C.J.M., Distel B., van Zonneveld A.-J.,
 RA Geurts van Kessel A., van Mourik J.A., Pannekoek H.;
 RT "Construction of cDNA coding for human von Willebrand factor using
 RT antibody probes for colony-screening and mapping of the chromosomal
 RT gene.";
 RL Nucleic Acids Res. 13:4699-4717(1985).
 RN [11]
 RP SEQUENCE OF 1-177 FROM N.A.
 RX MEDLINE=88111704; PubMed=2828057;
 RA Bonthron D., Orkin S.H.;
 RT "The human von Willebrand factor gene. Structure of the 5' region.";
 RL Eur. J. Biochem. 171:51-57(1988).
 RN [12]
 RP SEQUENCE OF 2621-2813 FROM N.A.
 RX MEDLINE=85244588; PubMed=3874428;
 RA Ginsburg D., Handin R.I., Bonthron D.T., Donlon T.A., Bruns G.A.P.,
 RA Latt S.A., Orkin S.H.;
 RT "Human von Willebrand factor (vWF): isolation of complementary DNA
 RT (cDNA) clones and chromosomal localization.";
 RL Science 228:1401-1406(1985).
 RN [13]
 RP SEQUENCE OF 2731-2813 FROM N.A.
 RX MEDLINE=85201687; PubMed=3873280;
 RA Lynch D.C., Zimmerman T.S., Collins C.J., Brown M., Morin M.J.,
 RA Ling E.H., Livingston D.M.;
 RT "Molecular cloning of cDNA for human von Willebrand factor:
 RT authentication by a new method.";
 RL Cell 41:49-56(1985).
 RN [14]
 RP REVISIONS.
 RA Lynch D.C.;
 RL Submitted (JUL-1991) to the EMBL/GenBank/DBJ databases.
 RN [15]
 RP SEQUENCE OF 2731-2813 FROM N.A.
 RX MEDLINE=87260814; PubMed=3496594;
 RA Collins C.J., Underdahl J.P., Levene R.B., Ravera C.P.,
 RA Morin M.J., Dombalagian M.J., Ricca G., Livingston D.M.,
 RA Lynch D.C.;
 RT "Molecular cloning of the human gene for von Willebrand factor and
 RT identification of the transcription initiation site.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4393-4397(1987).
 RN [16]
 RP DISULFIDE BONDS.

```

RT mutations cluster in one disulfide loop between proposed platelet
RT glycoprotein Ib binding sequences.*;
RT J. Clin. Invest. 87:1220-1226(1991).
RT [26]
RP VARIANTS TRP-I306; CYS-I308; MET-I316; GLN-I341 AND HIS-I399.
RX MEDLINE-91185602; PubMed-1672694;

Query Match      28.0%; Score 46; DB 1; Length 2813;
Best Local Similarity 41.2%; Pred. No. 1.6e+02;
Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 7 QGSDVCEPKYQTVSEPI 23
   | : | | : | : | : |
DB 2314 QNADQCPEYECVDFV 2330

RESULT 15
IPFSG_MUSLU
IID IPFG_MUSLU STANDARD; PRT; 122 AA.
AC P81481;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE DOUBLE-HEADED PROTEASE INHIBITOR, SUBMANDIBULAR GLAND.
OS Mustela lutreola (European mink).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustela.
NCBI_TaxID=9666;
RN [1]
RP SEQUENCE.
RX MEDLINE=94007749; PubMed=8403842;
RA Hochstrasser K., Wächter E., Reisinger P.W.M., Greim M.,
RT Albrecht G.J., Gebhard W.;
RT "Amino acid sequences of mammalian kazal-type proteinase inhibitors
RT from salivary glands.";
RT Comp. Biochem. Physiol. 106B:103-108(1993).
RZ -!- FUNCTION: THIS INHIBITOR IS COMPOSED OF TWO HOMOLOGOUS ACTIVELY
RZ INHIBITING HALVES: ONE WHICH INHIBITS TRYPSIN, THE OTHER WHICH
RZ INHIBITS ELASTASE.
RZ -!- SIMILARITY: BELONGS TO THE PROTEASE INHIBITORS KAZAL FAMILY.
RZ InterPro: IPR001239;
RZ InterPro: IPR002350;
RZ Pfam: PF00050; kazal; 2.
RZ PRINTS: PR00290; KAZALINHBTR.
RZ PROSITE: PS00282; KAZAL; 2.
RK Serine protease inhibitor; Repeat: Submandibular gland.
RFT DOMAIN 1 68 PSTI-TYPE.
RFT DOMAIN 69 122 PSTI-TYPE.
RFT ACT_SITE 30 31 REACTIVE BOND 1 (TRYPSIN).
RFT ACT_SITE 81 82 REACTIVE BOND 2 (ELASTASE).
RFT DISULFID 16 50 BY SIMILARITY.
RFT DISULFID 28 47 BY SIMILARITY.
RFT DISULFID 36 68 BY SIMILARITY.
RFT DISULFID 72 101 BY SIMILARITY.
RFT DISULFID 79 98 BY SIMILARITY.
RFT DISULFID 87 119 BY SIMILARITY.
RFT SEQUENCE 122 AA; 13710 MW; AAD20E149B464A0 CRC64;

Query Match      27.7%; Score 45.5; DB 1; Length 122;
Best Local Similarity 55.6%; Pred. No. 7.3;
Matches 10; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

QY 3 KYNTQSD-VCEPKYQTV 19
   ||||| : | : | : |
DB 18 KYNTTGEFACSRKQVP 35

Search completed: May 23, 2001, 15:36:19
Job time: 650 sec

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RP VARIANTS TRP-1306; CYS-1308 AND PRO-1613.
RX MEDLINE=91185601; PubMed=2010538;

DR PROSITE; PS00626; RCCL_2; UNKNOWN_4.
SQ SEQUENCE 1001 AA; 111855 MW; DE145FBFEAF0F8759 CRC64;

Query Match 30.2%; Score 49.5; DB 11; Length 1001;
Best Local Similarity 39.3%; Pred. No. 48;
Matches 11; Conservative 4; Mismatches 6; Indels 7; Gaps 1;

QY 5 NTQG-----SDVCEPKYQTVSEPIRW 25
|:|:| | | | | | | | | | | | | | | |
Db 167 NSEGIQIGLEDKSNVCIPHEVTGKPISW 194

RESULT 10
Q9LKA5
ID Q9LKA5 PRELIMINARY; PRT; 395 AA.
AC Q9LKA5;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE SIMILARITY TO DAG PROTEIN.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety pl,
RT TAC and BAC clones.";
RL DNA Res. 7:217-221(2000).
DR EMBL; AP000370; BAA97063.1; -.
SQ SEQUENCE 395 AA; 42869 MW; D15E5CCC89E2A33C CRC64;

Query Match 29.9%; Score 49; DB 10; Length 395;
Best Local Similarity 41.7%; Pred. No. 21;
Matches 10; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 NOKYNTQGSQSDVCEPKYQTVSEPIR 24
| | | | | | | | | | | | | | | |
Db 363 NNNYQQGGSGMQQPYQNNYPNR 386

RESULT 11
Q9NQ00
ID Q9NQ00 PRELIMINARY; PRT; 1276 AA.
AC Q9NQ00;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE NIEMANN-PICK TYPE C1 DISEASE PROTEIN.
GN NPC1.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Murakawa M., Freeman M.W.;
RT "Feline Niemann-Pick type C1 disease protein (NPC1).";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF258783; AAF72187.1; -.
SQ SEQUENCE 1276 AA; 141739 MW; CE9B7A0261691256 CRC64;

Query Match 29.9%; Score 49; DB 6; Length 1276;
Best Local Similarity 45.5%; Pred. No. 73;
Matches 10; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 9 SDVCEPKYQTVSEPIRWKLLML 30
| | | | | | | | | | | | | | | |
Db 244 SIVCGPRQPPTVPVWRILGL 265

RESULT 12
Q9JLG3
ID Q9JLG3 PRELIMINARY; PRT; 1277 AA.
AC Q9JLG3;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE NIEMANN-PICK TYPE C1 PROTEIN.
GN NPC1.
OS Cricetulus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RA Cruz J.C., Sugii S., Yu C., Chang T.-Y.;
RT "Role of Niemann-Pick Type C1 Protein in Intracellular Trafficking of
RT Low Density Lipoprotein-derived Cholesterol.";
RL J. Biol. Chem. 275:4013-4021(2000).
DR EMBL; AF182744; AAF31692.1; -.
SQ SEQUENCE 1277 AA; 142817 MW; 6B3D638094B4E156 CRC64;

Query Match 29.9%; Score 49; DB 11; Length 1277;
Best Local Similarity 45.5%; Pred. No. 73;
Matches 10; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 9 SDVCEPKYQTVSEPIRWKLLML 30
| | | | | | | | | | | | | | | |
Db 244 SIVCGPRQPPTVPVWRILGL 265

RESULT 13
Q9VBW7
ID Q9VBW7 PRELIMINARY; PRT; 653 AA.
AC Q9VBW7;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE CG13661 PROTEIN.
GN CG13661.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,

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Query Match      29.3%; Score 48; DB 10; Length 53;
Best Local Similarity 52.9%; Pred. No. 3.7;
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:28:31 ; Search time 184.73 Seconds
(without alignments)
7.117 Million cell updates/sec

Title: US-08-887-977-10_COPY_207_229

Perfect score: 123

Sequence: 1 GLELLFGFFIPLMFMYCTIV 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_0401.*
1: /SID56/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID56/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID56/gcgdata/geneseq/geneseq/AA1982.DAT.*
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21: /SID56/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID56/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	123	100.0	365	19	W48086 Human dendritic ce
2	123	100.0	365	21	Y97077 Primate (human) ch
3	67	54.5	355	14	R33420 Human IL-8 recepto
4	67	54.5	355	17	B09990 Human IL-8 recepto
5	67	54.5	358	16	R80952 Recombinant high a
6	67	54.5	360	13	R28273 Sequence in a low
7	67	54.5	360	16	R80758 Interleukin 8 rece
8	67	54.5	360	16	R80953 Recombinant high a
9	67	54.5	1064	16	R70124 IL8-R type 2-GBP 1
10	66	53.7	302	19	W70001 Rodent chemokine r
11	66	53.7	351	20	Y23825 A7 times membrane

12	66	53.7	359	15	R53747 Seven transmembran
13	66	53.7	359	19	W48728 Murine V31 seven t
14	66	53.7	359	21	B21691 Murine 7TM recepto
15	66	53.7	378	21	B21699 7TM receptor prote
16	66	53.7	474	21	B36479 Rat SNORF36 recept
17	65	52.8	342	19	W80806 STRL33 protein seq
18	65	52.8	342	19	W54041 Human HBMBU14 prot
19	65	52.8	342	20	Y39366 Platelet factor-4
20	65	52.8	342	20	W97783 Human HIV/SIV rece
21	65	52.8	342	20	W97784 African green monk
22	65	52.8	342	20	W97785 Pig-tailed macaque
23	65	52.8	354	13	R53932 Interleukin 8 (IL-
24	65	52.8	355	13	R28272 Sequence in a high
25	65	52.8	355	16	R80950 Recombinant high a
26	65	52.8	357	21	B19605 Human CC chemokine
27	65	52.8	357	21	Y90615 Human G protein-co
28	65	52.8	357	21	Y90649 Human mutant G pro
29	65	52.8	369	19	W51405 Mouse protease-act
30	64	52.0	312	15	R48717 G-protein coupled
31	64	52.0	312	17	W02689 Interleukin-8 rece
32	64	52.0	350	13	R27791 Interleukin-8 rece
33	64	52.0	350	16	R68811 Interleukin 8 rece
34	64	52.0	350	16	R80756 Recombinant high a
35	64	52.0	350	17	B09989 Human IL-8 recepto
36	64	52.0	350	17	B09989 Human IL-8 recepto
37	64	52.0	1060	16	R70123 IL8-R type 1-GBP 1
38	63	51.2	29	19	W39999 Peptide effecting
39	63	51.2	209	21	B58414 Lung cancer associ
40	63	51.2	269	21	Y94446 Rhodopsin family t
41	63	51.2	269	21	Y44366 Seven transmembran
42	63	51.2	355	15	R52749 C-C chemokine rece
43	63	51.2	355	18	W26588 Human MIP-1 alpha/
44	63	51.2	355	18	W25751 Human MIP-lalpha/R
45	63	51.2	355	21	B20571 Human CC-chemokine

ALIGNMENTS

RESULT 1

W48086 ID W48086 standard; Protein; 365 AA.

XX AC W48086;

XX DT 11-JUN-1998 (first entry)

XX DE Human dendritic cell chemokine receptor.

XX DE Human; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta; receptor; dendritic cell; macrophage; inflammation; asthma.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Misc-difference 193 /note= "encoded by CAN"

XX FT W09801557-A2.

XX PN 15-JAN-1998.

XX PD 02-JUL-1997; 97WO-US10819.

XX PF 04-JUN-1997; 97US-0048593.

XX PR 05-JUL-1996; 96US-0675814.

XX PR 11-OCT-1996; 96US-0028329.

XX PA (SCHE) SCHERING CORP.

XX PI Gish KC, Schall TJ, Vicari A, Wang W, Zlotnik A;

XX XX WPI; 1998-101054/09.

DR N-PSDB; V15418.
XX Novel chemokines, e.g. thymus expressed chemokine - used for
PT treating inflammatory conditions including asthma.
XX
XX Claim 3; Page 94-95; 202pp; English.
XX
XX The present sequence represents human dendritic cell chemokine receptor.
CC Antibodies which bind to the protein can be used in detecting or
CC diagnosing various immunological conditions related to expression
CC of the protein. The nucleic acid can be used for screening and
CC isolating DNA clones for the chemokines, especially from other
CC species. The chemokine can be used in the treatment of conditions
CC associated with abnormal physiology or development, including
CC inflammatory conditions such as asthma.
XX
XX Sequence 365 AA;
SQ

Query Match 100.0%; Score 123; DB 19; Length 365;
Best Local Similarity 100.0%; Pred. No. 2e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLELLFGFFIPLMFIFCYTFIV 23
Db 207 glellfgffiplmfifcytfiv 229

RESULT 2
Y97077
ID Y97077 standard; Protein; 365 AA.
XX
XX Y97077;
XX
XX
XX 04-DEC-2000 (first entry)
XX
XX Primate (human) chemokine receptor CCR6.
XX
XX MIP-3-alpha; chemokine; CCR6 receptor; ligand; cytostatic; agonist;
KW antagonist; anti-psoriatic; dermatological; immunosuppressive;
KW anti-inflammatory.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 193
FT /note= "Encoded by CAN#"
FT
XX
XX W0200046248-A1.
PN
XX
XX 10-AUG-2000.
PD
XX
XX 02-FEB-2000; 2000WO-US00511.
PF
XX
XX 03-FEB-1999; 99US-0244281.
PR
XX
XX (SCHE) SCHERING CORP.
PA
XX
XX Oldham ER, Homey B, Dieu-Nosjean M, Caux C, Zlotnik A;
PI
XX
XX WPI; 2000-543477/49.
DR
XX
XX N-PSDB; A51971.
DR
XX
XX Novel methods for modulating the migration of cells within or to the
PT skin using MIP-3-alpha or CCR6 agonists or antagonists, useful for
PT treating skin disorders, e.g. cancer
XX
XX Disclosure; Page 53-54; 61pp; English.
PS
XX
XX The MIP-3-alpha chemokine is expressed in inflamed skin cells. This
CC chemokine is the ligand for the CCR6 receptor. MIP-3-alpha or CCR6
CC agonists or antagonists can be used to modulate the migration of a cell
CC within or to the skin of a mammal. MIP-3-alpha can be used to purify a

CC population of cells expressing a MIP-3-alpha receptor. The methods are
CC useful for treating a mammalian subject with a skin disease or condition,
CC e.g. cancer, metastasis, psoriasis, atopic or contact dermatitis,
CC systemic lupus erythematosus and lichen ruber planus, or for treating
CC skin transplants or grafts.
XX
XX Sequence 365 AA;
SQ

Query Match 100.0%; Score 123; DB 21; Length 365;
Best Local Similarity 100.0%; Pred. No. 2e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLELLFGFFIPLMFIFCYTFIV 23
Db 207 glellfgffiplmfifcytfiv 229

RESULT 3
R33420
ID R33420 standard; Protein; 355 AA.
XX
XX R33420;
AC
XX
XX 26-JUL-1993 (first entry)
DT
XX
XX Human IL-8 receptor from clone p2.
XX
XX Interleukin-8 receptor; probes; gene therapy; gro receptor;
KW Intracellular-calcium mobilising; ligand-binding; MIP-2 receptor.
KW
XX
XX Homo sapiens.
OS
XX
XX W09306229-A.
PN
XX
XX 01-APR-1993.
PD
XX
XX 14-SEP-1992; 92WO-US07641.
PF
XX
XX 13-SEP-1991; 91US-0759568.
PR
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICE.
PA
XX
XX Murphy PM;
PI
XX
XX WPI; 1993-117549/14.
DR
XX
XX N-PSDB; Q38747.
DR
XX
XX New interleukin-8 receptor aminoacid sequence - and corresp. cDNA
PT expressed in Xenopus laevis oocytes or transfected host cells,
PT for screening ligands of IL-8 receptor and gene therapy
XX
XX Claim 1; Fig 3; 39pp; English.
PS
XX
XX cDNA libraries from 2 and 3.5 kb fractions of poly(A)+ RNA from HL60
CC neutrophils sep'd. of a sucrose gradient were made in UnizAP. The
CC libraries were screened with F3R oligonucleotide probe (from rabbit
CC IL-8 receptor) and under low stringency with a p2 cDNA probe
CC synthesised from random primers, to isolated the clone p2, encoding
CC human IL-8 receptor protein. The presence or absence of the DNA
CC encoding IL-8R or related MIP-2 receptor may be detected using
CC portions of the p2 clone as probes. P2 may also be used to screen
CC for ligands of IL-8R and may also be used in gene therapy to treat a
CC patient deficient in IL-8R. The IL-8R is a gro receptor and has
CC intracellular calcium-mobilising and ligand-binding properties.
XX
XX Sequence 355 AA;
SQ

Query Match 54.5%; Score 67; DB 14; Length 355;
Best Local Similarity 62.5%; Pred. No. 0.009;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 FGFFIPLMFIFCYTF 21
 ||| :|| :| :||| |
 Db 213 fgfipllmficygf 228

RESULT 4
 B09990
 ID B09990 standard; Protein; 355 AA.
 AC B09990;
 XX

DT 20-OCT-2000 (first entry)

DE Human IL-8 receptor protein hIL8RB.

KW IL-8 receptor protein; hIL8RA; hIL8RB; human; interleukin-8; drug;
 KW treatment; inflammatory disease; anti-tumor.
 XX

OS Homo sapiens.

XX JP08103276-A.

PN JP08103276-A.
 XX

PD 23-APR-1996.
 XX

PF 06-OCT-1994; 94JP-0242534.
 XX

PR 06-OCT-1994; 94JP-0242534.
 XX

FA (TAKE) TAKEDA CHEM IND LTD.
 XX

XX WPI; 1996-253878/26.
 DR

DR N-PSDB; A40128.
 XX

PT Recombinant human interleukin 8 receptor protein, - its prepn. and

PT application.
 XX

XX Example 2; Fig 4; 22pp; Japanese.

CC This invention describes a novel expression vector which carries a DNA
 CC encoding human interleukin 8 receptor protein and is expressed by
 CC pAKKO1.11/hIL8RA or pAKKO1.11/hIL8RB. Also claimed are (I) CHO cell
 CC containing the above expression vector, (II) the preparation of a
 CC recombinant human interleukin 8 receptor protein in which the above CHO
 CC cell is cultured under a condition enabling the expression of a DNA
 CC coding human interleukin 8 receptor protein, (III) a CHO cell
 CC containing a recombinant human interleukin 8 receptor protein which can
 CC be prepared, by culturing the above CHO cell under a condition enabling
 CC the expression of a DNA coding human interleukin 8 receptor protein or
 CC its cell membrane fraction, (IV) a recombinant human interleukin 8
 CC receptor protein isolated from a CHO cell containing the above
 CC recombinant human interleukin 8 receptor protein, its partial peptide or
 CC their salt, (V) the screening of human interleukin 8 receptor agonist or
 CC antagonist in which the above CHO cell or its cell membrane fraction is
 CC used or the above recombinant human interleukin 8 receptor protein, its
 CC partial peptide or their salt is used (VI) a kit for screening the human
 CC interleukin 8 receptor agonist or antagonist containing the above CHO
 CC cell or its cell membrane fraction or the above recombinant human
 CC interleukin 8 receptor protein, its partial peptide or their salt, (VII)
 CC a human interleukin 8 receptor agonist or antagonist prepared by using
 CC the above screening method or the above screening kit or its salt, (VII)
 CC an activation promoter or a migration promoter of neutrophils containing
 CC the above agonist or its salt, and an activation inhibitor or a migration
 CC inhibitor containing the above antagonist or its salt. The agonist or the
 CC antagonist can be used in drug compositions for the prevention and
 CC treatment of inflammatory diseases and anti-tumor agents. The screening
 CC method can select an agonist or an antagonist advantageously. This
 CC sequence represents the human IL-8 receptor protein hIL8RB which is
 CC described in the method of the invention.
 XX

SQ Sequence 355 AA;

Query Match 54.5%; Score 67; DB 17; Length 355;

Best Local Similarity 62.5%; Pred. No. 0.009;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 FGFFIPLMFIFCYTF 21
 ||| :|| :| :||| |
 Db 213 fgfipllmficygf 228

RESULT 5

R80952
 ID R80952 standard; Protein; 358 AA.
 XX

AC R80952;
 XX

DT 24-APR-1996 (first entry)

XX Recombinant high affinity Interleukin-8 receptor subtype B.

DE IL-8A; IL-8B; receptor; monoclonal antibody; inflammatory disorder;
 KW anaphylaxis; systemic lupus erythematosus; rheumatoid arthritis;
 KW systemic necrotizing vasculitis; psoriasis; asthma; allergy; ARDS;
 KW adult respiratory distress syndrome; neutrophil detection.
 XX

OS Oryctolagus cuniculus.

XX WO9525126-A1.
 PN

XX 21-SEP-1995.
 PD

XX 09-MAR-1995; 95WO-US03032.
 PF

XX 02-MAY-1994; 94US-0237937.
 PR

PR 15-MAR-1994; 94US-0210250.
 XX

XX (REPK) REPLIGEN CORP.
 PA

XX (UYBO-) UNIV BOSTON.
 PA

XX Greenfield EA, Larosa GJ, Navarro J, Thomas KM;
 PI

PI Witt DF;
 XX

XX WPI; 1995-336945/43.
 DR

DR N-PSDB; Q99951.
 XX

XX Monoclonal antibody against recombinant IL-8 receptor polypeptide -

PT useful for treating inflammatory disorders, for detecting

PT neutrophil(s) and for isolating IL-8 receptor from liq.mixt.

XX Claim 6; Fig 3A-B; 74pp; English.

CC Monoclonal antibodies were raised against recombinant interleukin-8
 CC (IL-8) receptor subtypes A and B from both human and rabbit sources
 CC (R80950-53 encoded by Q99949-52). The A subtype receptor (IL-8RA) is
 CC a high affinity receptor and the B subtype receptor (IL-8RB) is a
 CC low affinity receptor. The monoclonal antibody (mAb) pref. binds to
 CC the IL-8 binding domain thus blocking its activation. The mAbs are
 CC useful for treating inflammatory disorders (see key words) and for
 CC detecting the presence of neutrophils in a biological sample. The
 CC mAbs are also useful in the isolation of IL-8 receptors from a mixture.

XX Sequence 358 AA;

Query Match 54.5%; Score 67; DB 16; Length 358;

Best Local Similarity 62.5%; Pred. No. 0.0091;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 FGFFIPLMFIFCYTF 21
 ||| :|| :| :||| |
 Db 216 fgfipllmficygf 231

RESULT 6
 R28273

ID R28273 standard; Protein; 360 AA.
 XX
 AC R28273;
 XX
 DT 04-APR-1993 (first entry)
 XX
 DE Sequence in a low affinity recombinant human interleukin-8
 DE (IL-8) receptor polypeptide in 4AB.
 XX
 KW IL-8 receptor polypeptide; G-protein-coupled receptor.
 KW
 XX Homo sapiens.
 OS
 PN W09218641-A.
 XX
 PD 29-OCT-1992.
 XX
 PF 10-APR-1992; 92WO-US02977.
 XX
 PR 10-APR-1991; 91US-0685101.
 PR 09-JUL-1991; 91US-0726606.
 PR 09-DEC-1991; 91US-0803842.
 XX
 PA (REPK) REPLIGEN CORP.
 PA (UTBO-) UNIV BOSTON.
 XX
 PI Navarro J, Thomas KM, Witt DP;
 XX
 DR WPI: 1992-382123/46.
 DR N-PSDB; Q30012.
 XX
 PT Recombinant mammalian interleukin-8 receptor - used for screening
 PT interleukin-8 binding antagonists, used to treat inflammation
 XX
 PS Disclosure; Fig 2; 71pp; English.
 XX
 CC Rabbit high affinity IL-8 receptor gene was isolated from rabbit
 CC peritoneal neutrophils and used as a source of poly(A)+ RNA, to
 CC produce a rabbit neutrophil cDNA library. 250,000 recombinant
 CC plaques were screened for those which hybridized to an antisense
 CC oligonucleotide (Q30015). This probe was designed based on the
 CC sequence derived from the second transmembrane domain of G-protein-
 CC coupled receptors. After tertiary screening, six plaques were
 CC isolated. The insert of one of these plaques, termed F3R was of 2.5
 CC kb in size. This insert was sequenced. The protein deduced from
 CC the F3R clone demonstrates that it belongs to the family of
 CC G-protein-coupled receptors. The deduced protein sequence
 CC indicates seven putative transmembrane segments. A human
 CC peripheral blood leukocyte lambda gt10 cDNA library (5' stretch) was
 CC screened with a 652 bp EcoRI/BamHI fragment (including nucleotides
 CC -27 to 625) of the rabbit F3R clone. After tertiary screening
 CC several human clones which hybridized to the rabbit IL-8 probe
 CC were isolated. The insert of one such clone, termed 4AB was
 CC sequenced (Q30012).
 XX
 SQ Sequence 360 AA;
 Query Match 54.5%; Score 67; DB 13; Length 360;
 Best Local Similarity 62.5%; Pred. No. 0.0091;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 OY 6 FGFFIPLMFIMFCYTF 21
 ||| :||: | :||| |
 Db 218 fgfvpllmfcygf 233
 RESULT 7
 R80758
 ID R80758 standard; Protein; 360 AA.
 XX
 AC R80758;
 XX

DT 26-MAR-1996 (first entry)
 XX
 DE Interleukin 8 receptor B.
 XX
 KW Interleukin; IL-8; inflammation; psoriasis; dermatitis;
 KW rheumatoid arthritis; inflammatory bowel disease;
 KW chronic lung inflammation; treatment; antibody;
 KW affinity purification; detection.
 XX
 OS Homo sapiens.
 XX
 PN US5440021-A.
 XX
 PD 08-AUG-1995.
 XX
 PF 29-MAR-1991; 91US-0677211.
 XX
 PR 25-FEB-1994; 94US-0202056.
 PR 29-MAR-1991; 91US-0677211.
 XX
 PA (CHUN/) CHUNTHARAPAI A.
 PA (HEBE/) HEBERT C.
 PA (KIMK/) KIM K J.
 PA (LEEJ/) LEE J.
 XX
 PI Chuntharapai A, Hebert C, Kim KJ, Lee J;
 XX
 DR WPI: 1995-283151/37.
 DR N-PSDB; Q99008.
 XX
 PT New antibodies against interleukin 8 type B receptor - used to treat
 PT or prevent inflammation, also for detecting receptor expression and
 PT purific.
 XX
 PS Disclosure; Columns 53-56; 62pp; English.
 XX
 CC Antibodies directed against the interleukin-8 receptor B can be used
 CC to treat or prevent inflammation e.g. psoriasis, dermatitis,
 CC rheumatoid arthritis and particularly inflammatory bowel disease and
 CC chronic lung inflammation. When immobilised, these antibodies may
 CC be used to detect interleukin-8 receptor B expression in cells and
 CC tissues and for affinity purification of interleukin-8 receptor B
 CC from cells.
 XX
 SQ Sequence 360 AA;
 Query Match 54.5%; Score 67; DB 16; Length 360;
 Best Local Similarity 62.5%; Pred. No. 0.0091;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 OY 6 FGFFIPLMFIMFCYTF 21
 ||| :||: | :||| |
 Db 218 fgfvpllmfcygf 233
 RESULT 8
 R80953
 ID R80953 standard; Protein; 360 AA.
 XX
 AC R80953;
 XX
 DT 24-APR-1996 (first entry)
 XX
 DE Recombinant high affinity interleukin-8 receptor subtype B.
 XX
 KW IL-8A; IL-8B; receptor; monoclonal antibody; inflammatory disorder;
 KW anaphylaxis; systemic lupus erythematosus; rheumatoid arthritis;
 KW systemic necrotising vasculitis; psoriasis; asthma; allergy; ARDS;
 KW adult respiratory distress syndrome; neutrophil detection.
 XX
 OS Homo sapiens.
 XX

PN W09525126-A1.
 XX
 PD 21-SEP-1995.
 XX
 PF 09-MAR-1995; 95WO-US03032.
 XX
 PR 02-MAY-1994; 94US-0237937.
 PR 15-MAR-1994; 94US-0210250.
 XX
 PA (REPK) REPLIGEN CORP.
 PA (UYBO-) UNIV BOSTON.
 XX
 PI Greenfield EA, Larosa GJ, Navarro J, Thomas KM;
 PI Witt DT;
 XX
 DR WPI: 1995-336945/43.
 XX
 DR N-PSDB; Q99952.
 XX
 PT Monoclonal antibody against recombinant IL-8 receptor polypeptide -
 PT useful for treating inflammatory disorders, for detecting
 PT neutrophil(s) and for isolating IL-8 receptor from liq.mixt.
 XX
 PS Claim 5; Fig 4A-B; 74pp; English.
 XX
 CC Monoclonal antibodies were raised against recombinant interleukin-8
 CC (IL-8) receptor subtypes A and B from both human and rabbit sources
 CC (R80950-53 encoded by Q99949-52). The A subtype receptor (IL-8rA) is
 CC a high affinity receptor and the B subtype receptor (IL-8rB) is a
 CC low affinity receptor. The monoclonal antibody (mAb) pref. binds to
 CC the IL-8 binding domain thus blocking its activation. The mAbs are
 CC useful for treating inflammatory disorders (see key words) and for
 CC detecting the presence of neutrophils in a biological sample. The
 CC mAbs are also useful in the isolation of IL-8 receptors from a mixture.
 XX
 SQ Sequence 360 AA;
 Query Match 54.5%; Score 67; DB 16; Length 360;
 Best Local Similarity 62.5%; Pred. No. 0.0091;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 Qy 6 FGFFPLMFIMFYCYTF 21
 Db 218 fgfvpllmficygf 233
 RESULT 9
 ID R70124 standard; Protein; 1064 AA.
 XX
 AC R70124;
 XX
 DT 14-FEB-1996 (first entry)
 XX
 DE IL-8 R type 2-GBP 130 fusion protein.
 XX
 KW Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;
 KW red blood cell; cytokine receptor; glycoporphin binding peptide 130;
 KW GBP 130; GBPH; glycoporphin binding peptide homologue; glycoporphin A.
 XX
 OS Chimeric Homo sapiens.
 OS Chimeric Plasmodium falciparum.
 XX
 PN W09506737-A.
 XX
 PD 09-MAR-1995.
 XX
 PF 01-SEP-1994; 94WO-GB01900.
 XX
 PR 03-SEP-1993; 93GB-0018350.
 PR 23-AUG-1994; 94GB-0017021.
 XX
 PA (PREN/) PRENDERCAST K F.

XX Prendergast KF;
 PI WPI: 1995-115452/15.
 DR
 XX
 PT New hybrid peptide(s) for binding cytokine(s) - comprising a
 PT malaria parasite peptide capable of binding a red blood cell and
 PT a receptor peptide.
 XX
 PS Example A; Page 80-82; 93pp; English.
 XX
 CC Hybrid peptides for binding cytokines, comprising a malaria parasite
 CC (Plasmodium falciparum) peptide (capable of binding to a red blood
 CC cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples
 CC of these hybrid peptides. R70124 is a fusion of interleukin 8 receptor
 CC type 2 and glycoporphin binding protein (GBP) 130. The use of cytokine
 CC receptors not normally found on RBCs means that the cytokine can bind
 CC harmlessly to the RBC without deleterious effect. The RBC protects the
 CC hybrid peptides from excretion from the kidney, and due to steric
 CC hindrance prevents the cytokines binding to a receptor in another cell.
 CC GBP 130 or GBPH (GBP homologue) are the pref. malaria parasite peptides
 CC used, others include EBA 175 (175 kDa erythrocyte binding antigen),
 CC PMMSA (pre major merozoite surface antigen) and the Duffy binding
 CC receptor molecule (eg. exhibited by Plasmodium vivax). These peptides
 CC bind to pref. glycoporphin A, B and C, sialo glycoproteins, found on
 CC the surface of RBCs. The hybrid peptides are thus used to lower
 CC the levels of free cytokines in the circulation to reduce pathological
 CC damage.
 XX
 SQ Sequence 1064 AA;
 Query Match 54.5%; Score 67; DB 16; Length 1064;
 Best Local Similarity 62.5%; Pred. No. 0.027;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 Qy 6 FGFFPLMFIMFYCYTF 21
 Db 212 fgfvpllmficygf 227
 RESULT 10
 ID W70001 standard; Protein; 302 AA.
 XX
 AC W70001;
 XX
 DT 20-OCT-1998 (first entry)
 XX
 DE Rodent chemokine receptor 941D12 amino acid sequence.
 XX
 KW Chemokine; primate; human; rodent; chemokine receptor; asthma;
 KW inflammatory response; immune response; leukocyte migration; GPCR;
 KW leukocyte adhesion; chemoattractant; modulation; antiviral response;
 KW cellular morphology modification response; G-protein coupled receptor;
 KW phosphoinositide lipid turnover; abnormal proliferation; regeneration;
 KW atrophy; 941D12.
 XX
 OS Mus sp.
 XX
 PN W09832858-A2.
 XX
 PD 30-JUL-1998.
 XX
 PF 22-JAN-1998; 98WO-US00902.
 XX
 PR 23-JAN-1997; 97US-0036715.
 XX
 PA (SCHE) SCHERING CORP.
 XX
 PI Gorman DM, Hedrick JA, Mattson JD, Soto-trejo H;
 PI Zlotnik A;
 XX

DR WPI: 1998-427954/36.
XX N-PSDB: V43795.

PT Rodent and primate chemokines and chemokine receptors - useful
PT diagnostically and therapeutically to treat conditions associated
PT with abnormal physiology or development e.g. inflammatory conditions
XX
PS Claim 5; Pages 97-99; 105pp; English.

XX This represents a rodent chemokine receptor 941D12 amino acid sequence.
CC The invention provides novel primate and rodent chemokines and chemokine
CC receptors. The chemokines, receptors and binding compounds (optionally
CC antibodies/fragments specifically binding the chemokines) are useful
CC therapeutically to treat conditions associated with abnormal physiology
CC or development e.g. inflammatory conditions such as asthma. Chemokines
CC are important in immune and inflammatory responses in that they induce
CC leukocyte migration and adhesion. They are also chemoattractants for
CC several cells involved in inflammation and can induce other biological
CC responses e.g. modulation of second messenger levels (e.g. Ca⁺⁺);
CC cellular morphology modification responses, phosphoinositide lipid
CC turnover, possible antiviral responses etc. The chemokine receptors of
CC the invention exhibit structural properties of G-protein coupled
CC receptors (GPCR), although their ligands have not yet been identified.
CC The chemokine and chemokine receptor polypeptides are useful to produce
CC ligand-receptor complexes in vivo or in assay techniques. Assays may
CC also involve chemical antagonists which block complex production or
CC utilise competitive binding. Binding compounds identified (agonists or
CC antagonists) can be used to modulate the physiological responses in cells
CC (especially neurons, macrophages or lymphocytes) to treat e.g. abnormal
CC proliferation, regeneration, generation and atrophy. The polypeptides
CC are also used to produce antibodies useful diagnostically, for drug
CC screening or for polypeptide purification. The polynucleotides are useful
CC to produce probes for detecting the polypeptides, and to isolate the
CC polypeptides or related sequences, especially from other species. They
CC also allow transformation of cells for polypeptide production.

XX Sequence 302 AA;

Query Match 53.7%; Score 66; DB 19; Length 302;
Best Local Similarity 45.5%; Pred. No. 0.011;
Matches 10; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 2 LELFGFFIPLMFMYFYTFIV 23
:: |||:: || ||:: |
Db 203 iqmgtlglflltmilcysgii 224

RESULT 11
Y23825 ID Y23825 standard; Protein; 351 AA.

XX AC Y23825;
XX
XX 15-SEP-1999 (first entry)
XX A7 times membrane penetrating type receptor protein ET60.
DE 7 times membrane-penetrating type receptor protein; ET60;
KW leukocyte function; control; drug.

XX Unidentified.
XX JP11155573-A.
XX 15-JUN-1999.
XX 27-NOV-1997; 97JP-0325823.
XX 27-NOV-1997; 97JP-0325823.
XX (ASAH) ASAH KASEI KOGYO KK.
PA
XX

DR WPI: 1999-398070/34.
XX N-PSDB: X86032.

PT New 7 times membrane-penetrating type receptor protein ET60 - useful
PT for detecting drug controlling function of leukocyte
XX
XX Claim 1; Page 17-18; 20pp; Japanese.

XX The present sequence represents a 7 times membrane-penetrating type
CC receptor protein ET60. The 7 times membrane-penetrating type
CC receptor protein ET60 can be used for detecting a drug controlling
CC the function of leukocyte.
XX Sequence 351 AA;

Query Match 53.7%; Score 66; DB 20; Length 351;
Best Local Similarity 45.5%; Pred. No. 0.013;
Matches 10; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 2 LELFGFFIPLMFMYFYTFIV 23
:: |||:: || ||:: |
Db 203 iqmgtlglflltmilcysgii 224

RESULT 12
R53747 ID R53747 standard; Protein; 359 AA.

XX AC R53747;
XX
XX 03-FEB-1995 (first entry)
XX Seven transmembrane receptor (V31) partial sequence of mouse.
DE Primer: seven transmembrane receptor; receptor; amplification; PCR;
KW polymerase chain reaction.
XX Mus musculus.

XX WO9412635-A.
XX 09-JUN-1994.
XX 17-NOV-1993; 93WO-US11153.
XX 17-NOV-1992; 92US-0977452.
XX (ICOS-) ICOS CORP.

XX Godiska R, Gray PW, Schweickart VL;
WPI: 1994-200264/24.
XX N-PSDB; Q66164.

PT DNA encoding seven transmembrane receptors - used to develop
PT prods. for use as therapeutic or diagnostic agents for conditions
PT involving the receptors.

PS Example 5; Page 61-62; 100pp; English.

XX Two primers (Q66148, Q66149) were used to amplify human genomic DNA
CC purified from leukocytes. Approximately 1000 clones were isolated
CC after the initial amplification reaction and probed with sequences
CC specific for seven transmembrane receptors IL8R1, AT2R and R20.
CC Clones which did not hybridise were then chosen for sequence
CC analysis. Three new clones were identified that appeared to encode
CC seven transmembrane receptor segments. Two more primers (Q66151,
CC Q66152) were used to isolate a full length version of one of the
CC human V31 clone (See Q66153). A fragment of the human clone was used
CC to isolate a V31 genomic clone of the mouse from a library.
XX Sequence 359 AA;

Query Match 53.7%; Score 66; DB 15; Length 359;
Best Local Similarity 42.9%; Pred. No. 0.013; Mismatches 5; Indels 0; Gaps 0;

Matches 9; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 3 ELLEGGFFPLMFIFCYTFIV 23

Db 207 qmvfgflvpmlamsfcylili 227

RESULT 13

W48728

ID W48728 standard; Protein; 359 AA.

AC W48728;

XX 25-SEP-1998 (first entry)

XX Murine V31 seven transmembrane (7TM) receptor.

XX V28; placenta; seven transmembrane receptor; 7TM; signal transduction;

KW immunology; inflammation; V31; ss.

XX Mus sp.

OS US5759804-A.

PN 02-JUN-1998.

XX 17-NOV-1993; 93US-0153848.

XX 17-NOV-1992; 92US-0977452.

XX (ICOS-) ICOS CORP.

XX Godiska R, Gray PW, Schweickart VL;

XX WPI: 1998-332132/29.

DR N-PSDB; V18351.

XX DNA encoding V28 seven transmembrane receptor polypeptide - useful

PT for producing recombinant polypeptide and anti-V28 antibodies, and

PT in screening assays for V28 agonists and antagonists

XX Example 5; Columns 55-58; 56pp; English.

PS The present sequence represents the murine V31 seven transmembrane

XX (7TM) receptor which is encoded by the murine V31 genomic DNA (V18351)

CC isolated from a mouse genomic library. The invention claims for the

CC full length V28 genomic DNA sequence isolated from a human placenta

CC genomic library. V28 (W48722) and V31 proteins are seven transmembrane

CC (7TM) receptors which are probably involved in signal transduction.

CC The invention also claims that cells transformed with V28 DNA can be

CC used to produce the recombinant polypeptide, to produce anti-V28

CC antibodies or in screening assays for V28 agonists or antagonists. The

CC antibodies, agonists and antagonists could then be used to modulate

CC V28 receptor-ligand binding, for e.g. in immunological and/or

CC inflammatory events in vivo.

XX Sequence 359 AA;

SQ

Query Match 53.7%; Score 66; DB 19; Length 359;
Best Local Similarity 42.9%; Pred. No. 0.013; Mismatches 5; Indels 0; Gaps 0;

Matches 9; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 3 ELLEGGFFPLMFIFCYTFIV 23

Db 207 qmvfgflvpmlamsfcylili 227

RESULT 14

B21691

ID B21691 standard; Protein; 359 AA.

XX B21691;

AC 26-JAN-2001 (first entry)

XX Murine 7TM receptor V31cDNA clone protein.

DE Seven transmembrane receptor; 7TM; heptahelical; serpentine;

XX G-protein-coupled; V28; V31; V112; R20; R2; R12; RM3; gene therapy;

XX cancer.

XX Mus sp.

OS US6107475-A.

PN 22-AUG-2000.

XX 26-APR-1999; 99US-0299843.

XX 17-MAY-1994; 94US-0245242.

XX 01-JUN-1998; 98US-0088337.

XX 17-NOV-1992; 92US-0977452.

XX 17-NOV-1993; 93US-0153848.

XX (ICOS-) ICOS CORP.

XX Schweickart VL, Gray PW, Godiska R;

XX WPI: 2000-571335/53.

DR N-PSDB; A91711.

XX Polynucleotide encoding seven transmembrane receptors, antibody

PT specific to the receptor, agonist and antagonist of the receptor useful

PT for treating inflammation in a mammal

XX Example 4; Columns 57-60; 61pp; English.

PS The present sequence is a novel seven transmembrane (7TM) receptors

XX (also known as heptahelical, serpentine or G-protein-coupled receptors).

CC The coding sequence for the present sequence may be used for gene

CC therapy for diseases such as cancer.

XX Sequence 359 AA;

SQ

Query Match 53.7%; Score 66; DB 21; Length 359;
Best Local Similarity 42.9%; Pred. No. 0.013; Mismatches 5; Indels 0; Gaps 0;

QY 3 ELLEGGFFPLMFIFCYTFIV 23

Db 207 qmvfgflvpmlamsfcylili 227

RESULT 15

B21699

ID B21699 standard; Protein; 378 AA.

XX B21699;

XX 26-JAN-2001 (first entry)

XX 7TM receptor protein.

XX Seven transmembrane receptor; 7TM; heptahelical; serpentine;

XX G-protein-coupled; V28; V31; V112; R20; R2; R12; RM3; gene therapy;

XX cancer.

XX Unidentified.

XX US6107475-A.

PN

```

XX 22-AUG-2000.
PD
XX
XX PF 26-APR-1999; 99US-0299843.
XX
XX PR 17-MAY-1994; 94US-0245242.
XX
XX PR 01-JUN-1998; 98US-0088337.
XX
XX PR 17-NOV-1992; 92US-0977452.
XX
XX PR 17-NOV-1993; 93US-0153848.
XX
XX PA (ICOS-) ICOS CORP.
XX
XX PI Schweickart VL, Gray PW, Godiska R;
XX
XX DR WPI; 2000-571335/53.
XX
XX DR N-PSDB; A91745.
XX
XX PT Polynucleotide encoding seven transmembrane receptors, antibody
XX specific to the receptor, agonist and antagonist of the receptor useful
XX for treating inflammation in a mammal
XX
XX PS Disclosure; Columns 111-112; 61pp; English.
XX
XX CC The present sequence is a novel seven transmembrane (7TM) receptors
XX (also known as heptahelical, serpentine or G-protein-coupled receptors).
XX CC The coding sequence for the present sequence may be used for gene
XX CC therapy for diseases such as cancer.
XX
XX SQ Sequence 378 AA;

Query Match 53.7%; Score 66; DB 21; Length 378;
Best Local Similarity 42.9%; Pred. No. 0.014;
Matches 9; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 3 ELLEGGFIPLMFMFCYTFIV 23
Db ::|||::|::|::|::|
227 qmvfgflvpmlamsfcylili 247

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Search completed: May 23, 2001, 15:28:31
Job time: 408 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 23, 2001, 15:30:07 ; Search time 95.91 Seconds
(without alignments)
4.607 Million cell updates/sec

Title: US-08-887-977-10_COPY_207_229
Perfect score: 123
Sequence: 1 GLELLFGFIPLMFIFCVTFIV 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA.*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	67	54.5	115	4	US-08-513-974B-356
2	67	54.5	355	1	US-07-759-568-1
3	67	54.5	355	1	US-08-450-393A-8
4	67	54.5	355	2	US-08-390-000A-5
5	67	54.5	355	4	US-08-446-669-8
6	67	54.5	355	5	PCT-US95-00476-8
7	67	54.5	360	1	US-08-202-056-7
8	66	53.7	359	3	US-08-153-848-24
9	66	53.7	359	3	US-09-299-843A-24
10	66	53.7	378	3	PCT-US93-11153-24
11	66	53.7	378	3	US-09-299-843A-66
12	65	52.8	342	2	US-08-742-011-2
13	65	52.8	354	1	US-07-759-568-2
14	65	52.8	407	2	US-08-742-440A-3
15	64	52.0	312	1	US-08-118-270-38
16	64	52.0	312	5	PCT-US93-08528-38
17	64	52.0	350	1	US-08-202-056-1
18	64	52.0	350	1	US-08-076-093A-2
19	64	52.0	350	1	US-08-450-393A-7
20	64	52.0	350	1	US-08-410-453A-1
21	64	52.0	350	1	US-08-701-265-2
22	64	52.0	350	1	US-08-410-454A-1
23	64	52.0	350	2	US-08-284-586-2
24	64	52.0	350	2	US-08-410-456A-1
25	64	52.0	350	2	US-08-805-478-2
26	64	52.0	350	2	US-08-802-627A-2
27	64	52.0	350	2	US-08-801-238-2

28	64	52.0	350	2	US-08-801-228-2	Sequence 2, Appli
29	64	52.0	350	3	US-09-104-296-2	Sequence 2, Appli
30	64	52.0	350	4	US-08-446-669-7	Sequence 7, Appli
31	64	52.0	350	5	PCT-US95-00476-7	Sequence 7, Appli
32	63	51.2	355	1	US-08-012-988A-2	Sequence 2, Appli
33	63	51.2	355	1	US-08-450-393A-5	Sequence 5, Appli
34	63	51.2	355	4	US-08-446-669-5	Sequence 5, Appli
35	63	51.2	355	5	PCT-US95-00476-5	Sequence 5, Appli
36	62	50.4	115	4	US-08-513-974B-351	Sequence 351, App
37	62	50.4	368	4	US-08-709-838-2	Sequence 2, Appli
38	62	50.4	368	4	US-08-829-839-2	Sequence 2, Appli
39	62	50.4	482	2	US-08-876-874-2	Sequence 2, Appli
40	61	49.6	358	1	US-08-153-848-19	Sequence 19, Appl
41	61	49.6	358	3	US-09-299-843A-19	Sequence 19, Appl
42	61	49.6	358	5	PCT-US93-11153-19	Sequence 19, Appl
43	61	49.6	361	2	US-08-902-294-2	Sequence 2, Appli
44	61	49.6	361	3	US-09-178-637-2	Sequence 2, Appli
45	61	49.6	378	1	US-08-383-750-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-513-974B-356
; Sequence 356, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ongi, Kazuhiko
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357

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; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236356
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189274
; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189273
; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189272
; FILING DATE: 11-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 45753
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 356:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-513-974B-356

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Query Match 54.5%; Score 67; DB 4; Length 115;
 Best Local Similarity 62.5%; Pred. No. 0.0058;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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QY 6 FGFFPLMFIMFCYTF 21
DB 74 FGFLVPLLMFLFCYGF 89

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RESULT 2
US-07-759-568-1
; Sequence 1, Application US/07759568
; Patent No. 5374506
; GENERAL INFORMATION:
; APPLICANT: Murphy, Philip M.
; TITLE OF INVENTION: Cloning of cDNA Encoding a Functional
; TITLE OF INVENTION: Human Interleukin-8 Receptor
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cushman, Darby & Cushman
; STREET: 1615 L Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 19910913
; APPLICATION NUMBER: US/07/759,568
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Scott, Watson T.
; REGISTRATION NUMBER: 26581
; REFERENCE/DOCKET NUMBER: WTS/5683/91535/WBH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 cush
; INFORMATION FOR SEQ ID NO: 1:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-759-568-1

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Query Match 54.5%; Score 67; DB 1; Length 355;
 Best Local Similarity 62.5%; Pred. No. 0.018;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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QY 6 FGFFPLMFIMFCYTF 21
DB 213 FGFLVPLLMFLFCYGF 228

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```

RESULT 3
US-08-450-393A-8
; Sequence 8, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/020US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816CooleyPA
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-450-393A-8

```

Query Match 54.5%; Score 67; DB 1; Length 355;
 Best Local Similarity 62.5%; Pred. No. 0.018;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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QY 6 FGFFPLMFIMFCYTF 21
DB 213 FGFLVPLLMFLFCYGF 228

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RESULT 4
US-08-390-000A-5

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; Sequence 5, Application US/083900000A
; Patent No. 5985383
; GENERAL INFORMATION:
; APPLICANT: Sealfon, Stuart C.
; TITLE OF INVENTION: Cloning and Expression of
; TITLE OF INVENTION: Gonadotropin-Releasing Hormone Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 17-FEB-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6923-052
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-390-000A-5

Query Match 54.5%; Score 67; DB 2; Length 355;
Best Local Similarity 62.5%; Pred. No. 0.018;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 6 FGFFPLMFMEFYCYTF 21
Db 213 FGFIPLMLFCYGF 228

RESULT 5
US-08-446-669-8
; Sequence 8, Application US/08446669
; Patent No. 6132987
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,669

; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Neeley, Richard
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-237/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; TELEX: 380816COOLEYPA
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-08-446-669-8

Query Match 54.5%; Score 67; DB 4; Length 355;
Best Local Similarity 62.5%; Pred. No. 0.018;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 6 FGFFPLMFMEFYCYTF 21
Db 213 FGFIPLMLFCYGF 228

RESULT 6
PCT-US95-00476-8
; Sequence 8, Application PC/TUS9500476
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 N. Figueroa Street, 5th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012-2628
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00476
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berliner, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-977-1001
; TELEFAX: 310-977-1003
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; PCT-US95-00476-8

Query Match 54.5%; Score 67; DB 5; Length 355;
Best Local Similarity 62.5%; Pred. No. 0.018;

Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 FGFFIPLMFIFCYTF 21
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 Db 213 FGFIPLMLFCYGF 228

RESULT 7

US-08-202-056-7
 ; Sequence 7, Application US/08202056
 ; Patent No. 5440021
 ; GENERAL INFORMATION:
 ; APPLICANT: Chuntharapai, Anan
 ; APPLICANT: Hebert, Caroline
 ; APPLICANT: Kim, Kyung Jin
 ; APPLICANT: Lee, James
 ; TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: patin (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/202,056
 ; FILING DATE: 25-FEB-1994
 ; CLASSIFICATION: 436
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/677211
 ; FILING DATE: 23-MAR-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Love, Richard B.
 ; REGISTRATION NUMBER: 34,659
 ; REFERENCE/DOCKET NUMBER: 706P3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415/225-5530
 ; TELEFAX: 415/952-9881
 ; TELEX: 910/371-7168
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 360 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; US-08-202-056-7

Query Match 54.5%; Score 67; DB 1; Length 360;
 Best Local Similarity 62.5%; Pred. No. 0.016;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 FGFFIPLMFIFCYTF 21
 ||| :||: |:||| |
 Db 218 FGFIPLMLFCYGF 233

RESULT 8

US-08-153-848-24
 ; Sequence 24, Application US/08153848
 ; Patent No. 5759804
 ; GENERAL INFORMATION:
 ; APPLICANT: Godiska, Ronald
 ; APPLICANT: Gray, Patrick W.
 ; APPLICANT: Schweikart, Vicki L.
 ; TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
 ; NUMBER OF SEQUENCES: 64
 ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ; ADDRESSEE: Bicknell
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/153,848
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/977,452
 ; FILING DATE: 17-NOV-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 5759804and, Greta E.
 ; REGISTRATION NUMBER: 35,302
 ; REFERENCE/DOCKET NUMBER: 31794
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 474-6300
 ; TELEFAX: (312) 474-0448
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 24:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 359 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-153-848-24

Query Match 53.7%; Score 66; DB 1; Length 359;
 Best Local Similarity 42.9%; Pred. No. 0.025;
 Matches 9; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 3 ELFGFFIPLMFIFCYTFIV 23
 :||| :||: |:||| |
 Db 207 QMVEGFLVPLMLAMSFVYLIII 227

RESULT 9

US-09-299-843A-24
 ; Sequence 24, Application US/09299843A
 ; Patent No. 6107475
 ; GENERAL INFORMATION:
 ; APPLICANT: Godiska, Ronald
 ; APPLICANT: Gray, Patrick W.
 ; APPLICANT: Schweikart, Vicki L.
 ; TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
 ; NUMBER OF SEQUENCES: 66
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ; ADDRESSEE: Borun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/299,843A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 09/088,337
;; FILING DATE: 01-JUN-1998
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/153,848
;; FILING DATE: 17-NOV-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/977,452
;; FILING DATE: 17-NOV-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Jill E. Uhl
;; REGISTRATION NUMBER: 43,213
;; REFERENCE/DOCKET NUMBER: 27866/32059B
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312) 474-6300
;; TELEFAX: (312) 474-0448
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 24:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 359 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-09-299-843A-24

Query Match 53.7%; Score 66; DB 3; Length 359;
Best Local Similarity 42.9%; Pred. No. 0.025;
Matches 9; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 3 ELLGFFIPLMFIFCYTFIV 23
Db 207 QMVFGFLVPLMAMSFCLYLI 227

RESULT 10
PCT-US93-11153-24
Sequence 24, Application PC/TUS9311153
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: Novel Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11153
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-299-843A-24

;; LENGTH: 359 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; PCT-US93-11153-24

Query Match 53.7%; Score 66; DB 5; Length 359;
Best Local Similarity 42.9%; Pred. No. 0.025;
Matches 9; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 3 ELLGFFIPLMFIFCYTFIV 23
Db 207 QMVFGFLVPLMAMSFCLYLI 227

RESULT 11
US-09-299-843A-66
Sequence 66, Application US/09299843A
Patent No. 6107475
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Jill E. Uhl
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-299-843A-66

Query Match 53.7%; Score 66; DB 3; Length 378;
Best Local Similarity 42.9%; Pred. No. 0.027;
Matches 9; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 3 ELFGFFPLMFMIFCYTFIV 23
::|||::| ||| |:
Db 227 QMWGFLVPLMAMSGCYLIII 247

RESULT 12
US-08-742-011-2
; Sequence 2, Application US/08742011
; Patent No. 5824504
; GENERAL INFORMATION:
; APPLICANT: Elshourbagy, Nabil A.
; APPLICANT: Bergsma, Derek J.
; APPLICANT: Ellis, Catherine E.
; TITLE OF INVENTION: Human 7-Transmembrane Receptor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,011
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T.
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: ATG50020P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-5090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 342 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-742-011-2

Query Match 52.8%; Score 65; DB 2; Length 342;
Best Local Similarity 47.6%; Pred. No. 0.034;
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 3 ELFGFFPLMFMIFCYTFIV 23
:: |||:: || ||| |:
Db 195 QMTLGFPLPLMTIVCVSVII 215

RESULT 13
US-07-759-568-2
; Sequence 2, Application US/07759568
; Patent No. 5374506
; GENERAL INFORMATION:
; APPLICANT: Murphy, Philip M.
; TITLE OF INVENTION: Cloning of cDNA Encoding a Functional
; TITLE OF INVENTION: Human Interleukin-8 Receptor
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cushman, Darby & Cushman
; STREET: 1615 L Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/759,568
; FILING DATE: 19910913
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Scott, Watson T.
; REGISTRATION NUMBER: 26581
; REFERENCE/DOCKET NUMBER: WTS/5683/91535/WBH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 cush
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 354 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-759-568-2

Query Match 52.8%; Score 65; DB 1; Length 354;
Best Local Similarity 62.5%; Pred. No. 0.035;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 FGFFPLMFMIFCYTF 21
|||::|||:| ||| |:
Db 213 FGFPLPLVLMFCYGF 228

RESULT 14
US-08-742-440A-3
; Sequence 3, Application US/08742440A
; Patent No. 5892014
; GENERAL INFORMATION:
; APPLICANT: Coughlin, Shaun
; APPLICANT: Ishihari, Hiroaki
; APPLICANT: Connolly, Andrew
; TITLE OF INVENTION: Protease Activated Receptor
; TITLE OF INVENTION: 3 and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bozicevic & Reed, LLP
; STREET: 285 Hamilton Avenue, Suite 200
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,440A
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela J.
; REGISTRATION NUMBER: 36,677
; REFERENCE/DOCKET NUMBER: UCAL/060PAT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-327-3400
; TELEFAX: 650-327-3231
; TELEX:

; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 407 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FEATURE:
 US-08-742-440A-3

Query Match 52.8%; Score 65; DB 2; Length 407;
 Best Local Similarity 55.6%; Pred. No. 0.04;
 Matches 10; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 6 FGFFPLMFIFCYTFV 23
 Db 284 FGFLPFVILIFCYTTLI 301

RESULT 15

US-08-118-270-38
 ; Sequence 38, Application US/08118270
 ; Patent No. 5508384
 ; GENERAL INFORMATION:

; APPLICANT: Murphy, Randall B.
 ; APPLICANT: Schuster, David I.
 ; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
 ; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
 ; NUMBER OF SEQUENCES: 348

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK
 ; STREET: 419 Seventh Street, N.W., Suite 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/118,270
 ; FILING DATE: 09-SEP-1993

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/943,236

; FILING DATE: 10-SEP-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Townsend, Kevin G.

; REGISTRATION NUMBER: 34,033

; REFERENCE/DOCKET NUMBER: MURPHY-2A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-628-5197

; TELEFAX: 202-737-3528

; TELEX: 248633

; INFORMATION FOR SEQ ID NO: 38:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 312 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-118-270-38

Query Match 52.0%; Score 64; DB 1; Length 312;
 Best Local Similarity 56.2%; Pred. No. 0.042;
 Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 6 FGFFPLMFIFCYTF 21
 Db 170 FGFLPFVILIMCYGF 185

Search completed: May 23, 2001, 15:30:07
 Job time: 414 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:32:01 ; Search time 110.15 seconds
(without alignments)
14.350 Million cell updates/sec

Title: US-08-887-977-10_COPY_207_229

Perfect score: 123

Sequence: 1 GLELLFGFFIPLMFIFCYTFIV 23

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_67:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	123	100.0	369	2 JC5068	G protein-coupled
2	67	54.5	358	2 A53752	interleukin-8 rece
3	67	54.5	359	2 A48921	interleukin-8 rece
4	67	54.5	360	2 A53611	interleukin-8 rece
5	66	53.7	378	2 A55735	G protein-coupled
6	65	52.8	354	2 A23669	interleukin-8 rece
7	65	52.8	355	2 J01231	interleukin-8 rece
8	64	52.0	350	2 A39445	interleukin-8 rece
9	63	51.2	355	2 A45177	chemokine (C-C) re
10	63	51.2	356	2 S42096	interleukin-8 rece
11	62.5	50.8	376	2 A48197	opsin, ocellar - A
12	62	50.4	351	1 A46525	complement C5a ana
13	62	50.4	352	1 S27357	complement C5a ana
14	62	50.4	367	2 J50349	interferon-inducib
15	62	50.4	482	2 S65766	G protein-coupled
16	61.5	50.0	376	2 B48197	opsin, lateral eye
17	61	49.6	378	2 A45680	G protein-coupled
18	61	49.6	378	2 B55735	lymphocyte-specifi
19	59	48.0	350	1 A37963	complement C5a ana
20	58	47.2	473	2 JC5835	anaphylatoxin C3a
21	57	46.3	557	2 T16619	hypothetical prote
22	56.5	45.9	360	2 A57160	chemokine (C-C) re
23	56	45.5	354	2 I58186	probable G protein
24	56	45.5	380	2 JC2434	kappa opiod recep
25	56	45.5	380	2 JC2338	kappa opiod recep
26	55	44.7	346	2 S29248	somatostatin recep
27	55	44.7	356	2 I49340	MIP-1 alpha recept
28	55	44.7	359	2 I49341	MIP-1 alpha recept
29	55	44.7	360	2 G02084	G protein-coupled

30	55	44.7	369	2 JC2083	somatostatin recep
31	55	44.7	369	2 A45291	somatostatin recep
32	55	44.7	369	2 B41795	somatostatin recep
33	55	44.7	369	2 D41795	somatostatin recep
34	55	44.7	380	2 A48227	kappa opiod recep
35	55	44.7	380	2 S36143	kappa opiod recep
36	55	44.7	380	2 A55259	kappa opiod recep
37	54	43.9	349	2 I59336	galanin receptor 1
38	54	43.9	350	2 JN0621	G protein-coupled
39	53	43.1	353	2 JC2492	G protein-coupled
40	53	43.1	355	2 I49339	macrophage inflam
41	53	43.1	363	2 I57955	somatostatin recep
42	53	43.1	364	2 JN0763	somatostatin recep
43	53	43.1	379	2 T19318	hypothetical prote
44	53	43.1	419	2 T25565	hypothetical prote
45	53	43.1	448	1 S29483	rhodopsin [similar

ALIGNMENTS

RESULT 1

JC5068

G protein-coupled receptor CKR-L3 - human

C:Species: Homo sapiens (man)

C>Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000

C:Accession: JC5068

R:Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.

Biochem. Biophys. Res. Commun. 227, 846-853, 1996

A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-lik

A:Reference number: JC5067; MUID:97040707

A:Accession: JC5068

A:Molecule type: DNA

A:Residues: 1-369 <ZAB>

A:Cross-references: EMBL:Z79784; NID:gl668737; PIDN:CAB02144.1; PID:gl668738

C:Comment: This protein belongs to the family of alpha chemokine receptors.

C:Genetics:

A:Gene: GDB:CMKBR6; STPL22; GPR29; CCR6; CKR-L3; GPR-CY4

A:Cross-references: GDB:5370639; OMIM:601835

A:Map position: 6q27-6q27

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

F:42-68/Domain: transmembrane #status predicted <TM1>

F:79-99/Domain: transmembrane #status predicted <TM2>

F:115-136/Domain: transmembrane #status predicted <TM3>

F:160-180/Domain: transmembrane #status predicted <TM4>

F:212-233/Domain: transmembrane #status predicted <TM5>

F:250-271/Domain: transmembrane #status predicted <TM6>

F:292-315/Domain: transmembrane #status predicted <TM7>

Query Match 100.0%; Score 123; DB 2; Length 369;

Best Local Similarity 100.0%; Pred. No. 1.2e-10;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GLELLFGFFIPLMFIFCYTFIV 23

|||||

DB 211 GLELLFGFFIPLMFIFCYTFIV 233

RESULT 2

A53752

interleukin-8 receptor (clone 5Bla) - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999

C:Accession: A53752

R:Prado, G.N.; Thomas, K.M.; Suzuki, H.; LaRosa, G.J.; Wilkinson, N.; Folco, E.; Nava

J. Biol. Chem. 269, 12391-12394, 1994

A:Title: Molecular characterization of a novel rabbit interleukin-8 receptor isotype.

A:Reference number: A53752; MUID:94230294

A:Accession: A53752

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-358 <PRA>
 A:Cross-references: GB:L24445; NID:g437661; PIDN:AAA31378.1; PID:g437662
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 54.5%; Score 67; DB 2; Length 358;
 Best Local Similarity 62.5%; Pred. No. 0.016;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 FGFFIPLMFIMFCYTF 21
 ||| :|| :|:| |
 Db 216 FGFIPLLMFICYVF 231

RESULT 3

Interleukin-8 receptor type B - mouse
 A:Alternate names: G-protein coupled receptor Gpcr16
 C:Species: Mus musculus (house mouse)
 C:Date: 20-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 05-Nov-1999
 C:Accession: A48921; A53677; I49348; I55421; H48909; I53774
 R:Cerretti, D.P.; Nelson, N.; Kozlosky, C.J.; Morrissey, P.J.; Copeland, N.G.; Gilbert, Genomics 18, 410-413, 1993
 A:Title: The murine homologue of the human interleukin-8 receptor type B maps near the
 A:Reference number: A48921; MUID:94117014
 A:Accession: A48921
 A:Molecule type: DNA
 A:Residues: 1-359 <CER>
 A:Cross-references: GB:L23637; NID:g435093; PIDN:AAA39305.1; PID:g435094
 R:Suzuki, H.; Prado, G.N.; Wilkinson, N.; Navarro, J.
 J. Biol. Chem. 269, 18263-18266, 1994
 A:Title: The N terminus of interleukin-8 (IL-8) receptor confers high affinity binding to
 A:Reference number: A53677; MUID:94308043
 A:Accession: A53677
 A>Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-359 <SUZ>
 A:Cross-references: GB:L26549
 A:Note: sequence extracted from NCBI backbone (NCBIP:149812)
 R:Lee, J.; Cacalano, G.; Canerato, T.; Toy, K.; Moore, M.W.; Wood, W.I.
 J. Immunol. 155, 2158-2164, 1995
 A:Title: Chemokine binding and activities mediated by the mouse IL-8 receptor.
 A:Reference number: I49348; MUID:95363183
 A:Accession: I49348
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-359 <RES>
 A:Cross-references: EMBL:U31207; NID:g950174; PIDN:AAC52239.1; PID:g950175
 R:Bozic, C.R.; Gerard, N.P.; von Uexkull-Guldenband, C.; Kolakowski, L.F.
 J. Biol. Chem. 269, 29355-29358, 1994
 A:Title: The murine interleukin 8 type B receptor homologue and its ligands. Expression
 A:Reference number: I55421; MUID:95050766
 A:Accession: I55421
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-359 <RE2>
 A:Cross-references: PIDN:AAA62109.1; PID:g293666
 R:Wilkie, T.M.; Chen, Y.; Gilbert, D.J.; Moore, K.J.; Yu, L.; Simon, M.I.; Copeland, N.C.
 Genomics 16, 175-184, 1993
 A:Title: Identification, chromosomal location, and genome organization of mammalian G-protein-coupled receptor
 A:Reference number: A48909; MUID:94116980
 A:Accession: H48909
 A>Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 145-258 <MIL>
 A:Cross-references: GB:L20337; NID:g438800; PIDN:AAA16853.1; PID:g438801
 R:Harada, A.; Kuno, K.; Nomura, H.; Mukaida, N.; Murakami, S.; Matsushima, K.
 Gene 142, 297-300, 1994
 A:Title: Cloning of a cDNA encoding a mouse homolog of the interleukin-8 receptor.
 A:Reference number: I53774; MUID:94252584
 A:Accession: I53774
 A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
 A:Residues: 1-359 <RE3>
 A:Cross-references: GB:D17630; NID:g493671; PIDN:BAA04536.1; PID:g493672
 C:Genetics:
 A:Gene: IL8rb
 A:Introns: #status absent
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
 F:49-74/Domain: transmembrane #status predicted <TM1>
 F:84-106/Domain: transmembrane #status predicted <TM2>
 F:120-141/Domain: transmembrane #status predicted <TM3>
 F:163-182/Domain: transmembrane #status predicted <TM4>
 F:213-234/Domain: transmembrane #status predicted <TM5>
 F:251-271/Domain: transmembrane #status predicted <TM6>
 F:308-328/Domain: transmembrane #status predicted <TM7>

Query Match 54.5%; Score 67; DB 2; Length 359;
 Best Local Similarity 62.5%; Pred. No. 0.016;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 FGFFIPLMFIMFCYTF 21
 ||| :|| :|:| |
 Db 217 FGFIPLLMFICYGF 232

RESULT 4

Interleukin-8 receptor type B - human
 A:Species: Homo sapiens (man)
 C:Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 05-Nov-1999
 C:Accession: I37898; I38712; A53611; A39446
 R:Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
 J. Biol. Chem. 269, 26381-26389, 1994
 A:Title: Comparison of the genomic organization and promoter function for human interleukin-8
 A:Reference number: I37898; MUID:95014476
 A:Accession: I37898
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-360 <RES>
 A:Cross-references: EMBL:U11869; NID:g511801; PIDN:AAB560556.1; PID:g511803
 A:Accession: I38712
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-15 <RE2>
 A:Cross-references: EMBL:U11872; NID:g511808; PIDN:AAA64380.1; PID:g511809; EMBL:U11876; NID:g511816; PID:g511817; EMBL:U11877; NID:g511818; PID:g511819; EMBL:U11878; J. Biol. Chem. 269, 11065-11072, 1994
 R:Spranger, H.; Lloyd, A.R.; Lautens, L.L.; Bonner, T.I.; Kelvin, D.J.
 A:Title: Structure, genomic organization, and expression of the human interleukin-8 r
 A:Reference number: A53611; MUID:94209273
 A:Accession: A53611
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 6-360 <SPR>
 A:Cross-references: GB:M99412; GB:L19593
 R:Murphy, P.M.; Tiffany, H.L.
 Science 253, 1280-1283, 1991
 A:Title: Cloning of complementary DNA encoding a functional human interleukin-8 recep
 A:Reference number: A39446; MUID:91368200
 A:Accession: A39446
 A>Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 6-360 <MUR>
 A:Cross-references: GB:M73969
 C:Comment: This receptor, unlike IL8RA, binds several peptides besides interleukin-8,
 C:Genetics:
 A:Gene: GDB:IL8RB; IL8RA
 A:Cross-references: GDB:127868; OMIM:146928
 A:Map position: 2q35-2q35
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 54.5%; Score 67; DB 2; Length 360;
Best Local Similarity 62.5%; Pred. No. 0.016;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 FGFFIPLMFIFCYTF 21
||| :||: |||| |

DB 218 FGFIPLMLFCYGF 233

RESULT 5

G protein-coupled receptor EB11 - mouse
A:Species: Mus musculus (house mouse)
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 24-Nov-1999
R:Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.
Genomics 23, 643-650, 1994
A:Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor
A:Reference number: A55735; MUID:95154835
A:Accession: A55735
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-378 <SCH>
A:Cross-references: GB:L31580; NID:g468340; PIDN:AAA74232.1; PID:g468341
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

Query Match 53.7%; Score 66; DB 2; Length 378;
Best Local Similarity 42.9%; Pred. No. 0.023;
Matches 9; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 3 ELLFGFIPLMFIFCYTFIV 23
:::|::|::| |::| |

DB 227 QMVFGLVPLAMSFYLI 247

RESULT 6

interleukin-8 receptor, high affinity - rabbit
N:Alternate names: fMLP receptor
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 05-Nov-1999
C:Accession: A23669
R:Thomas, K.M.; Pyun, H.Y.; Navarro, J.
J. Biol. Chem. 265, 20061-20064, 1990
A:Title: Molecular cloning of the fMet-Leu-Phe receptor from neutrophils.
A:Reference number: A23669; MUID:91056034
A:Accession: A23669
A:Molecule type: mRNA
A:Residues: 1-354 <THO>
A:Cross-references: GB:M58021; GB:J05705; NID:gi65442; PIDN:AAA31377.1; PID:gi65443
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein; neutrophil

Query Match 52.8%; Score 65; DB 2; Length 354;
Best Local Similarity 62.5%; Pred. No. 0.03;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 FGFFIPLMFIFCYTF 21
||| :||: |||| |

DB 213 FGFIPLMLFCYGF 228

RESULT 7

interleukin-8 receptor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Nov-1999
C:Accession: JQ1231; A46483
R:Beckmann, M.P.; Munger, W.E.; Kozlosky, C.; VandenBos, T.; Price, V.; Lyman, S.; Gerard

Biochem. Biophys. Res. Commun. 179, 784-789, 1991
A:Title: Molecular characterization of the interleukin-8 receptor.
A:Reference number: JQ1231; MUID:91378994
A:Accession: JQ1231

A:Molecule type: DNA

A:Residues: 1-355 <BEC>

A:Cross-references: GB:M74240; NID:gi65438; PIDN:AAA31375.1; PID:gi65439
R:Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.
J. Immunol. 148, 1261-1264, 1992

A:Title: Characterization of complementary DNA clones encoding the rabbit IL-8 receptor

A:Reference number: A46483; MUID:92148149

A:Accession: A46483

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-355 <LEE>

A:Cross-references: GB:M82873; NID:gi65440; PIDN:AAA31376.1; PID:gi65441

A:Experimental source: neutrophils

A>Note: sequence extracted from NCBI backbone (NCBIN:81526, NCBI:81530)

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 52.8%; Score 65; DB 2; Length 355;
Best Local Similarity 62.5%; Pred. No. 0.03;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 FGFFIPLMFIFCYTF 21
||| :||: |||| |

DB 214 FGFIPLMLFCYGF 229

RESULT 8

A39445
interleukin-8 receptor type A - human
N:Alternate names: interleukin-8 receptor, high-affinity
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1993 #sequence_revision 12-Apr-1996 #text_change 05-Nov-1999
C:Accession: I37449; I38710; I38711; A39445
R:Molliereau, C.; Muscatelli, F.; Mattei, M.G.; Vassart, G.; Parmentier, M.
Genomics 16, 248-251, 1993
A:Title: The high-affinity interleukin 8 receptor gene (IL8RA) maps to the 2q33-q36 r-

A:Reference number: I37449; MUID:93252387

A:Accession: I37449

A:Molecule type: DNA

A:Residues: 1-350 <RES>

A:Cross-references: EMBL:X65858; NID:gi312046; PIDN:CAA46688.1; PID:gi312047

R:Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.

J. Biol. Chem. 269, 26381-26389, 1994

A:Title: Comparison of the genomic organization and promoter function for human inter

A:Reference number: I37898; MUID:95014476

A:Accession: I38710

A:Molecule type: DNA

A:Residues: 1-350 <RE2>

A:Cross-references: EMBL:U11870; NID:gi511804; PIDN:AAA64378.1; PID:gi511805

A:Accession: I38711

A:Molecule type: mRNA

A:Residues: 1-16 <RE3>

A:Cross-references: EMBL:U11871; NID:gi511806; PIDN:AAA64379.1; PID:gi733002

R:Holmes, W.E.; Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.

Science 253, 1278-1280, 1991

A:Title: Structure and functional expression of a human interleukin-8 receptor.

A:Reference number: A39445; MUID:91368199

A:Accession: A39445

A:Molecule type: mRNA

A:Residues: 1-275, 'T', 277-350 <HOL>

A:Cross-references: GB:M68932; NID:gi86369; PIDN:AAA59159.1; PID:gi86370

C:Genetics:

A:Gene: GDB:IL8RA

A:Cross-references: GDB:135039; OMIM:146929

A:Map position: 2q35-2q35

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein

Query Match 52.0%; Score 64; DB 2; Length 350;
 Best Local Similarity 62.5%; Pred. No. 0.042;
 Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 6 FGFFIPLMFIFCYTF 21
 |||||:|:|:|:|:|:|
 Db 209 FGFIPLFLVLMFCYGF 224

RESULT 9

A45177
 chemokine (C-C) receptor 1 - human
 N:Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor
 C:Species: Homo sapiens (man)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
 C:Accession: A45177; I55671
 R:Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.
 Cell 72, 415-425, 1993
 A:Title: Molecular cloning, functional expression, and signaling characteristics of a C-C chemokine receptor
 A:Reference number: A45177; MUID:93161416
 A:Accession: A45177
 A:Molecule type: mRNA
 A:Status: nucleic acid sequence not shown
 A:Residues: 1-355 <NEQ>
 A:Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
 A:Experimental source: HL60 cells
 A:Note: sequence extracted from NCBI backbone (NCBIP:124876)
 R:Gao, J.
 J. Exp. Med. 177, 1421-1427, 1993
 A:Title: Structure and functional expression of the human macrophage inflammatory 1 alpha receptor
 A:Reference number: I55671; MUID:93240122
 A:Accession: I55671
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 1-355 <RES>
 A:Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
 C:Genetics:

A:Gene: GDB:CMKBR1; CMKR-1
 A:Cross-references: GDB:138446; OMIM:601159
 A:Map position: 3p21-3p21
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane
 F:36-60/Domain: transmembrane #status predicted <TM1>
 F:71-91/Domain: transmembrane #status predicted <TM2>
 F:108-129/Domain: transmembrane #status predicted <TM3>
 F:147-171/Domain: transmembrane #status predicted <TM4>
 F:205-223/Domain: transmembrane #status predicted <TM5>
 F:240-264/Domain: transmembrane #status predicted <TM6>
 F:288-305/Domain: transmembrane #status predicted <TM7>
 F:5/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:24-273,106-183/Disulfide bonds: #status predicted
 F:345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 51.2%; Score 63; DB 2; Length 355;
 Best Local Similarity 57.9%; Pred. No. 0.059;
 Matches 11; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 5 LFQFFIPLMFIFCYTFIV 23
 |||||:|:|:|:|:|:|
 Db 205 LFGLVPLLLVMIICYTGII 223

RESULT 10

S42096
 interleukin-8 receptor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-Aug-1999
 C:Accession: S42096
 R:Gobl, A.E.; Wang, S.; Zhou, Y.; Oeberg, K.
 submitted to the EMBL Data Library, February 1994
 A:Description: Molecular cloning of the rat IL8 receptor.

A:Reference number: S42096
 A:Accession: S42096
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-356 <GOB>
 A:Cross-references: EMBL:X77797
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 51.2%; Score 63; DB 2; Length 356;
 Best Local Similarity 56.2%; Pred. No. 0.059;
 Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 6 FGFFIPLMFIFCYTF 21
 |||||:|:|:|:|:|:|
 Db 217 YGFLPLLLIMFCYGF 232

RESULT 11

A48197
 opsin, ocular - Atlantic horseshoe crab
 C:Species: Limulus polyphemus (Atlantic horseshoe crab)
 C>Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 13-Aug-1999
 C:Accession: A48197
 R:Smith, W.C.; Price, D.A.; Greenberg, R.M.; Battelle, B.A.
 Proc. Natl. Acad. Sci. U.S.A. 90, 6150-6154, 1993
 A:Title: Opsins from the lateral eyes and ocelli of the horseshoe crab, Limulus polyphemus
 A:Reference number: A48197; MUID:93317641
 A:Accession: A48197
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-376 <SMI>
 A:Cross-references: EMBL:L03792; NID:g156644; PIDN:AAA28274.1; PID:g156645
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: chromoprotein; G protein-coupled receptor; lipoprotein; photoreceptor; retinal
 F:318/Binding site: retinal (Lys) (covalent) #status predicted

Query Match 50.8%; Score 62.5; DB 2; Length 376;
 Best Local Similarity 47.8%; Pred. No. 0.073;
 Matches 11; Conservative 7; Mismatches 2; Indels 3; Gaps 1;

QY 4 LLFG---FFIPLMFIFCYTFIV 23
 ::||:|:|:|:|:|:|
 Db 213 IIVGLAVYFLPLITMIYCYFFIV 235

RESULT 12

A46525
 complement C5a anaphylatoxin receptor - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A46525
 R:Gerard, C.; Bao, L.; Orozco, O.; Pearson, M.; Kunz, D.; Gerard, N.P.
 J. Immunol. 149, 2600-2606, 1992
 A:Title: Structural diversity in the extracellular faces of peptidergic G-protein-coupled receptors
 A:Reference number: A46525; MUID:93017861
 A:Accession: A46525
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-351 <GER>
 A:Cross-references: GB:S46665; GB:L05630; NID:g257519; PIDN:AAB97774.1; PID:g257520
 A:Experimental source: BALB/C
 A:Note: sequence extracted from NCBI backbone (NCBIP:116075)
 C:Function:
 A:Description: mediates the inflammatory and chemotactic responses of polymorphonuclear leukocytes
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: chemotaxis; G protein-coupled receptor; glycoprotein; inflammation; polymorphonuclear leukocyte
 F:1-37/Domain: extracellular #status predicted <EX1>
 F:38-61/Domain: transmembrane #status predicted <TM1>
 F:62-71/Domain: intracellular #status predicted <IN1>

JE0349

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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:36:19 ; Search time 62.39 Seconds
(without alignments)
12.628 Million cell updates/sec

Title: US-08-887-977-10_COPY_207_229
Perfect score: 123
Sequence: 1 GLELLFGFFIPLMFIFCVTFIV 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues
Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	123	100.0	374	1 CRR6_HUMAN	P51684 homo sapien
2	103	83.7	367	1 CRR6_MOUSE	O54689 mus musculus
3	74	60.2	369	1 CRR9_MOUSE	Q9wut7 mus musculus
4	67	54.5	353	1 IL8B_GORGO	Q28422 gorilla gor
5	67	54.5	353	1 IL8B_MACMU	Q28519 macaca mula
6	67	54.5	353	1 IL8B_PANTR	Q28807 pan troglod
7	67	54.5	358	1 IL8B_RABIT	P35344 oryctolagus
8	67	54.5	359	1 IL8B_MOUSE	P35343 mus musculus
9	67	54.5	360	1 IL8B_HUMAN	P25025 homo sapien
10	66	53.7	356	1 IL8B_CANFA	O97571 canis fami
11	66	53.7	378	1 CRR7_MOUSE	P47774 mus musculus
12	65	52.8	342	1 BONZ_CERAE	O18983 cercopithec
13	65	52.8	342	1 BONZ_HUMAN	O00574 homo sapien
14	65	52.8	342	1 BONZ_MACNE	O19024 macaca neme
15	65	52.8	343	1 BONZ_MACMU	Q9xt45 macaca mula
16	65	52.8	355	1 IL8A_RABIT	P21109 oryctolagus
17	65	52.8	357	1 CRR9_HUMAN	P51686 homo sapien
18	65	52.8	360	1 IL8B_BOVIN	Q28003 bos taurus
19	65	52.8	369	1 PAR3_MOUSE	O08675 mus musculus
20	64	52.0	350	1 IL8A_GORGO	P55919 gorilla gor
21	64	52.0	350	1 IL8A_HUMAN	P25024 homo sapien
22	64	52.0	350	1 IL8A_PANTR	P55920 pan troglod
23	63	51.2	355	1 CRR1_HUMAN	P32246 homo sapien
24	63	51.2	359	1 IL8B_RAT	P33407 rattus norv
25	62.5	50.8	376	1 OPS2_LIMPO	P35361 limulus pol
26	62	50.4	345	1 C5AR_CAVPO	O70129 cavia porce
27	62	50.4	347	1 C5AR_MOUSE	P30993 mus musculus
28	62	50.4	349	1 IL8A_RAT	P70612 rattus norv
29	62	50.4	352	1 C5AR_CANFA	P30992 canis fami
30	62	50.4	352	1 C5AR_RAT	P97520 rattus norv
31	62	50.4	355	1 CKR1_MACMU	P56482 macaca mula
32	62	50.4	367	1 CCR3_MOUSE	O88410 mus musculus
33	62	50.4	368	1 CCR3_HUMAN	P49682 homo sapien

ALIGNMENTS

RESULT	ID	CKR6_HUMAN	STANDARD;	PRT;	374 AA.
34	AC	P51684; Q92846; P78553;			
35	DT	01-OCT-1996 (Rel. 34, Created)			
36	DT	15-JUL-1998 (Rel. 36, Last sequence update)			
37	DT	01-OCT-2000 (Rel. 40, Last annotation update)			
38	DE	C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CCR-6) (LARC			
39	DE	RECEPTOR) (GPR-CY4) (GPCY4) (CHEMOKINE RECEPTOR-LIKE 3) (CKR-L3)			
40	DE	(DRY6)			
41	GN	CCR6 OR CMKBR6 OR STRL22 OR GPR29 OR CKRL3.			
42	OS	Homo sapiens (Human).			
43	OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
44	OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
45	OX	NCBI_TaxID=9606;			
	RN	[1]			
	RP	SEQUENCE FROM N.A., AND FUNCTION.			
	RX	MEDLINE-97313465; PubMed-9169459;			
	RA	Baba M., Imai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K.,			
	RA	Nomiyama H., Yoshie O.;			
	RT	*Identification of CCR6, the specific receptor for a novel			
	RT	lymphocyte-directed CC chemokine LARC.;			
	RL	J-Biol.-Chem.-272:14893-14898(1997).			
	[2]				
	RN	SEQUENCE FROM N.A.			
	RP	Lautens L.L., Modi W., Bonner T.I.;			
	RL	Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.			
	[3]				
	RN	SEQUENCE FROM N.A.			
	RP	MEDLINE-97040707; PubMed-8886020;			
	RX	Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G.;			
	RA	"Molecular cloning and RNA expression of two new human chemokine			
	RT	receptor-like genes.;"			
	RL	Biochem. Biophys. Res. Commun. 227:846-853(1996).			
	[4]				
	RN	SEQUENCE FROM N.A.			
	RP	McCoy R., Perlmuter D.H.;			
	RA	Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.			
	[5]				
	RN	SEQUENCE FROM N.A.			
	RP	MEDLINE-97224503; PubMed-9070937;			
	RX	Liao F., Lee H.-H., Farber J.M.;			
	RA	"Cloning of STRL22, a new human gene encoding a G-protein-coupled			
	RT	receptor related to chemokine receptors and located on chromosome			
	RL	6q27.;"			
	RL	Genomics 40:175-180(1997).			
	CC	-!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-			
	CC	ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE			
	CC	INTRACELLULAR CALCIUM IONS LEVEL.			
	CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
	CC	-!- TISSUE SPECIFICITY: SPLEEN, LYMPH NODES, APPENDIX, AND FETAL			
	CC	LIVER. EXPRESSED IN LYMPHOCYTES, T CELLS AND B CELLS BUT NOT IN			
	CC	NATURAL KILLER CELLS, MONOCYTES, OR GRANULOCYTES.			
	CC	-!- INDUCTION: INTERLEUKIN-2.			
	CC	-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
	CC	-!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-6 IS THE INITIATOR.			

O88680 cavia porce
Q16581 homo sapien
P35360 limulus pol
P75240 pan troglod
Q92213 cavia porce
P32248 homo sapien
O16018 cambarellus
P79175 gorilla gor
P21730 homo sapien
O00247 mus musculus
O55197 rattus norv

C3AR_CAVPO
C3AR_HUMAN
OPSL_LIMPO
C5AR_PANTR
CRR3_CAVPO
CKR7_HUMAN
OPSD_CAMSC
C5AR_GORGO
C5AR_HUMAN
PAR3_MOUSE
C3AR_MOUSE
C3AR_RAT

62 50.4 475 1
62 50.4 482 1
61.5 50.0 376 1
61 49.6 340 1
61 49.6 358 1
61 49.6 378 1
59 48.0 301 1
59 48.0 340 1
59 48.0 350 1
59 48.0 374 1
59 48.0 477 1
58 47.2 473 1

RESULT 1
CKR6_HUMAN
ID CKR6_HUMAN STANDARD; PRT; 374 AA.
AC P51684; Q92846; P78553;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CCR-6) (LARC
DE RECEPTOR) (GPR-CY4) (GPCY4) (CHEMOKINE RECEPTOR-LIKE 3) (CKR-L3)
DE (DRY6)
GN CCR6 OR CMKBR6 OR STRL22 OR GPR29 OR CKRL3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND FUNCTION.
RX MEDLINE-97313465; PubMed-9169459;
RA Baba M., Imai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K.,
RA Nomiyama H., Yoshie O.;

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U45984; AAB62714.1; -
CC EMBL; 279784; CAB02144.1; ALT_INIT
CC EMBL; U60000; AAB06949.1; -
CC EMBL; U68030; AAC51124.1; -
CC EMBL; U68032; AAC51125.1; -
CC HSSP; P34996; IDDD.
CC GCRDB; GCR_1037; -
CC GCRDB; GCR_1075; -
CC GCRDB; GCR_1906; -
CC GCRDB; GCR_1919; -
CC GCRDB; GCR_1941; -
CC GCRDB; GCR_2110; -
CC MIM; 601835; -
CC InterPro; IPR000276; -
CC Pfam; PF00001; 7tm1.1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PROSITE; PS00237; G_PROTEIN_RECF_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECF_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
KW DOMAIN 1 47 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 48 74 1 (POTENTIAL).
FT DOMAIN 75 83 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 84 104 2 (POTENTIAL).
FT DOMAIN 105 119 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 120 141 3 (POTENTIAL).
FT DOMAIN 142 159 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 160 180 4 (POTENTIAL).
FT DOMAIN 181 211 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 212 238 5 (POTENTIAL).
FT DOMAIN 239 254 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 255 279 6 (POTENTIAL).
FT DOMAIN 280 303 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 304 321 7 (POTENTIAL).
FT DOMAIN 322 374 CYTOPLASMIC (POTENTIAL).
FT DISULFID 118 197 BY SIMILARITY.
FT CARBOHYD 7 7 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 23 23 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 60 60 G -> A (IN REF. 4).
FT CONFLICT 74 74 Y -> N (IN REF. 4).
FT CONFLICT 86 86 L -> V (IN REF. 4).
FT CONFLICT 164 164 S -> T (IN REF. 5).
FT CONFLICT 182 182 T -> S (IN REF. 4).
FT CONFLICT 192 192 Q -> L (IN REF. 4).
FT CONFLICT 206 206 E -> V (IN REF. 4).
FT CONFLICT 225 225 I -> F (IN REF. 4).
FT CONFLICT 370 374 SSFTM -> VLVHVIIES (IN REF. 4).
SQ SEQUENCE 374 AA; 42494 MW; D7F963534E990BC4 CRC64;

Query Match 100.0%; Score 123; DB 1; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.6e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLELLFGFFPIPLMFICYTFIV 23
Db 216 GLELLFGFFPIPLMFICYTFIV 238

RESULT 2
CKR6_MOUSE
ID CKR6_MOUSE STANDARD; PRT; 367 AA.
AC O54689;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)

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DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CCR-6) (KY411).
GN CCR6 OR CMKBR6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Yanagihara S., Komura E., Yamaguchi Y.;
RT "Mouse G protein-coupled receptor KY411.";
RL Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99077268; PubMed=9862452;
RA Varona R., Zaballos A., Gutierrez J., Martin P., Roncal F.,
RA Albar J.P., Ardavin C., Marquez G.;
RT "Molecular cloning, functional characterization and mRNA expression
RT analysis of the murine chemokine receptor CCR6 and its specific ligand
RT MIP-3alpha.";
RL FEBS Lett. 440:188-194(1998).
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-
CC ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE
CC INTRACELLULAR CALCIUM IONS LEVEL.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB009369; BAA23776.1; -
CC EMBL; AJ222714; CAA10956.1; -
CC MGD; MGI:1333797; Cmkbr6.
CC InterPro; IPR000276; -
CC Pfam; PF00001; 7tm1.1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PROSITE; PS00237; G_PROTEIN_RECF_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECF_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
KW DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 40 66 1 (POTENTIAL).
FT TRANSMEM 67 75 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 76 96 2 (POTENTIAL).
FT TRANSMEM 97 111 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 112 133 3 (POTENTIAL).
FT DOMAIN 134 151 4 (POTENTIAL).
FT TRANSMEM 152 172 5 (POTENTIAL).
FT TRANSMEM 173 203 6 (POTENTIAL).
FT TRANSMEM 204 230 7 (POTENTIAL).
FT TRANSMEM 231 246 8 (POTENTIAL).
FT TRANSMEM 247 271 9 (POTENTIAL).
FT TRANSMEM 272 295 10 (POTENTIAL).
FT TRANSMEM 296 313 11 (POTENTIAL).
FT TRANSMEM 314 367 12 (POTENTIAL).
FT CARBOHYD 110 189 BY SIMILARITY.
FT CARBOHYD 2 2 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 35 35 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 367 AA; 42102 MW; 6A309AF833B1117E CRC64;

Query Match 83.7%; Score 103; DB 1; Length 367;
Best Local Similarity 73.9%; Pred. No. 1.3e-06;
Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 GLELLFGFFPIPLMFICYTFIV 23
Db 208 GLELLFGFFPIPLMFICYTFIV 230

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[illegible]

FT	DOMAIN	323	369	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	32	32	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	119	198	BY SIMILARITY.
SQ	SEQUENCE	369 AA;	41913 MW;	6971F76F0A24B4AE CRC64;
Query Match		60.2%;	Score 74;	DB 1; Length 369;
Best Local Similarity		54.5%;	Pred. No. 0.0071;	
Matches 12;	Conservative	4;	Mismatches 6;	Indels 0; Gaps 0;
QY	2	LELFGGFRIPLMFIFCYTFIV	23	
DB	217	LKVTGLGFFLPPVWMAFCYTI	238	
RESULT	4			
IL8B	GORG			
ID	IL8B_GORG	STANDARD;	PRT;	353 AA.
AC	Q28422;			
DT	01-NOV-1997	(Rel. 35, Created)		
DT	01-NOV-1997	(Rel. 35, Last sequence update)		
DT	01-NOV-1997	(Rel. 35, Last annotation update)		
DE	HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (FRAGMENT).			
GN	IL8RB OR CXCR2.			
OS	Gorilla gorilla gorilla (Lowland gorilla).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Gorilla.			
OX	NCBI_TaxID=9595;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96175151; PubMed=9110929;			
RA	Alvarez V., Coto E., Setien F., Gonzalez S., Gonzalez-Roces S.,			
RA	Lopez-Larrea C.;			
RL	Immunogenetics 43:261-267(1996).			
CC	!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL			
CC	NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR			
CC	CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A			
CC	G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND			
CC	MESSENGER-SYSTEM. THIS-RECEPTOR BINDS-TO IL-8 WITH A HIGH AFFINITY			
CC	AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.			
CC	!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	use by non-profit institutions as long as its content is in no way			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announcement/			
CC	or send an email to license@isb-sib.ch).			
DR	EMBL; AJ132336; CAB3480.1;			
DR	MGD; MGI:1341902; Cmkbr10.			
DR	InterPro; IPR000174;			
DR	InterPro; IPR000248;			
DR	InterPro; IPR000276;			
DR	InterPro; IPR000355;			
DR	InterPro; IPR000496;			
DR	InterPro; IPR001277;			
DR	InterPro; IPR001718;			
DR	Pfam; PF00001; 7tm1.1;			
DR	PRINTS; PR00237; GPCRHHODPSN.			
DR	PRINTS; PR00241; ANGIOTENSINR.			
DR	PRINTS; PR00425; BRADYKININR.			
DR	PRINTS; PR00427; INTRLEUKIN8R.			
DR	PRINTS; PR00641; CHEMOKINER7.			
DR	PRINTS; PR00645; LCRIORPHANR.			
DR	PRINTS; PR00657; CCHEMOKINER.			
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.			
DR	PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein.			
FT	DOMAIN	1	49	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	50	76	1 (POTENTIAL).
FT	DOMAIN	77	85	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	86	106	2 (POTENTIAL).
FT	DOMAIN	107	120	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	121	142	3 (POTENTIAL).
FT	DOMAIN	143	160	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	161	181	4 (POTENTIAL).
FT	DOMAIN	182	210	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	211	238	5 (POTENTIAL).
FT	DOMAIN	239	254	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	255	280	6 (POTENTIAL).
FT	DOMAIN	281	304	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	305	322	7 (POTENTIAL).
FT	DOMAIN	<1	45	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	46	72	1 (POTENTIAL).
FT	DOMAIN	73	81	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	82	102	2 (POTENTIAL).
FT	DOMAIN	103	117	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	118	139	3 (POTENTIAL).
FT	DOMAIN	140	160	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	161	180	4 (POTENTIAL).
FT	DOMAIN	181	205	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	206	228	5 (POTENTIAL).
FT	DOMAIN	229	248	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	249	270	6

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FT DOMAIN 271 291 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 292 312 7 (POTENTIAL).
FT DOMAIN 313 >353 CYTOPLASMIC (POTENTIAL).
FT DISULFID 116 193 BY SIMILARITY.
FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 353 353
SQ SEQUENCE 353 AA; 39919 MW; 1FF04E31A7E825B4 CRC64;

Query Match 54.5%; Score 67; DB 1; Length 353;
Best Local Similarity 62.5%; Pred. No. 0.054;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 FGFFIPLMFICYTF 21
DB 215 FGFIPLLMFCYGF 230

RESULT 5
IL8B_MACMU
ID IL8B_MACMU STANDARD; PRT; 353 AA.
AC Q28519;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (FRAGMENT).
GN IL8RB OR CXCR2
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96175151; PubMed=9110929;
RA Alvarez V., Coto E., Setien F., Gonzalez S., Gonzalez-Roces S.,
RA Lopez-Larrea C.;
RT "Characterization of interleukin-8 receptors in non-human primates.";
CC "-!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
CC AND TO GROM/MSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
CC "-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC "-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC
CC EMBL; X91116; CAA62565.1;
CC HSP; P34996; 1DD0.
CC InterPro; IPR000276;
CC Pfam; PF00001; 7tm_1; 1.
CC PROSITE; PS00237; G-PROTEIN_RECEPTOR_F1_1; 1.
CC PROSITE; PS0262; G-PROTEIN_RECEPTOR_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Chemoaxis.
FT NON_TER 1 1
FT DOMAIN <1 45 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 46 72 1 (POTENTIAL).
FT DOMAIN 73 81 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 82 102 2 (POTENTIAL).
FT DOMAIN 103 117 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 118 139 3 (POTENTIAL).
FT DOMAIN 140 160 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 161 180 4 (POTENTIAL).

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FT DOMAIN 181 205 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 206 228 5 (POTENTIAL).
FT DOMAIN 229 248 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 249 270 6 (POTENTIAL).
FT DOMAIN 271 291 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 292 312 7 (POTENTIAL).
FT DOMAIN 313 >353 CYTOPLASMIC (POTENTIAL).
FT DISULFID 116 193 BY SIMILARITY.
FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 353 353
SQ SEQUENCE 353 AA; 39947 MW; EC8B38130657C713 CRC64;

Query Match 54.5%; Score 67; DB 1; Length 353;
Best Local Similarity 62.5%; Pred. No. 0.054;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 FGFFIPLMFICYTF 21
DB 215 FGFIPLLMFCYGF 230

RESULT 6
IL8B_PANTR
ID IL8B_PANTR STANDARD; PRT; 353 AA.
AC Q28607;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (FRAGMENT).
GN IL8RB OR CXCR2
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96175151; PubMed=9110929;
RA Alvarez V., Coto E., Setien F., Gonzalez S., Gonzalez-Roces S.,
RA Lopez-Larrea C.;
RT "Characterization of interleukin-8 receptors in non-human primates.";
CC "-!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
CC AND TO GROM/MSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
CC "-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC "-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC
CC EMBL; X91113; CAA62563.1;
CC HSP; P34996; 1DD0.
CC InterPro; IPR000276;
CC Pfam; PF00001; 7tm_1; 1.
CC PROSITE; PS00237; G-PROTEIN_RECEPTOR_F1_1; 1.
CC PROSITE; PS0262; G-PROTEIN_RECEPTOR_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Chemoaxis.
FT NON_TER 1 1
FT DOMAIN <1 45 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 46 72 1 (POTENTIAL).
FT DOMAIN 73 81 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 82 102 2 (POTENTIAL).
FT DOMAIN 103 117 EXTRACELLULAR (POTENTIAL).

```

FT TRANSMEM 118 139 3 (POTENTIAL).
 FT DOMAIN 140 160 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 161 180 4 (POTENTIAL).
 FT DOMAIN 181 205 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 206 228 5 (POTENTIAL).
 FT DOMAIN 229 248 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 249 270 6 (POTENTIAL).
 FT DOMAIN 271 291 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 292 312 7 (POTENTIAL).
 FT DOMAIN 313 >353 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 116 193 BY SIMILARITY.
 FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT NON_TER 353 353
 SQ SEQUENCE 353 AA; 39998 MW; E745ACD9EC10C1E2 CRC64;

Query Match 54.5%; Score 67; DB 1; Length 353;
 Best Local Similarity 62.5%; Pred. No. 0.054; 3; Indels 0; Gaps 0;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 6 FGFFPLMFMYCYTF 21
 ||| :||: |:||| |
 Db 215 FGFIPLMLFCYGF 230

RESULT 7
 IL8B_RABIT
 ID IL8B_RABIT STANDARD; PRT; 358 AA.
 AC P35344;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GRO/MGSA RECEPTOR).
 DE RECEPTOR.
 GN IL8RB OR CXCR2.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ALBINO; TISSUE=Blood;
 RX MEDLINE=94230294; PubMed=8175642;
 RA Prado G.N., Thomas K.M., Suzuki H., Larosa G.J., Wilkinson N.C.,
 RA Folco E., Navarro J.;
 RT Molecular characterization of a novel rabbit interleukin-8 receptor
 RT isotype.;
 RL J. Biol. Chem. 269:12391-12394(1994).
 CC -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
 CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
 CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
 CC G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER SYSTEM. THE AFFINITY OF THIS RECEPTOR IS IL-8 >> NAP-2 >
 CC MSGA (GRO).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: EXPRESSED PREFERENTIALLY IN NEUTROPHILS.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC
 CC EMBL: L24445; AAA31378.1; -
 CC PIR: A53752; A53752.
 CC GCRDb; GCR_0861; -
 CC InterPro; IPR000057; -
 CC InterPro; IPR000174; -
 CC InterPro; IPR000276; -
 CC Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00427; INTRLEUKIN8R.
 DR PROSITE; PR00573; INTRLEUKIN8R.
 DR PROSITE; PR00237; G-PROTEIN RECP_FL_1; 1.
 DR PROSITE; PR00237; G-PROTEIN RECP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Chemotaxis.
 FT DOMAIN 1 46 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 47 73 1 (POTENTIAL).
 FT DOMAIN 74 82 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 83 103 2 (POTENTIAL).
 FT DOMAIN 104 118 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 119 140 3 (POTENTIAL).
 FT DOMAIN 141 161 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 162 181 4 (POTENTIAL).
 FT DOMAIN 182 206 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 207 229 5 (POTENTIAL).
 FT DOMAIN 230 249 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 250 271 6 (POTENTIAL).
 FT DOMAIN 272 292 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 293 313 7 (POTENTIAL).
 FT DOMAIN 314 358 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 117 194 BY SIMILARITY.
 SQ SEQUENCE 358 AA; 40632 MW; 6899716944D6126A CRC64;

Query Match 54.5%; Score 67; DB 1; Length 358;
 Best Local Similarity 62.5%; Pred. No. 0.055;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 6 FGFFPLMFMYCYTF 21
 ||| :||: |:||| |
 Db 216 FGFIPLMLFCYVF 231

RESULT 8
 IL8B_MOUSE
 ID IL8B_MOUSE STANDARD; PRT; 359 AA.
 AC P35343;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GRO/MGSA RECEPTOR).
 DE RECEPTOR.
 GN IL8RB OR CXCR2 OR CMKAR2 OR GPCR16.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94117014; PubMed=8288247;
 RA Cerretti D.P., Nelson N., Kozlosky C.J., Morrissey P.J.,
 RA Copeland N.G., Gilbert D.J., Jenkins N.A., Dosik J.K., Mock B.A.;
 RT "The murine homologue of the human interleukin-8 receptor type B maps
 RT near the lty-lsh-Bcg disease resistance locus.";
 RL Genomics 18:410-413(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RX MEDLINE=95050766; PubMed=7961909;
 RA Bozic C.R., Gerard N.P., von Uexkull-Guldenband C.,
 RA Kolakowski L.F. Jr., Conklyn M.J., Breslow R., Showell H.J.,
 RA Gerard C.;
 RT "The murine interleukin 8 type B receptor homologue and its ligands.
 RT Expression and biological characterization.";
 RL J. Biol. Chem. 269:29355-29358(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV;
 RX MEDLINE=95363183; PubMed=7636264;

RA Lee J., Cacalano G., Camerato T., Toy K., Moore M.W., Wood W.I.;
 RT "Chemokine binding and activities mediated by the mouse IL-8
 receptor.";
 RL J. Immunol. 155:2158-2164(1995).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94252584; PubMed=8194768;
 RA Harada A., Kuno K., Nomura H., Mukaida N., Murakami S., Matsushima K.;
 RT "Cloning of a cDNA encoding a mouse homolog of the interleukin-8
 receptor.";
 RL Gene 142:297-300(1994).
 RN [5]
 RP SEQUENCE OF 145-258 FROM N.A.
 RX MEDLINE=94116980; PubMed=8288218;
 RA Wilkie T.M., Chen Y., Gilbert D.J., Moore K.J., Yu L., Simon M.I.,
 RT "Identification, chromosomal location, and genome organization of
 mammalian G-protein-coupled receptors.";
 RL Genomics 18:175-184(1993).
 CC -1- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
 NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
 CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
 G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
 AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 DR EMBL; L23637; AAA39305.1; -
 DR EMBL; L13239; AAA62109.1; -
 DR EMBL; U31207; AAC52239.1; -
 DR EMBL; D17630; BAA04536.1; -
 DR EMBL; L20337; AAA16853.1; -
 DR PIR; A53677; A53677.
 DR GCRdb; GCR_0550; -
 DR GCRdb; GCR_0812; -
 DR GCRdb; GCR_0838; -
 DR GCRdb; GCR_1027; -
 DR GCRdb; GCR_1670; -
 DR MGD; MGI:105303; Cmkar2.
 DR InterPro; IPR000057; -
 DR InterPro; IPR000174; -
 DR InterPro; IPR000276; -
 DR Pfam; PF00001; 7tm1.1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00427; INTRLEUKIN8R.
 DR PRINTS; PR00573; INTRLEUKIN8R.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Chemotaxis.
 DR DOMAIN 1 47
 DR TRANSMEM 48 74
 DR DOMAIN 75 83
 DR TRANSMEM 84 104
 DR DOMAIN 105 119
 DR TRANSMEM 120 141
 DR DOMAIN 142 162
 DR TRANSMEM 163 182
 DR DOMAIN 183 207
 DR TRANSMEM 208 230
 DR DOMAIN 231 250
 DR TRANSMEM 251 272
 DR DOMAIN 273 293
 DR EXTRACELLULAR (POTENTIAL).
 DR 1 (POTENTIAL).
 DR CYTOPLASMIC (POTENTIAL).
 DR 2 (POTENTIAL).
 DR EXTRACELLULAR (POTENTIAL).
 DR 3 (POTENTIAL).
 DR CYTOPLASMIC (POTENTIAL).
 DR 4 (POTENTIAL).
 DR EXTRACELLULAR (POTENTIAL).
 DR 5 (POTENTIAL).
 DR CYTOPLASMIC (POTENTIAL).
 DR 6 (POTENTIAL).
 DR EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 294 314 7 (POTENTIAL).
 FT DOMAIN 315 359 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 23 23 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 118 195 BY SIMILARITY.
 SQ SEQUENCE 359 AA; 40425 MW; 74BD166E9B679F88 CRC64;
 Query Match 54.5%; Score 67; DB 1; Length 359;
 Best Local Similarity 62.5%; Pred. No. 0.055;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 6 FGFEPLMFIMFYCYTF 21
 Db 217 FGFLVPLLLMLFCYGF 232
 RESULT 9
 IL8B_HUMAN STANDARD; PRT; 360 AA.
 ID IL8B_HUMAN
 AC P25025;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GRO/MGSA
 RECEPTOR) (IL-8 RECEPTOR TYPE 2) (CDW128B).
 GN IL8RB OR CXCR2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91368200; PubMed=1891716;
 RA Murphy P.M., Tiffany H.L.;
 RT "Cloning of complementary DNA encoding a functional human
 interleukin-8 receptor.";
 RL Science 253:1280-1283(1991).
 RN [2]
 RP SEQUENCE FROM N.A. AND CHARACTERIZATION.
 RX MEDLINE=93205012; PubMed=8384312;
 RA Carretti D.P., Kozlosky C.J., Vanden Bos T., Nelson N., Gearing D.P.,
 RA Beckmann M.P.;
 RT "Molecular characterization of receptors for human interleukin-8,
 GRO/melanoma growth-stimulatory activity and neutrophil activating
 peptide-2.";
 RL Mol. Immunol. 30:359-367(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94209273; PubMed=7512557;
 RA Sprenger H., Lloyd A.R., Lautens L.L., Bonner T.I., Kelvin D.J.;
 RT "Structure, genomic organization, and expression of the human
 interleukin-8 receptor B gene.";
 RL J. Biol. Chem. 269:11065-11072(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=95014476; PubMed=7929358;
 RA Ahuja S.K., Shetty A., Tiffany H.L., Murphy P.M.;
 RT "Comparison of the genomic organization and promoter function for
 human interleukin-8 receptors A and B.";
 RL J. Biol. Chem. 269:26381-26389(1994).
 RN [5]
 RP CHARACTERIZATION.
 RX MEDLINE=92355587; PubMed=1379593;
 RA Lee J., Horuk R., Rice G.C., Bennett G.L., Camerato T., Wood W.I.;
 RT "Characterization of two high affinity human interleukin-8
 receptors.";
 RL J. Biol. Chem. 267:16283-16287(1992).
 CC -1- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
 NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
 CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
 G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY

CC AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -!- DATABASE: NAME=PROW; NOTE=CD guide Cdw128b entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw128b.htm".
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 CC
 CC EMBL; M73969; AAA83148.1; -
 CC EMBL; M94582; AAA36108.1; -
 CC EMBL; M9412; AAC14460.1; -
 CC EMBL; L19593; AAB59437.1; -
 CC EMBL; L11869; AAB60656.1; -
 CC PIR; A39446; A39446.
 CC PIR; A53611; A53611.
 CC HSP; P34996; 1DD0.
 CC GCRDb; GCR_0077; -
 CC GCRDb; GCR_0610; -
 CC GCRDb; GCR_1001; -
 CC GCRDb; GCR_1339; -
 CC GCRDb; GCR_1831; -
 CC MIM; 146928; -
 CC InterPro; IPR000057; -
 CC InterPro; IPR000174; -
 CC InterPro; IPR000276; -
 CC Pfam; PF00001; 7tm.1; 1.
 CC PRINTS; PR00237; GPCRHHODOPSN.
 CC PRINTS; PR00427; INTRLEUKN8R.
 CC PRINTS; PR00573; INTRLEUKN8R.
 CC PROSITE; PS00237; G-PROTEIN_RECEPTOR_F1_1; 1.
 CC PROSITE; PS00262; G-PROTEIN_RECEPTOR_F1_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein;
 CC Chemotaxis.

FT DOMAIN 1 48 - - - - - EXTRACELLULAR (POTENTIAL);
 FT TRANSMEM 49 75 1 (POTENTIAL).
 FT DOMAIN 76 84 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 85 105 2 (POTENTIAL).
 FT DOMAIN 106 120 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 121 142 3 (POTENTIAL).
 FT DOMAIN 143 163 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 164 183 4 (POTENTIAL).
 FT DOMAIN 184 208 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 209 231 5 (POTENTIAL).
 FT DOMAIN 232 251 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 252 273 6 (POTENTIAL).
 FT DOMAIN 274 294 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 295 315 7 (POTENTIAL).
 FT DOMAIN 316 360 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 119 196 BY SIMILARITY.
 SQ SEQUENCE 360 AA; 40759 MW; 564F04A8BCC0A197 CRC64;

Query Match 54.5%; Score 67; DB 1; Length 360;
 Best Local Similarity 62.5%; Pred. No. 0.055;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 6 FGFFIPLMFIFCYTF 21
 ||| :|| :||| |
 Db 218 FGFIPLMLFCYGF 233

RESULT 10
 IL8B_CANFA STANDARD; PRT; 356 AA.
 AC 097571;
 DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GRO/MGSA
 DE RECEPTOR).
 GN IL8RB OR CXCR2.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BEAGLE;
 RA Chang Y.F., Novosel V., Chang C.F.;
 RT "The isolation and sequence of canine interleukin-8 receptor
 RT homolog".
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
 CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
 CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
 CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER SYSTEM. THE AFFINITY OF THIS RECEPTOR IS IL-8 >> NAP-2 >
 CC MGSA (GRO).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC
 CC EMBL; AF047047; AAC98968.1; -
 CC InterPro; IPR000057; -
 CC InterPro; IPR000174; -
 CC InterPro; IPR000276; -
 CC InterPro; IPR000355; -
 CC InterPro; IPR001277; -
 CC Pfam; PF00001; 7tm.1; 1.
 CC PRINTS; PR00237; GPCRHHODOPSN.
 CC PRINTS; PR00427; INTRLEUKN8R.
 CC PRINTS; PR00573; INTRLEUKN8R.
 CC PRINTS; PR00645; LCR1ORPHNR.
 CC PRINTS; PR00657; CCEHEMOKNER.
 CC PROSITE; PS00237; G-PROTEIN_RECEPTOR_F1_1; 1.
 CC PROSITE; PS00262; G-PROTEIN_RECEPTOR_F1_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein;
 CC Chemotaxis.
 FT DOMAIN 1 46 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 47 73 1 (POTENTIAL).
 FT DOMAIN 74 82 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 83 103 2 (POTENTIAL).
 FT DOMAIN 104 118 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 119 140 3 (POTENTIAL).
 FT DOMAIN 141 161 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 162 181 4 (POTENTIAL).
 FT DOMAIN 182 206 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 207 229 5 (POTENTIAL).
 FT DOMAIN 230 249 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 250 269 6 (POTENTIAL).
 FT DOMAIN 270 290 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 291 311 7 (POTENTIAL).
 FT DOMAIN 312 356 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SEQUENCE 356 AA; 40505 MW; 2B67DD4E9DD39B15 CRC64;

Query Match 53.7%; Score 66; DB 1; Length 356;
 Best Local Similarity 71.4%; Pred. No. 0.074;
 Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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QY 6 FGFIPLMFIMFY 19
    ||| :||| :|||
Db 216 FGFIPLMFIMFY 229

RESULT 11
ID CKR7_MOUSE STANDARD; PRT; 378 AA.
AC P47774;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 7 PRECURSOR (C-C CKR-7) (CCR-7)
DE (MIP-3 BETA RECEPTOR) (EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 1)
DE (EB11).
GN CKR7 OR CMKBR7 OR EB11 OR EB11H.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6/CBA; TISSUE=Thymus;
RX MEDLINE=95154835; PubMed=7851893;
RA Schweickart V.L., Raport C.J., Godiska R., Byers M.G., Eddy R.L. Jr.,
RA Shows T.B., Gray P.W.;
RT "Cloning of human and mouse EB11, a lymphoid-specific
RT G-protein-coupled receptor encoded on human chromosome 17q12-q21.2.";
RL Genomics 23:643-650(1994).
CC -!- FUNCTION: RECEPTOR FOR THE MIP-3-BETA CHEMOKINE. PROBABLE MEDIATOR
CC OF EBV EFFECTS ON B LYMPHOCYTES OR OF NORMAL LYMPHOCYTE FUNCTIONS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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DR EMBL; L31580; AAA74232.1;
DR MGD; MGI:103011; Cmkbr7.
DR InterPro; IPR000276;
DR InterPro; IPR001718;
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PR00641; CHEMOKINER7.
DR PROSITE; PS00237; G_PROTEIN_RECF_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECF_F1_2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 378 C-C CHEMOKINE RECEPTOR TYPE 7.
FT DOMAIN 25 59 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 60 86 1 (POTENTIAL).
FT DOMAIN 87 95 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 96 116 2 (POTENTIAL).
FT DOMAIN 117 130 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 131 152 3 (POTENTIAL).
FT DOMAIN 153 170 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 171 191 4 (POTENTIAL).
FT DOMAIN 192 219 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 220 247 5 (POTENTIAL).
FT DOMAIN 248 263 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 264 289 6 (POTENTIAL).
FT DOMAIN 290 313 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 314 331 7 (POTENTIAL).
FT DOMAIN 332 378 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 129 210 BY SIMILARITY.
SQ SEQUENCE 378 AA; 42941 MW; ACBIA422CF54AA54 CRC64;

QY 3 ELLFGFFIPLMFIMFY 23
    ::||| :||| :|||
Db 227 QMVFGFLVPLMAMSFYLI 247

RESULT 12
ID BONZ_CERAE STANDARD; PRT; 342 AA.
AC O18983;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE G PROTEIN-COUPLED RECEPTOR BONZO.
GN BONZO.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97373958; PubMed=9230441;
RA Deng H.K., Unutmaz D., Kewalramani V.N., Littman D.R.;
RT "Expression cloning of new receptors used by simian and human
RT immunodeficiency viruses.";
RL Nature 388:296-300(1997).
CC -!- FUNCTION: ORPHAN RECEPTOR. COULD BE A CHEMOKINE RECEPTOR. USED AS
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC -----
DR EMBL; AF007859; AAB64225.1;
DR GCRdb; GCR_2411;
DR InterPro; IPR000276;
DR InterPro; IPR002235;
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR01105; BONZOORPHANR.
DR PROSITE; PS00237; G_PROTEIN_RECF_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECF_F1_2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 33 59 1 (POTENTIAL).
FT DOMAIN 60 88 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 89 103 2 (POTENTIAL).
FT DOMAIN 104 125 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 126 143 3 (POTENTIAL).
FT DOMAIN 144 164 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 165 187 4 (POTENTIAL).
FT DOMAIN 188 215 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 216 231 5 (POTENTIAL).
FT TRANSMEM 232 259 6 (POTENTIAL).
FT DOMAIN 260 275 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 276 293 7 (POTENTIAL).
FT DOMAIN 294 342 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 102 180 BY SIMILARITY.
FT CARBOHYD 16 16 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 342 AA; 39226 MW; 6CBFE389C6E5919E CRC64;
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Query Match      52.8%; Score 65; DB 1; Length 342;
Best Local Similarity 47.6%; Pred. No. 0.096;
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 3 ELLFGFFIPLMFIMFYTFIV 23
   :  |||:|:|  |||:|:|  :
Db 195 QMTLGFLLPMLAMIVCYSVII 215

RESULT 13
BONZ_HUMAN
ID BONZ_HUMAN STANDARD; PRT; 342 AA.
AC O00574; O00575;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE G PROTEIN-COUPLED RECEPTOR BONZO (G PROTEIN-COUPLED RECEPTOR STRL33).
GN BONZO OR STRL33 OR TYMSTR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97373958; PubMed=9230441;
RA Deng H.K., Unutmaz D., Kewalramani V.N., Littman D.R.;
RT "Expression cloning of new receptors used by simian and human
   immunodeficiency viruses."
RL Nature 388:296-300(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97311099; PubMed=9166430;
RA Liao F., Alkhatib G., Feden K.W.C., Sharma G., Berger E.A.,
RA Farber J.M.;
RT "STRL33, A novel chemokine receptor-like protein, functions as a
   fusion cofactor for both macrophage-tropic and T cell line-tropic
   HIV-1."
RL J. Exp. Med. 185:2015-2023(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Blood;
RC MEDLINE=97431687; PubMed=9285716;
RA Loetscher M., Amara A., Oberlin E., Brass N., Legler D.F.,
RA Loetscher P., D'Apuzzo M., Meese E.U., Rousset D., Virelizier J.L.,
RA Baggiolini M., Arenzana-Seisdedos F., Moser B.;
RT "TYMSTR, a putative chemokine receptor selectively expressed in
   activated T cells, exhibits HIV-1 coreceptor function."
RL Curr. Biol. 7:652-660(1997).
CC -!- FUNCTION: ORPHAN RECEPTOR. COULD BE A CHEMOKINE RECEPTOR. USED AS
   A CORECEPTOR BY SIVS AND BY STRAINS OF HIV-2 AND M-TROPIC HIV-1.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN LYMPHOID TISSUES AND ACTIVATED T
   CELLS.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
CC EMBL; AF007545; AAB64221.1;
CC EMBL; U73529; AAB61456.1;
CC EMBL; U73531; AAB61457.1;
CC EMBL; Y13248; CAA73698.1;
CC MIM; 605163;
CC GCRDB; GCR_1328;
CC GCRDB; GCR_1330;
CC GCRDB; GCR_2393;

InterPro; IPR000276;
InterPro; IPR002235;
Pfam; PF00001; 7tm.1; 1.
PRINTS; PR00237; GPCRHDOPSN.
PRINTS; PR01105; BONZOORPHANR.
PRINTS; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.
DOMAIN 1 32
TRANSSEM 33 59
DOMAIN 60 68
TRANSSEM 69 89
DOMAIN 90 103
TRANSSEM 104 125
DOMAIN 126 143
TRANSSEM 144 164
DOMAIN 165 187
TRANSSEM 188 215
DOMAIN 216 231
TRANSSEM 232 259
DOMAIN 260 275
TRANSSEM 276 293
DOMAIN 294 342
DISULFID 102 180
FT CARBOHYD 16 16
FT VARIANT 25 25
SQ SEQUENCE 342 AA; 39280 MW; 9FBC02556D1082E CRC64;

Query Match      52.8%; Score 65; DB 1; Length 342;
Best Local Similarity 47.6%; Pred. No. 0.096;
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 3 ELLFGFFIPLMFIMFYTFIV 23
   :  |||:|:|  |||:|:|  :
Db 195 QMTLGFLLPMLAMIVCYSVII 215

RESULT 14
BONZ_MACNE
ID BONZ_MACNE STANDARD; PRT; 342 AA.
AC O19024;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE G PROTEIN-COUPLED RECEPTOR BONZO.
GN BONZO.
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97373958; PubMed=9230441;
RA Deng H.K., Unutmaz D., Kewalramani V.N., Littman D.R.;
RT "Expression cloning of new receptors used by simian and human
   immunodeficiency viruses."
RL Nature 388:296-300(1997).
CC -!- FUNCTION: ORPHAN RECEPTOR. COULD BE A CHEMOKINE RECEPTOR. USED AS
   A CORECEPTOR BY SIVS AND BY STRAINS OF HIV-2 AND M-TROPIC HIV-1.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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   or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF007545; AAB64221.1;
CC EMBL; U73529; AAB61456.1;
CC EMBL; U73531; AAB61457.1;
CC EMBL; Y13248; CAA73698.1;
CC MIM; 605163;
CC GCRDB; GCR_1328;
CC GCRDB; GCR_1330;
CC GCRDB; GCR_2393;

```

DR EMBL; AF007858; AAB64224.1; -;
 DR GCRDB; GCR_2409; -;
 DR InterPro; IPR000276; -;
 DR Pfam; PF00001; 7tm1.1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PRINTS; PR01105; BONZOORPHANR.
 DR PROSITE; PS00237; G_PROTEIN_RECP_FL_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 32
 FT TRANSMEM 33 59
 FT DOMAIN 60 68
 FT TRANSMEM 69 89
 FT DOMAIN 90 103
 FT TRANSMEM 104 125
 FT DOMAIN 126 143
 FT TRANSMEM 144 164
 FT DOMAIN 165 187
 FT TRANSMEM 188 215
 FT DOMAIN 216 231
 FT TRANSMEM 232 259
 FT DOMAIN 260 275
 FT TRANSMEM 276 293
 FT DOMAIN 294 342
 FT DISULFID 102 180
 FT CARBOHYD 16 16
 SQ SEQUENCE 342 AA; 39297 MW; 55F9F68CB62D2DF5 CRC64;

Query Match 52.8%; Score 65; DB 1; Length 342;
 Best Local Similarity 47.6%; Pred. No. 0.096;
 Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 3 ELLFGFFPLMFIMFCYTFIV 23
 :: |||:: || ||:
 Db 195 QMTLGFLLAMIVCYSVII 215

RESULT 15
 BONZ_MACMU STANDARD; PRT; 343 AA.
 ID BONZ_MACMU
 AC Q9XT45;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE G PROTEIN-COUPLED RECEPTOR BONZO (G PROTEIN-COUPLED RECEPTOR STRL33).
 GN BONZO OR STRL33.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Margulies B.J., Hauer D.A., Clements J.E.;
 RT "Identification and characterization of thirteen rhesus macaque
 chemokine receptors and chemokine receptor homologues";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: ORPHAN RECEPTOR. COULD BE A CHEMOKINE RECEPTOR. USED AS
 CC A CORECEPTOR BY SIVS AND BY STRAINS OF HIV-2 AND M-TROPIC HIV-1.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF124380; AAD31419.1; -;

DR InterPro; IPR000276; -;
 DR Pfam; PF00001; 7tm1.1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PRINTS; PR01105; BONZOORPHANR.
 DR PROSITE; PS00237; G_PROTEIN_RECP_FL_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 33
 FT TRANSMEM 34 60
 FT DOMAIN 61 69
 FT TRANSMEM 70 90
 FT DOMAIN 91 104
 FT TRANSMEM 105 126
 FT DOMAIN 127 144
 FT TRANSMEM 145 165
 FT DOMAIN 166 188
 FT TRANSMEM 189 216
 FT DOMAIN 217 232
 FT TRANSMEM 233 260
 FT DOMAIN 261 276
 FT TRANSMEM 277 294
 FT DOMAIN 295 343
 FT CARBOHYD 17 17
 FT DISULFID 103 181
 SQ SEQUENCE 343 AA; 39423 MW; 48DB2544949EB83F CRC64;

Query Match 52.8%; Score 65; DB 1; Length 343;
 Best Local Similarity 47.6%; Pred. No. 0.096;
 Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 3 ELLFGFFPLMFIMFCYTFIV 23
 :: |||:: || ||:
 Db 196 QMTLGFLLAMIVCYSVII 216

Search completed: May 23, 2001, 15:36:20
 Job time: 651 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:35:16 ; Search time 189.03 Seconds
(without alignments)
14.261 Million cell updates/sec

Title: US-08-887-977-10_COPY_207_229
Perfect score: 123
Sequence: 1 GLELLFGFFPLMFIMFCYTFIV 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_unclassified.*
- 13: sp_vertebrate.*
- 14: sp_virus.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	103	83.7	367	11	Q9R1V0	Q9R1V0 mus musculus
2	71	57.7	368	13	O42444	O42444 oncorhynch
3	67	54.5	111	4	Q9P2T6	Q9P2T6 homo sapien
4	66	53.7	521	11	Q9QXZ9	Q9QXZ9 mus musculus
5	65.5	53.3	342	13	Q93239	Q93239 cyprinus ca
6	65	52.8	174	6	Q9TU48	Q9TU48 bos taurus
7	65	52.8	174	6	Q9TQ57	Q9TQ57 bos taurus
8	65	52.8	339	11	Q9J371	Q9J371 mus musculus
9	65	52.8	342	6	Q9TV16	Q9TV16 pan troglod
10	65	52.8	343	6	Q9XT45	Q9XT45 macaca mula
11	65	52.8	343	6	Q9N0Z0	Q9N0Z0 cercocebus
12	65	52.8	352	11	Q9JK47	Q9JK47 mus musculus
13	65	52.8	369	4	Q9UQ06	Q9UQ06 homo sapien
14	63	51.2	478	4	Q9UHM6	Q9UHM6 homo sapien
15	62	50.4	367	11	O88410	O88410 mus musculus
16	62	50.4	367	11	Q9QWN6	Q9QWN6 mus musculus
17	62	50.4	415	4	O15185	O15185 homo sapien
18	62	50.4	475	11	Q9QW69	Q9QW69 cavia porce
19	61	49.6	367	11	Q9J1I9	Q9J1I9 rattus norv

20	60	48.8	337	4	Q9Y271	Q9Y271 homo sapien
21	59	48.0	392	13	O93281	O93281 gallus gall
22	58	47.2	270	5	O45125	O45125 drosophila
23	57	46.3	350	6	Q9TUEL	Q9TUEL oryctolagus
24	56.5	45.9	360	4	Q9ULY7	Q9ULY7 homo sapien
25	56.5	45.9	360	4	Q9ULY6	Q9ULY6 homo sapien
26	56	45.5	355	6	Q9MYJ8	Q9MYJ8 callithrix
27	56	45.5	546	13	Q9IAJ3	Q9IAJ3 pimephales
28	55	44.7	144	11	O08840	O08840 rattus norv
29	55	44.7	238	6	Q97523	Q97523 sus scrofa
30	55	44.7	360	6	Q97663	Q97663 macaca mula
31	55	44.7	360	6	Q9TV17	Q9TV17 macaca mula
32	54.5	44.3	341	5	Q9UANO	Q9UANO papilio gla
33	54	43.9	372	13	O93237	O93237 cyprinus ca
34	54	43.9	377	5	O02464	O02464 manduca sex
35	54	43.9	571	6	Q9TSE9	Q9TSE9 ovis aries
36	53	43.1	351	6	Q9MYJ9	Q9MYJ9 oryctolagus
37	53	43.1	355	11	Q9JLY8	Q9JLY8 rattus norv
38	53	43.1	364	4	O9UJ15	O9UJ15 homo sapien
39	53	43.1	379	5	O9XVS5	O9XVS5 caenorhabdi
40	53	43.1	419	5	P91096	P91096 caenorhabdi
41	53	43.1	469	4	Q9NSD7	Q9NSD7 homo sapien
42	53	43.1	1087	5	O22490	O22490 caenorhabdi
43	52.5	42.7	395	2	O9PPI4	O9PPI4 campylobact
44	52	42.3	138	6	O97777	O97777 elephas max
45	52	42.3	148	6	O9TS32	O9TS32 bos sp. c5a

ALIGNMENTS

RESULT 1
Q9R1V0
ID Q9R1V0 PRELIMINARY; PRT; 367 AA.
AC Q9R1V0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE CC-CHEMOKINE-LARC-SPECIFIC-RECEPTOR
GN MCCR6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Tanaka Y.;
RT "Molecular Cloning of Murine Homologue of CCR6, the Specific Receptor
for CC Chemokine LARC";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB016031; BAA82443.1; -;
DR INTERPRO; IPR000190; -;
DR INTERPRO; IPR000276; -;
DR INTERPRO; IPR000355; -;
DR PFAM; PF000001; 7tm_1; 1;
DR PRINTS; PRO0237; GPCRHHODPSN.
DR PRINTS; PRO0635; ANGIOTENSINR.
DR PRINTS; PRO0657; CCHEMOKINER..
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 367 AA; 42082 MW; 207FD98B2F7A6DD3 CRC64;

Query Match 83.7%; Score 103; DB 11; Length 367;
Best Local Similarity 73.9%; Pred. No. 1.3e-06;
Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 GLELLFGFFPLMFIMFCYTFIV 23
|||||
Db 208 GLELLFGFFPLMFIMFCYTFII 230

RESULT 2

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042444
ID O42444 PRELIMINARY: PRT: 368 AA.
AC O42444;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE INTERLEUKIN-8-LIKE RECEPTOR.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Zou J., Daniels G.D., Cunningham C., Secombes C.J.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ003159; CAA05917.1; -
DR INTERPRO: IPR000276; -
DR PFAM: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODOPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
SQ SEQUENCE 368 AA; 41523 MW; BE28E2D4C47E821A CRC64;

Query Match 57.7%; Score 71; DB 13; Length 368;
Best Local Similarity 47.8%; Pred. No. 0.029;
Matches 11; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 GLELLFGFFPLMFIFCYTFIV 23
DB 216 GLQICMGFCPLPLLVVFCYAGII 238

RESULT 3
Q9P2T6 PRELIMINARY: PRT: 111 AA.
AC Q9P2T6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE IL-8 RECEPTOR TYPE B (FRAGMENT).
GN CXCR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kato H., Tsuchiya N., Tokunaga K.;
RT "Detection of single nucleotide polymorphisms in the coding region of
human CXCR2-chemokine receptor CXCR1, CXCR2, and CXCR3.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB032734; BAA92296.1; -
KW Receptor.
FT NON_TER 1 1
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12947 MW; 1425DC123439A1BB CRC64;

Query Match 54.5%; Score 67; DB 4; Length 111;
Best Local Similarity 62.5%; Pred. No. 0.037;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 FGFFPLMFIFCYTF 21
DB 28 FGFIPLLMFICYGF 43

RESULT 4
Q9QXZ9 PRELIMINARY: PRT: 521 AA.
ID Q9QXZ9
AC Q9QXZ9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)

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DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE MELANOPSIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-RETINA.
RX MEDLINE=20098934; PubMed=10632589;
RA Provencio I., Rodriguez I.R., Jiang G., Hayes W.P., Moreira E.F.,
RA Rolliag M.D.;
RT "A novel human opsin in the inner retina.";
RL J. Neurosci. 20:600-605(2000).
DR EMBL: AF147789; AAF24979.1; -
DR INTERPRO: IPR000276; -
DR INTERPRO: IPR001760; -
DR PFAM: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODOPSN.
DR PROSITE: PS00238; OPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
DR PROSITE: PS00238; OPSIN; 1.
SQ SEQUENCE 521 AA; 57231 MW; 50FD1CBB05669DA9 CRC64;

Query Match 53.7%; Score 66; DB 11; Length 521;
Best Local Similarity 64.7%; Pred. No. 0.18;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 FGFIPLMFIFCYTFI 22
DB 241 FVFPLPLLIIFCYIFI 257

RESULT 5
Q93239 PRELIMINARY: PRT: 342 AA.
ID Q93239;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE CXCR CHEMOKINE RECEPTOR-2.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RA Fujiki K., Nakao M., Shin D., Yano T.;
RT "cDNA cloning of a carp homologue-2 of mammalian interleukin-8
receptors.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB010713; BAA31470.1; -
DR INTERPRO: IPR000276; -
DR PFAM: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODOPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
SQ SEQUENCE 342 AA; 38481 MW; 8946E5ED5E34B39 CRC64;

Query Match 53.3%; Score 65.5; DB 13; Length 342;
Best Local Similarity 54.2%; Pred. No. 0.15;
Matches 13; Conservative 3; Mismatches 5; Indels 3; Gaps 1;

QY 1 GLELL---FGFIPLMFIFCYTF 21
DB 191 GLRIHLHTLGFPLVAVMFCYGF 214

RESULT 6
Q9TU48

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ID Q9TU48 PRELIMINARY; PRT; 174 AA.
AC Q9TU48;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE INTERLEUKIN 8 RECEPTOR-LIKE PROTEIN (FRAGMENT).
GN IL8R.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Grosse W.M., Kappes S.M., Laegreid W.W., Keele J.W.,
RA Chitko-McKown C.G., Heaton M.P.;
RT "Single Nucleotide Polymorphism (SNP) Discovery and Linkage Mapping of
RT Bovine Cytokine Genes.";
RL Mamm. Genome 10:1062-1069(1999).
DR EMBL; AF140650; AAF07867.1; -
DR INTERPRO; IPR000174; -
DR INTERPRO; IPR000276; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00427; INTRLEUKIN8R.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 174 174
SQ SEQUENCE 174 AA; 20107 MW; D20E223B08FE8B36 CRC64;

Query Match 52.8%; Score 65; DB 6; Length 174;
Best Local Similarity 62.5%; Pred. No. 0.1;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 6 FGFFIPLMFIMFYTF 21
Db 66 FGFLPLLLVLMFCYGF 81

Query Match 52.8%; Score 65; DB 6; Length 174;
Best Local Similarity 62.5%; Pred. No. 0.1;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 6 FGFFIPLMFIMFYTF 21
Db 66 FGFLPLLLVLMFCYGF 81
```

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SQ SEQUENCE 174 AA; 20116 MW; D21C877CEC5BAFC6 CRC64;

Query Match 52.8%; Score 65; DB 6; Length 174;
Best Local Similarity 62.5%; Pred. No. 0.1;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 6 FGFFIPLMFIMFYTF 21
Db 66 FGFLPLLLVLMFCYGF 81

RESULT 8
Q9JJ71 PRELIMINARY; PRT; 339 AA.
AC Q9JJ71;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE CYSLT1.
GN MCYSLT1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CELL;
RA Ogasawara H., Izumi T., Shimizu T.;
RT "mouse CysLT1.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB044087; BAA96809.1; -
SQ SEQUENCE 339 AA; 39160 MW; 27BF72C0F3F0F00F CRC64;

Query Match 52.8%; Score 65; DB 11; Length 339;
Best Local Similarity 50.0%; Pred. No. 0.17;
Matches 11; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 2 LELFGFFIPLMFIMFYTFIV-23
Db 194 VSLFFGIIPFVTIIVCYTMII 215

RESULT 9
Q9TV16 PRELIMINARY; PRT; 342 AA.
AC Q9TV16;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE G PROTEIN-COUPLED RECEPTOR STRL33.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=STRL33(BONZO);
RA Brussel A., Pretet J.L., Girard M., Butor C.;
RT "Sequences and Predicted Structures of Chimpanzee STRL33 (Bonzo) and
RT gpr15 (Bos).";
RL AIDS Res. Hum. Retroviruses 15:0-0(1999).
DR EMBL; AF084229; AAD52041.1; -
DR INTERPRO; IPR000248; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR000355; -
DR INTERPRO; IPR001277; -
DR INTERPRO; IPR002235; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00241; ANGIOTENSINR.
DR PRINTS; PR00645; LCR1ORPHANR.
```

DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01105; BONZOORPHANR.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 342 AA; 39273 MW; 5B58003797806B2A CRC64;

Query Match 52.8%; Score 65; DB 6; Length 342;
Best Local Similarity 47.6%; Pred. No. 0.18;
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

OY 3 ELLFGFFIPLMFIFCYTFIV 23
:: |||:: || ||: |:
Db 195 QMTLGFLLPLLMIVCYSVII 215

RESULT 10
Q9XT45 PRELIMINARY; PRT; 343 AA.
AC Q9XT45;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE CHEMOKINE RECEPTOR BONZO.
GN STRL33.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Marquies B.J., Hauer D.A., Clements J.E.;
RT "Identification of Thirteen Rhesus Macaque Chemokine Receptors.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF124380; AAD31419.1;
DR INTERPRO; IPR000248;
DR INTERPRO; IPR000276;
DR INTERPRO; IPR000355;
DR INTERPRO; IPR001277;
DR INTERPRO; IPR002235;
DR PFAM; PF00001; 7tm_1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00241; ANGIOTENSINR.
DR PRINTS; PR00645; LCRIORPHANR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01105; BONZOORPHANR.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 343 AA; 39423 MW; 48DB2544949EB83F CRC64;

Query Match 52.8%; Score 65; DB 6; Length 343;
Best Local Similarity 47.6%; Pred. No. 0.18;
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

OY 3 ELLFGFFIPLMFIFCYTFIV 23
:: |||:: || ||: |:
Db 196 QMTLGFLLPLLMIVCYSVII 216

RESULT 11
Q9N020 PRELIMINARY; PRT; 343 AA.
AC Q9N020;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE STRL33.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecus.

OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20261727; PubMed=10799581;
RA Pohlmann S., Lee B., Meister S., Krumbiegel M., Leslie G., Doms R.W.,
RA Kirchhoff F.;
RT "Simian immunodeficiency virus utilizes human and sooty mangabey but
not rhesus macaque STRL33 for efficient entry.";
RL J. Virol. 74:5075-5082(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Pohlmann S., Lee B., Meister S., Krumbiegel M., Leslie G., Doms R.W.,
RA Kirchhoff F.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF237559; AAF68392.1;
SQ SEQUENCE 343 AA; 39588 MW; A75B7A0751C13455 CRC64;

Query Match 52.8%; Score 65; DB 6; Length 343;
Best Local Similarity 47.6%; Pred. No. 0.18;
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

OY 3 ELLFGFFIPLMFIFCYTFIV 23
:: |||:: || ||: |:
Db 196 QMTLGFLLPLLMIVCYSVII 216

RESULT 12
Q9JK47 PRELIMINARY; PRT; 352 AA.
AC Q9JK47;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE LEUKOTRIENE D4 RECEPTOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RA Mollerup J., Jorgensen S., Hougaard C., Hoffmann E.K.;
RT "Cloning and functional expression of a murine leukotriene D4
receptor.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF263370; AAF73047.1;
KW Receptor.
SQ SEQUENCE 352 AA; 40667 MW; F25A465107B4282D CRC64;

Query Match 52.8%; Score 65; DB 11; Length 352;
Best Local Similarity 50.0%; Pred. No. 0.18;
Matches 11; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 2 LELLFGFFIPLMFIFCYTFIV 23
: | ||| |:: | ||| |:
Db 207 VSLFGFIIPFTIIVCYTMI 228

RESULT 13
Q9UQ06 PRELIMINARY; PRT; 369 AA.
AC Q9UQ06;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CHEMOKINE RECEPTOR CCR9 (CC CHEMOKINE RECEPTOR 9A).
GN CCR9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

```
RN
RP SEQUENCE FROM N.A.
RA Zaballos A., Gutierrez J., Varona R., Ardavin C., Marquez G.;
RT "Identification of the orphan chemokine receptor GPR-9-6 as CCR9, the
RT receptor for the chemokine TECK."
RL J. Immunol. 162:5671-5675(1999).
RN
RP SEQUENCE FROM N.A.
RA Yu C.-R., Peden K.W.C., Farber J.M.;
RT "CCR9A and CCR9B, Two Receptors for the Chemokine CCL25 (TECK/Ckbeta-
RT 15).";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ132337; CAB43477.1; -
DR EMBL; AF145439; AAF66699.1; -
DR INTERPRO; IPR000248; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR000355; -
DR INTERPRO; IPR001277; -
DR INTERPRO; IPR001718; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PRINTS; PR00241; ANGIOTENSINR.
DR PRINTS; PR00641; CHEMOKINER7.
DR PRINTS; PR00645; LCRIORPHANR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW RECEPTOR.
SQ SEQUENCE 369 AA; 42015 MW; F27CEAOCFB66B44C CRC64;

Query Match 52.8%; Score 65; DB 4; Length 369;
Best Local Similarity 45.5%; Pred. No. 0.19;
Matches 10; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 2 LELFGFFPLPMFMFCYTFIV 23
|:::|:::|:::|:::|:::|
Db 217 LKVLGFFLPFVVMACCYTHII 238

RESULT 14
QY Q9UHM6 PRELIMINARY; PRT; 478 AA.
ID Q9UHM6;
AC Q9UHM6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE MELANOPSIN.
DE MOP.
GN MOP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN
RP SEQUENCE FROM N.A.
RA Medline-20098934; PubMed-10632589;
RX Provencio I., Rodriguez I.R., Jiang G., Hayes W.P., Moreira E.F.,
RA Rollag M.D.;
RT "A novel human opsin in the inner retina.";
RL J. Neurosci. 20:600-605(2000).
DR EMBL; AF147788; AAF24978.1; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR001760; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PRINTS; PR00238; OPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
DR PROSITE; PS00238; OPSIN; 1.
SQ SEQUENCE 478 AA; 52635 MW; A8022F5B5AA1198F CRC64;

Query Match 51.2%; Score 63; DB 4; Length 478;
Best Local Similarity 58.8%; Pred. No. 0.43;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 6 FGFFPLPMFMFCYTFI 22
|:::|:::|:::|:::|:::|
Db 242 FVFPLLIILIIYCYIFI 258

RESULT 15
QY Q88410 PRELIMINARY; PRT; 367 AA.
ID Q88410;
AC Q88410;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE CHEMOKINE RECEPTOR CXCR3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=98318636; PubMed=9653165;
RA Soto H., Wang W., Strieter R.M., Copeland N.G., Gilbert D.J.,
RA Jenkins N.A., Hedrick J., Zlotnik A.;
RT "The CC chemokine 6ckine binds the CXCR3 chemokine receptor CXCR3.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:8205-8210(1998).
DR EMBL; AF045146; AAC40163.1; -
DR INTERPRO; IPR000276; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
SQ SEQUENCE 367 AA; 41016 MW; 029FBB778E3CD4EA CRC64;

Query Match 50.4%; Score 62; DB 11; Length 367;
Best Local Similarity 45.5%; Pred. No. 0.47;
Matches 10; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 2 LELFGFFPLPMFMFCYTFIV 23
|:::|:::|:::|:::|:::|
Db 217-LQLVAGFLLPLVWVAYAHIL 238

Search completed: May 23, 2001, 15:35:16
Job time: 622 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:28:31 ; Search time 184.73 seconds
(without alignments)
4.951 Million cell updates/sec

Title: US-08-887-977-10_COPY_230_245
Perfect score: 78
Sequence: 1 KTLVQAQSKRHKRAIR 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_0401.*
1: /SID56/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID56/gcgdata/geneseq/geneseq/AA1981.DAT.*
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22: /SID56/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	100.0	365	19 W48086	Human dendritic ce
2	78	100.0	365	21 Y97077	Primate (human) ch
3	49	62.8	357	21 B19605	Human CC chemokine
4	49	62.8	357	21 Y90615	Human G protein-co
5	48	61.5	358	15 R33745	Partial sequence o
6	48	61.5	358	21 B21689	Human 7TM receptor
7	48	61.5	359	15 R53747	Seven transmembran
8	48	61.5	359	19 W48728	Murine V31 seven t
9	48	61.5	359	21 B21691	Murine 7TM recepto
10	48	61.5	361	20 W97348	An Epstein-barr vi
11	48	61.5	378	15 R34079	Epstein Barr virus

12	48	61.5	378	15 R53744	Putative seven tra
13	48	61.5	378	19 W48724	Human V31 seven tr
14	48	61.5	378	19 W56164	G-protein coupled
15	48	61.5	378	19 W36222	Epstein Barr virus
16	48	61.5	378	21 B21688	Human 7TM receptor
17	48	61.5	378	21 B21699	7TM receptor prote
18	48	61.5	378	21 Y90629	Human G protein-co
19	48	61.5	378	22 B50859	Human CCR7. Homo
20	48	61.5	410	15 R53743	Putative seven tra
21	48	61.5	410	19 W48723	Polypeptide sequen
22	48	61.5	410	21 B21687	Genomic clone of 7
23	45	57.7	302	19 W70001	Rodent chemokine r
24	45	57.7	351	20 Y23825	A7 times membrane
25	45	57.7	357	21 Y90649	Human mutant G pro
26	44.5	57.1	332	18 W26766	Human chemokine re
27	44.5	57.1	352	18 W27407	Human CCR5. Homo
28	44.5	57.1	352	18 W27123	Human chemokine re
29	44.5	57.1	352	18 W27125	Macaque chemokine
30	44.5	57.1	352	18 W07602	Human G-protein ch
31	44.5	57.1	352	19 W23835	Human CC chemokine
32	44.5	57.1	352	20 W88232	HIV-1 co-receptor
33	44.5	57.1	352	21 Y80128	Human G-protein ch
34	44.5	57.1	360	16 R79166	Human monocyte che
35	44.5	57.1	360	18 W35833	Human monocyte che
36	44.5	57.1	371	19 W23834	Human CC chemokine
37	44.5	57.1	374	16 R79165	Human monocyte che
38	44.5	57.1	439	20 Y41280	Fusion protein con
39	43	55.1	355	17 W03376	CC-chemokine recep
40	43	55.1	355	17 W03377	CC-chemokine recep
41	43	55.1	355	17 W03378	CC-chemokine recep
42	43	55.1	355	18 W31850	Human eosinophil e
43	43	55.1	355	18 W27124	Human chemokine re
44	43	55.1	355	18 W10100	Human C-C chemokin
45	43	55.1	355	19 W51744	Human C-C chemokin

ALIGNMENTS

RESULT 1	
W48086	
ID W48086 standard; Protein: 365 AA.	
AC W48086;	
XX	
DT 11-JUN-1998 (first entry)	
XX	Human dendritic cell chemokine receptor.
DE	Human; thymus expressed chemokine: TECK; MIP-3alpha; MIP-3beta;
KW	receptor; dendritic cell; macrophage; inflammation; asthma.
XX	
OS Homo sapiens.	
XX	
PH Key Location/Qualifiers	
FT Misc-difference 193	/note= "encoded by CAN"
FT	
XX	
PN W09801557-A2.	
XX	
PD 15-JAN-1998.	
XX	
PF 02-JUL-1997; 97WO-US10819.	
PR	
PR 04-JUN-1997; 97US-0048593.	
PR 05-JUL-1996; 96US-0675814.	
PR 11-OCT-1996; 96US-0028329.	
XX	(SCHE) SCHERING CORP.
PA	
XX	
XX	Gish KC, Schall TJ, Vicari A, Wang W, Zlotnik A;
XX	WPI; 1998-101054/09.
DR	

DR N-PSDB; V15418.
 XX Novel chemokines, e.g. thymus expressed chemokine - used for
 PT treating inflammatory conditions including asthma.
 XX
 PS Claim 3; Page 94-95; 202pp; English.
 XX
 CC The present sequence represents human dendritic cell chemokine receptor.
 CC Antibodies which bind to the protein can be used in detecting or
 CC diagnosing various immunological conditions related to expression
 CC of the protein. The nucleic acid can be used for screening and
 CC isolating DNA clones for the chemokines, especially from other
 CC species. The chemokine can be used in the treatment of conditions
 CC associated with abnormal physiology or development, including
 CC inflammatory conditions such as asthma.
 XX
 SQ Sequence 365 AA;

Query Match 100.0%; Score 78; DB 19; Length 365;
 Best Local Similarity 100.0%; Pred. No. 6.3e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KTLVQNSKRHKAIR 16
 |||||
 DB 230 ktlvqnskrhkair 245

RESULT 2
 Y97077
 ID Y97077 standard; Protein; 365 AA.
 XX
 AC Y97077;
 XX
 DT 04-DEC-2000 (first entry)
 DE
 XX
 DE Primate (human) chemokine receptor CCR6.
 XX
 KW MIP-3-alpha; chemokine; CCR6 receptor; ligand; cytostatic; agonist;
 KW antagonist; anti-psoriatic; dermatological; immunosuppressive;
 KW anti-inflammatory.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 193
 FT /note= "Encoded by CAN#"
 XX
 PN WO200046248-A1.
 XX
 PD 10-AUG-2000.
 XX
 PF 02-FEB-2000; 2000WO-US00511.
 XX
 PR 03-FEB-1999; 99US-0244281.
 XX
 PA (SCHE) SCHERING CORP.
 XX
 PI Oldham ER, Honey B, Dieu-Nosjean M, Caux C, Zlotnik A;
 XX
 DR WPI; 2000-543477/49.
 DR N-PSDB; A51971.
 XX
 PT Novel methods for modulating the migration of cells within or to the
 PT skin using MIP-3-alpha or CCR6 agonists or antagonists, useful for
 PT treating skin disorders, e.g. cancer
 XX
 PS Disclosure; Page 53-54; 61pp; English.
 XX
 CC The MIP-3-alpha chemokine is expressed in inflamed skin cells. This
 CC chemokine is the ligand for the CCR6 receptor. MIP-3-alpha or CCR6
 CC agonists or antagonists can be used to modulate the migration of a cell
 CC within or to the skin of a mammal. MIP-3-alpha can be used to purify a

CC population of cells expressing a MIP-3-alpha receptor. The methods are
 CC useful for treating a mammalian subject with a skin disease or condition,
 CC e.g. cancer, metastasis, psoriasis, atopic or contact dermatitis,
 CC systemic lupus erythematosus and lichen ruber planus, or for treating
 CC skin transplants or grafts.
 XX
 SQ Sequence 365 AA;

Query Match 100.0%; Score 78; DB 21; Length 365;
 Best Local Similarity 100.0%; Pred. No. 6.3e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KTLVQNSKRHKAIR 16
 |||||
 DB 230 ktlvqnskrhkair 245

RESULT 3
 B19605
 ID B19605 standard; Protein; 357 AA.
 XX
 AC B19605;
 XX
 DT 22-JAN-2001 (first entry)
 XX
 DE Human CC chemokine receptor GPR-9-6.
 XX
 KW GPR-9-6; human; chemokine receptor; TECK; cancer; leukaemia;
 KW lymphoma; carcinoma; inflammation; Crohn's disease; colitis;
 KW therapy; diagnosis.
 XX
 OS Homo sapiens.
 XX
 PN WO200053635-A1.
 XX
 PD 14-SEP-2000.
 XX
 PF 10-MAR-2000; 2000WO-US06240.
 XX
 PR 11-MAR-1999; 99US-0266464.
 XX
 PA (LEUK-) LEUKOSITE INC.
 XX
 PI Andrew DP, Zabel BA, Ponath PD;
 XX
 DR WPI; 2000-572263/53.
 XX
 PT Antibody or its antigen-binding fragment which binds to the mammalian
 PT CC chemokine receptor GPR-9-6, useful for treating inflammatory
 PT diseases, cancer or inhibiting GPR-9-6-mediated homing of leukocytes to
 PT mucosal tissue -
 XX
 PS Disclosure; Fig 14A-B; 114pp; English.
 XX
 CC The present sequence is that of human GPR-9-6, a CC chemokine
 CC receptor that is expressed on the majority of thymocytes and also
 CC on a subset of memory CD4 lymphocytes that traffic to mucosal
 CC sites, suggesting a dual role in T cell development and mucosal
 CC immune response. The invention relates to an antibody that binds
 CC to GPR-9-6 and blocks the binding of a ligand, such as TECK (see
 CC B19607), to the receptor. Also provided is a method of identifying
 CC agents which can bind to GPR-9-6 and inhibit the binding of a
 CC ligand and/or modulate a function of GPR-9-6. The antibodies can
 CC be used to detect or measure expression of GPR-9-6 receptor. They
 CC are useful for treating an inflammatory disease, cancer and
 CC inhibiting GPR-9-6-mediated homing of leukocytes to mucosal tissue.
 CC The cancer treated is acute or chronic leukaemia (e.g., acute T-cell
 CC lymphoblastic leukaemia, acute B-cell lymphoblastic leukaemia,
 CC chronic T-cell lymphoblastic leukaemia, chronic B-cell lymphoblastic
 CC leukaemia), lymphoma (e.g., Hodgkin's disease, T cell lymphoma) or
 CC carcinoma (e.g. breast, melanoma, myeloma, or adenoma). The
 CC inflammatory diseases treated are Crohn's disease, colitis

CC (claimed), inflammatory bowel disease, mastitis, vaginitis,
 CC cholangitis or pericholangitis, chronic bronchitis, asthma, graft
 CC versus host disease, hypersensitivity pneumonitis, collagen
 CC diseases, sarcoidosis, and other idiopathic conditions. Other
 CC diseases that can be treated by the antibodies are autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis), infectious
 CC diseases (e.g. bacterial and viral infections), atherosclerosis,
 CC retinosis, AIDS, pancreatitis, insulin-dependent diabetes mellitus,
 CC and diseases in which angiogenesis or neovascularization play a role.
 XX
 SQ Sequence 357 AA;

Query Match 62.8%; Score 49; DB 21; Length 357;
 Best Local Similarity 53.3%; Pred. No. 0.79;
 Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 TLVQAQNSKRHKRAIR 16
 ||||| : |||||
 Db 228 tliqakskkhkalk 242

RESULT 4
 Y90615
 ID Y90615 standard; Protein: 357 AA.
 XX
 AC Y90615;
 XX

DT 21-AUG-2000 (first entry)

DE Human G protein-coupled receptor GPR9-6.

KW G protein-coupled receptor; GPCR: constitutively active;
 KW intracellular loop 3; transmembrane domain 6; drug screening;
 KW agonist; antagonist.

OS Homo sapiens.
 XX
 PN WO200022129-A1.
 XX

PD 20-APR-2000.

PF 12-OCT-1999; 99WO-US23938.

PR 13-OCT-1998; 98US-0170496.

XX (AREN-) ARENA PHARM INC.

PI Behan DP, Chalmers DT, Liaw CW;

DR WPI: 2000-329165/28.

DR N-PSDB; A30596.

XX Non-endogenous constitutively activated human G protein-coupled
 PT receptors, useful for identifying agonists for use as pharmaceutical
 PT agents
 XX

PS Example 1; Page 119-120; 341pp; English.

XX The invention relates to constitutively active, non-endogenous versions
 CC of endogenous human orphan G protein-coupled receptors (GPCRs, Y90643-
 CC Y90677 and Y90683-Y90687), and to DNA encoding them (A30709-A30743 and
 CC A30775-A30779). The mutant proteins of the invention contain a
 CC mutation in a portion of the protein comprising intracellular loop 3
 CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
 CC is substituted for an endogenous residue in IC3 at a position 16 amino
 CC acids N-terminal of an endogenous proline in TM6 to form a sequence
 CC X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or
 CC Ala, and is preferably Lys. When the endogenous residue at this position
 CC is Lys, this residue is replaced by His, Arg or preferably Ala. The 15
 CC amino acid stretch between the substituted amino acid and the Pro may be
 CC endogenous, non-endogenous, or a mixture of endogenous and non-endogenous
 CC residues. The constitutively active GPCRs are useful for identifying

CC antagonists, agonists and partial agonists for use as pharmaceutical
 CC agents. The mutant proteins are also useful in research settings for
 CC elucidating the roles of the receptors in normal and diseased conditions.
 CC Antagonists for a particular GPCR are useful for treating diseases and
 CC disorders associated with that receptor. Because the novel mutant GPCRs
 CC are constitutively active, they can be used directly for screening of
 CC compounds without the need for endogenous ligands. The present
 CC sequence represents a human wild-type GPCR referred to in an
 XX exemplification of the invention.
 SQ Sequence 357 AA;

Query Match 62.8%; Score 49; DB 21; Length 357;
 Best Local Similarity 53.3%; Pred. No. 0.79;
 Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 TLVQAQNSKRHKRAIR 16
 ||||| : |||||
 Db 228 tliqakskkhkalk 242

RESULT 5
 R53745
 ID R53745 standard; Protein: 358 AA.
 XX
 AC R53745;
 XX

DT 02-FEB-1995 (first entry)

DE Partial sequence of seven transmembrane receptor (V31).

KW Primer; seven transmembrane receptor; receptor; amplification; PCR;
 KW polymerase chain reaction.

OS Homo sapiens.
 XX
 PN WO9412635-A.
 XX

PD 09-JUN-1994.

PF 17-NOV-1993; 93WO-US11153.

PR 17-NOV-1992; 92US-0977452.

XX (ICOS-) ICOS CORP.

XX Godiska R, Gray PW, Schweickart VL;

DR WPI: 1994-200264/24.

DR N-PSDB; Q66162.

XX DNA encoding seven transmembrane receptors - used to develop
 PT prods. for use as therapeutic or diagnostic agents for conditions
 PT involving the receptors.
 XX

PS Example 3; Page 56-57; 100pp; English.

XX Two primers (Q66148, Q66149) were used to amplify human genomic DNA
 CC purified from leukocytes. Approximately 1000 clones were isolated
 CC after the initial amplification reaction and probed with sequences
 CC specific for seven transmembrane receptors IL8R1, ATR2 and R20.
 CC Clones which did not hybridise were then chosen for sequence
 CC analysis. Three new clones were identified that appeared to encode
 CC seven transmembrane receptor segments. Two more primers (Q66151,
 CC Q66152) were used to isolate a full length version of one of these
 CC clones designated V31 (See Q66153). This is the sequence encoded
 CC by exon 3 of the V31 genomic clone
 XX

SQ Sequence 358 AA;

Query Match 61.5%; Score 48; DB 15; Length 358;

```

Best Local Similarity 56.2%; Pred. No. 1.2;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHKAIR 16
Db 228 rtlqarnfernkalk 243

RESULT 6
ID B21689 standard; Protein; 358 AA.
XX AC B21689;
XX DT 26-JAN-2001 (first entry)
XX DE Human 7TM receptor V31-B cDNA clone exon 1 protein.
XX KW Seven transmembrane receptor; 7TM; heptahelical; serpentine;
KW G-protein-coupled; V28; V31; V112; R20; R2; RM3; gene therapy;
KW cancer.
XX OS Homo sapiens.
XX PN US6107475-A.
XX PD 22-AUG-2000.
XX PF 26-APR-1999; 99US-0299843.
XX PR 17-MAY-1994; 94US-0245242.
XX PR 01-JUN-1998; 98US-0088337.
XX PR 17-NOV-1992; 92US-0977452.
XX PR 17-NOV-1993; 93US-0153848.
XX PA (ICOS-) ICOS CORP.
XX PI Schweickart VL, Gray PW, Godiska R;
XX WPI: 2000-571335/53.
XX DR N-PSDB; A91709.
XX PT Polynucleotide encoding seven transmembrane receptors, antibody
XX specific to the receptor, agonist and antagonist of the receptor useful
XX for treating inflammation in a mammal.
XX PS Example 3; Columns 49-52; 61pp; English.
XX CC The present sequence is a novel seven transmembrane (7TM) receptors
XX (also known as heptahelical, serpentine or G-protein-coupled receptors).
XX CC The coding sequence for the present sequence may be used for gene
XX therapy for diseases such as cancer.
XX SQ Sequence 358 AA;

Query Match 61.5%; Score 48; DB 21; Length 358;
Best Local Similarity 56.2%; Pred. No. 1.2;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHKAIR 16
Db 228 rtlqarnfernkalk 243

RESULT 7
ID R53747 standard; Protein; 359 AA.
XX AC R53747;
XX DT 03-FEB-1995 (first entry)
XX PR 17-NOV-1992; 92US-0977452.

```

```

DE Seven transmembrane receptor (V31) partial sequence of mouse.
XX KW Primer: seven transmembrane receptor; receptor; amplification; PCR;
XX KW polymerase chain reaction.
XX OS Mus musculus.
XX PN W09412635-A.
XX PD 09-JUN-1994.
XX PF 17-NOV-1993; 93WO-US11153.
XX PR 17-NOV-1992; 92US-0977452.
XX PA (ICOS-) ICOS CORP.
XX PI Godiska R, Gray PW, Schweickart VL;
XX WPI: 1994-200264/24.
XX DR N-PSDB; Q66164.
XX PT DNA encoding seven transmembrane receptors - used to develop
XX prods. for use as therapeutic or diagnostic agents for conditions
XX involving the receptors.
XX PS Example 5; Page 61-62; 100pp; English.
XX CC Two primers (Q66148, Q66149) were used to amplify human genomic DNA
XX purified from leukocytes. Approximately 1000 clones were isolated
XX after the initial amplification reaction and probed with sequences
XX specific for seven transmembrane receptors IL8R1, AT2R and R20.
XX CC Clones which did not hybridise were then chosen for sequence
XX analysis. Three new clones were identified that appeared to encode
XX seven transmembrane receptor segments. Two more primers (Q66151,
XX Q66152) were used to isolate a full length version of one of the
XX human V31 clone (See Q66153). A fragment of the human clone was used
XX to isolate a V31 genomic clone of the mouse from a library.
XX SQ Sequence 359 AA;

Query Match 61.5%; Score 48; DB 15; Length 359;
Best Local Similarity 56.2%; Pred. No. 1.2;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHKAIR 16
Db 228 rtlqarnfernkalk 243

RESULT 8
ID W48728 standard; Protein; 359 AA.
XX AC W48728;
XX DT 25-SEP-1998 (first entry)
XX DE Murine V31 seven transmembrane (7TM) receptor.
XX KW V28; placenta; seven transmembrane receptor; 7TM; signal transduction;
XX KW immunology; inflammation; V31; ss.
XX OS Mus sp.
XX PN US5759804-A.
XX PD 02-JUN-1998.
XX PF 17-NOV-1993; 93US-0153848.
XX PR 17-NOV-1992; 92US-0977452.

```

XX PA (ICOS-) ICOS CORP.
 XX PI Godiska R, Gray PW, Schweickart VL;
 XX PI WPI; 1998-332132/29.
 DR N-PSDB; V18351.
 XX DNA encoding V28 seven transmembrane receptor polypeptide - useful
 PT for producing recombinant polypeptide and anti-V28 antibodies, and
 PT in screening assays for V28 agonists and antagonists
 XX PS Example 5; Columns 55-58; 56pp; English.
 XX The present sequence represents the murine V31 seven transmembrane
 CC (7TM) receptor which is encoded by the murine V31 genomic DNA (V18351)
 CC isolated from a mouse genomic library. The invention claims for the
 CC full length V28 genomic DNA sequence isolated from a human placenta
 CC genomic library. V28 (W48722) and V31 proteins are seven transmembrane
 CC (7TM) receptors which are probably involved in signal transduction.
 CC The invention also claims that cells transformed with V28 DNA can be
 CC used to produce the recombinant polypeptide, to produce anti-V28
 CC antibodies or in screening assays for V28 agonists or antagonists. The
 CC antibodies, agonists and antagonists could then be used to modulate
 CC V28 receptor-ligand binding, for e.g. in immunological and/or
 CC inflammatory events in vivo.
 XX SQ Sequence 359 AA;

Query Match 61.5%; Score 48; DB 19; Length 359;
 Best Local Similarity 56.2%; Pred. No. 1.2;
 Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTLVQAQNSKRHKRAIR 16
 :||:|:|:|:|:|:|:
 Db 228 rtlqarfernkalk 243

RESULT -- 9

B21691 ID B21691 standard; Protein; 359 AA.
 XX AC B21691;
 XX DT 26-JAN-2001 (first entry)
 XX DE Murine 7TM receptor V31cDNA clone protein.
 XX KW Seven transmembrane receptor; 7TM; heptahelical; serpentine;
 KW G-protein-coupled; V28; V31; V112; R20; R2; R12; RM3; gene therapy;
 KW Cancer.
 XX OS Mus sp.
 XX PN US6107475-A.
 XX PD 22-AUG-2000.
 XX PF 26-APR-1999; 99US-0299843.
 XX PR 17-MAY-1994; 94US-0245242.
 PR 01-JUN-1998; 98US-0088337.
 PR 17-NOV-1992; 92US-0977452.
 PR 17-NOV-1993; 93US-0153848.
 XX PA (ICOS-) ICOS CORP.
 XX PI Schweickart VL, Gray PW, Godiska R;
 XX WPI; 2000-571335/53.
 DR N-PSDB; A91711.
 XX

PT Polynucleotide encoding seven transmembrane receptors, antibody
 PT specific to the receptor, agonist and antagonist of the receptor useful
 PT for treating inflammation in a mammal
 XX Example 4; Columns 57-60; 61pp; English.
 XX The present sequence is a novel seven transmembrane (7TM) receptors
 CC (also known as heptahelical, serpentine or G-protein-coupled receptors).
 CC The coding sequence for the present sequence may be used for gene
 CC therapy for diseases such as cancer.
 XX SQ Sequence 359 AA;

Query Match 61.5%; Score 48; DB 21; Length 359;
 Best Local Similarity 56.2%; Pred. No. 1.2;
 Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
 OY 1 KTLVQAQNSKRHKRAIR 16
 :||:|:|:|:|:|:
 Db 228 rtlqarfernkalk 243

RESULT 10
 W97348 ID W97348 standard; Protein; 361 AA.
 XX AC W97348;
 XX DT 12-MAY-1999 (first entry)
 XX DE An Epstein-barr virus-induced G-protein coupled receptor.
 XX KW Epstein-barr virus-induced G-protein coupled receptor; EBI 3;
 KW splicing variant; EBI 1; vaccine; infection; HIV-1; HIV-2; pain;
 KW cancer; anorexia; bulimia; asthma; Parkinson's disease;
 KW acute heart failure; hypotension; hypertension; urinary retention;
 KW osteoporosis; angina pectoris; myocardial infarction; ulcer; allergy;
 KW benign prostatic hypertrophy; psychotic disorder; neurological disorder;
 KW anxiety; schizophrenia; manic-depression; delirium; dementia;
 KW severe mental retardation; dyskinesias; Huntington's disease;
 KW Gilles de la Tourette's syndrome.

OS Homo sapiens.
 XX EP894854-A2.
 XX PD 03-FEB-1999.
 XX PF 04-DEC-1997; 97EP-0309791.
 XX PR 29-JUL-1997; 97US-0902294.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 XX PA Zhu Y;
 XX PI
 XX WPI; 1999-108346/10.
 DR N-PSDB; X15857.
 XX PT New Epstein-barr virus-induced G-protein coupled receptor (EBI 3)
 PT gene and protein - useful as diagnostic reagents and for prevention
 PT and treatment of HIV infections and cancer
 XX Claim 2; Page 7; 20pp; English.

XX The present sequence represents a Epstein-barr virus-induced G-protein
 CC coupled receptor (EBI 3), which is a splicing variant of EBI 1. EBI 3
 CC antibodies are useful for inducing an immune response to immunize and
 CC prevent disease, and for isolating EBI 3 clones or purifying the
 CC polypeptides by affinity chromatography. EBI 3 polypeptides can be
 CC administered directly or as a vaccine to inoculate against disease.
 CC Diseases diagnosed, prevented and treated include: bacterial, fungal,

CC viral and protozoan infections, particularly infections caused by HIV1-
 CC or HIV-2; pain; cancers; anorexia; bulimia; asthma; Parkinson's disease;
 CC acute heart failure; hypotension; hypertension; urinary retention;
 CC osteoporosis; angina pectoris; myocardial infarction; ulcers; allergies;
 CC benign prostatic hypertrophy; and psychotic and neurological disorders,
 CC including anxiety, schizophrenia, manic depression, delirium, dementia,
 CC severe mental retardation and dyskinesias, such as Huntington's disease
 CC or Gilles de la Tourette's syndrome.
 XX
 SQ Sequence 361 AA;

Query Match 61.5%; Score 48; DB 20; Length 361;
 Best Local Similarity 56.2%; Pred. No. 1.2;
 Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTLVQAQNSKRHKAIR 16
 Db 231 rtlqarnfernkalk 246

RESULT 11
 R54079
 ID R54079 standard; Protein: 378 AA.
 XX
 AC R54079;

DT 03-FEB-1995 (first entry)

DE Epstein Barr virus induced (EBI-1) polypeptide.

XX Epstein Barr virus; EBV; induction; detection; diagnosis;
 KW Lymphocytes; antigen; growth; differentiation; mediator;
 KW infectious mononucleosis.
 XX

OS Homo sapiens.

Key Location/Qualifiers
 FT Region 1..24
 FT /label= Hydrophobic region.
 FT /note= "Predicted to be a signal peptide for
 FT membrane translocation."
 FT Modified-site 36
 FT /note= "Potential N-linked glycosylation site."
 FT Region 60..86
 FT /label= Hydrophobic region.
 FT Region 96..116
 FT /label= Hydrophobic region.
 FT Region 131..152
 FT /label= Hydrophobic region.
 FT Region 151..159
 FT /note= "This sequences motif
 FT (S-[I/V]-D-R-[Y/F]-X-X-X) is highly
 FT conserved among a large number of G-protein
 FT coupled receptors."
 FT Region 171..191
 FT /label= Hydrophobic region.
 FT Region 220..247
 FT /label= Hydrophobic region.
 FT Region 264..289
 FT /label= Hydrophobic region.
 FT Modified-site 292
 FT /note= "Potential N-linked glycosylation site."
 FT Region 314..331
 FT /label= Hydrophobic region.

XX WO9412519-A.

XX PD 09-JUN-1994.

XX PF 08-OCT-1993; 93WO-US09636.

XX PR 25-NOV-1992; 92US-0980518.

XX (BGHM) BRIGHAM & WOMENS HOSPITAL.
 PA Birkenbach M, Kieff E;

XX WPI; 1994-200183/24.

XX DR N-PSDB; Q64125.
 XX

PT DNA coding for Epstein Barr Virus induced (EBI) polypeptide(s)
 and antibodies to EBI1, 2 and 3 - useful for detecting EBV by
 PT hybridisation or by immunoassay
 XX

PS Claim 8; Page 54-56; 84pp; English.

XX EBV infected B lymphocytes recapitulate features of antigen
 stimulation in enlarging, increasing RNA synthesis, expressing
 CC activation antigens and adhesion molecules, secreting Ig and
 CC proliferating. Unlike antigen stimulated B lymphocytes, EBV
 CC infected B lymphocytes continue to proliferate (in vitro) as
 CC immortalised lymphoblastoid cell lines. Because of the similar
 CC effects of EBV and antigen, EBV induced genes are likely to include
 CC mediators of antigen induced B lymphocyte growth or differentiation.
 XX

SQ Sequence 378 AA;

Query Match 61.5%; Score 48; DB 15; Length 378;

Best Local Similarity 56.2%; Pred. No. 1.3;

Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTLVQAQNSKRHKAIR 16

Db 248 rtlqarnfernkalk 263

RESULT 12

R53744

ID R53744 standard; Protein: 378 AA.

XX R53744;

XX 02-FEB-1995 (first entry)

XX Putative seven transmembrane receptor (V31).

XX Primer; seven transmembrane receptor; receptor; amplification; PCR;
 KW polymerase chain reaction.
 XX

XX Homo sapiens.

XX WO9412635-A.

XX PD 09-JUN-1994.

XX PF 17-NOV-1993; 93WO-US11153.

XX PR 17-NOV-1992; 92US-0977452.

XX (ICOS-) ICOS CORP.

XX Godiska R, Gray PW, Schweickart VL;

XX WPI; 1994-200264/24.

XX DR N-PSDB; Q66160.
 XX

PT DNA encoding seven transmembrane receptors - used to develop
 prod. for use as therapeutic or diagnostic agents for conditions
 PT involving the receptors.
 XX

PS Claim 1; Page 52-53; 100pp; English.

XX A human cDNA encoding the seven transmembrane receptor V31 was
 CC isolated by first amplifying a partial cDNA clone from a human

CC the lymphocyte receptor protein. This method can be used to screen for
CC agonists or antagonists to the lymphocyte receptor protein. The method
CC can be modified and used to screen for agonists or antagonists to the
CC immune-cell specific lymphocyte receptor polypeptide or the neuronal type
CC oploid receptor polypeptide.
XX
SQ Sequence 378 AA;

Search completed: May 23, 2001, 15:28:32
Job time: 409 sec

Query Match 61.5%; Score 48; DB 19; Length 378;
Best Local Similarity 56.2%; Pred. No. 1.3;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHKRAIR 16
:|:|:|:|:|:|:|:|:
Db 248 rtilqarnfernkalk 263

RESULT 15
W53622
ID W53622 standard; Protein; 378 AA.
XX
AC W53622;
XX
DT 09-JUL-1998 (first entry)
XX
DE Epstein Barr virus induced protein 1 (EBI-1).
XX
KW Assessing; monitoring; foetal development; placental development;
KW Epstein Barr virus; EBV; induced gene 1; EBI-1.
XX
OS Homo sapiens.
XX
PN US5744301-A.
XX
PD 28-APR-1998.
XX
PF 02-FEB-1995; 95US-0383750.
XX
PR 02-FEB-1995; 95US-0383750.
PR 25-NOV-1992; 92US-0980518.
PR 30-NOV-1994; 94US-0352678.
XX
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
XX
PI Birkenbach M, Kieff E;
XX
DR WPI; 1998-271060/24.
DR N-PSDB; V25490.

PT Assessing or monitoring foetal or placental development - comprises
PT detecting the level or size of Epstein Barr virus induced nucleic
PT acid or protein in maternal serum samples
XX

PS Example 2; Columns 37-40; 45pp; English.

XX
CC The present sequence was used in the development of a novel method
CC for assessing or monitoring foetal or placental development. The
CC method comprises taking a maternal serum sample, and detecting the
CC level or size of Epstein Barr virus (EBV) induced gene or protein 3
CC (EBI-3) to obtain a result, which can be compared to a control to
CC assess or monitor foetal or placental development.
XX
SQ Sequence 378 AA;

Query Match 61.5%; Score 48; DB 19; Length 378;
Best Local Similarity 56.2%; Pred. No. 1.3;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHKRAIR 16
:|:|:|:|:|:|:|:|:
Db 248 rtilqarnfernkalk 263

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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:30:07 ; Search time 95.91 Seconds
(without alignments)
3.205 Million cell updates/sec

Title: US-08-887-977-10_COPY_230_245

Perfect score: 78

Sequence: 1 KTLVQANSRRHRAIR 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	61.5	358	1	US-08-153-848-19
2	48	61.5	358	3	US-09-299-843A-19
3	48	61.5	358	5	PCT-US93-11153-19
4	48	61.5	359	1	US-08-153-848-24
5	48	61.5	359	3	US-09-299-843A-24
6	48	61.5	359	5	PCT-US93-11153-24
7	48	61.5	361	2	US-08-902-294-2
8	48	61.5	361	3	US-09-178-637-2
9	48	61.5	378	1	US-08-383-750-2
10	48	61.5	378	1	US-08-383-751A-2
11	48	61.5	378	1	US-08-153-848-15
12	48	61.5	378	3	US-08-352-678-2
13	48	61.5	378	3	US-09-299-843A-15
14	48	61.5	378	3	US-09-299-843A-66
15	48	61.5	378	4	US-09-251-545-1
16	48	61.5	378	5	PCT-US93-09636-2
17	48	61.5	378	5	PCT-US93-11153-15
18	48	61.5	410	1	US-08-153-848-7
19	48	61.5	410	3	US-09-299-843A-7
20	48	61.5	410	5	PCT-US93-11153-7
21	44.5	57.1	344	3	US-08-466-343D-9
22	44.5	57.1	347	1	US-08-461-244-3
23	44.5	57.1	352	3	US-08-466-343D-2
24	44.5	57.1	352	4	US-09-087-232A-13
25	44.5	57.1	360	1	US-08-450-393A-4
26	44.5	57.1	360	4	US-08-446-669-4
27	44.5	57.1	360	5	PCT-US95-00476-4

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29	44.5	57.1	374	4	US-08-446-669-2	Sequence 2, Appli
30	44.5	57.1	374	5	PCT-US95-00476-2	Sequence 2, Appli
31	42	53.8	3174	2	US-08-477-451-3	Sequence 3, Appli
32	40	51.3	354	1	US-07-759-568-2	Sequence 2, Appli
33	38	48.7	170	4	US-08-875-573-6	Sequence 6, Appli
34	38	48.7	360	4	US-08-875-573-20	Sequence 20, Appli
35	38	48.7	523	4	US-08-948-564-8	Sequence 8, Appli
36	37	47.4	355	1	US-08-012-988A-2	Sequence 2, Appli
37	37	47.4	355	1	US-08-450-393A-5	Sequence 5, Appli
38	37	47.4	355	4	US-08-446-669-5	Sequence 5, Appli
39	37	47.4	355	5	PCT-US95-00476-5	Sequence 5, Appli
40	37	47.4	879	1	US-08-220-151-2	Sequence 2, Appli
41	37	47.4	879	1	US-08-220-151-3	Sequence 3, Appli
42	37	47.4	879	1	US-08-413-118-2	Sequence 2, Appli
43	37	47.4	879	1	US-08-413-118-3	Sequence 3, Appli
44	37	47.4	879	1	US-08-413-118-106	Sequence 106, App
45	37	47.4	879	3	US-08-473-446-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-153-848-19
: Sequence 19, Application US/08153848
: Patent No. 5759804
: GENERAL INFORMATION:
: APPLICANT: Godiska, Ronald
: APPLICANT: Gray, Patrick W.
: APPLICANT: Schweikart, Vicki L.
: TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
: NUMBER OF SEQUENCES: 64
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
: ADDRESSEE: Bicknell
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION NUMBER: US/08/153,848
: FILING DATE:
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/977,452
: FILING DATE: 17-NOV-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: No. 5759804and, Greta E.
: REGISTRATION NUMBER: 35,302
: REFERENCE/DOCKET NUMBER: 31794
: TELEPHONE: (312) 474-6300
: TELEFAX: (312) 474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 358 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-153-848-19

Query Match 61.5% Score 48; DB 1; Length 358;
Best Local Similarity 56.2%; Pred. No. 0.62;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTLVQAQNSKRHKRAIR 16
:||||:|:|:|:
Db 228 RTLLQARNFERNKAIR 243

RESULT 2

US-09-299-843A-19
; Sequence 19, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,843A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/088,337
; FILING DATE: 01-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jill E. Uhl
; REGISTRATION NUMBER: 43,213
; REFERENCE/DOCKET NUMBER: 27866/32059B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX:

; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-299-843A-19

Query Match 61.5%; Score 48; DB 3; Length 358;
Best Local Similarity 56.2%; Pred. No. 0.62;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTLVQAQNSKRHKRAIR 16
:||||:|:|:|:
Db 228 RTLLQARNFERNKAIR 243

RESULT 3

PCT-US93-11153-19
; Sequence 19, Application PC/TUS9311153
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald

; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: Novel Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11153
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-11153-19

Query Match 61.5%; Score 48; DB 5; Length 358;
Best Local Similarity 56.2%; Pred. No. 0.62;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTLVQAQNSKRHKRAIR 16
:||||:|:|:|:
Db 228 RTLLQARNFERNKAIR 243

RESULT 4

US-08-153-848-24
; Sequence 24, Application US/08153848
; Patent No. 5759804
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/153.848
;; FILING DATE: 17-NOV-1992
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/977,452
;; FILING DATE: 17-NOV-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: No. 5759804and, Greta E.
;; REGISTRATION NUMBER: 35,302
;; REFERENCE/DOCKET NUMBER: 31794
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312) 474-6300
;; TELEFAX: (312) 474-0448
;; TELEX: 25-3856
;; INFORMATION FOR SEQ ID NO: 24:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 359 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-153-848-24

Query Match 61.5%; Score 48; DB 1; Length 359;
Best Local Similarity 56.2%; Pred. No. 0.62;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHKRAIR 16
Db 228 RTLLQARNFERNKAIK 243

RESULT 5

US-09-299-843A-24
; Sequence 24, Application US/09299843A
; Patent No. 6107475

;; GENERAL INFORMATION:
;; APPLICANT: Godiska, Ronald
;; APPLICANT: Gray, Patrick W.
;; APPLICANT: Schweikart, Vicki L.
;; TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
;; NUMBER OF SEQUENCES: 66
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
;; ADDRESSEE: Borun
;; STREET: 6300 Sears Tower, 233 South Wacker Drive
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60606
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/299,843A
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 09/088,337
;; FILING DATE: 01-JUN-1998
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/153,848
;; FILING DATE: 17-NOV-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/977,452
;; FILING DATE: 17-NOV-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Jill E. Uhl
;; REGISTRATION NUMBER: 43,213
;; REFERENCE/DOCKET NUMBER: 27866/32059B

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312) 474-6300
;; TELEFAX: (312) 474-0448
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 24:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 359 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-09-299-843A-24

Query Match 61.5%; Score 48; DB 3; Length 359;
Best Local Similarity 56.2%; Pred. No. 0.62;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHKRAIR 16
Db 228 RTLLQARNFERNKAIK 243

RESULT 6

PCT-US93-11153-24
; Sequence 24, Application PC/TUS9311153
; GENERAL INFORMATION:

;; APPLICANT: Godiska, Ronald
;; APPLICANT: Gray, Patrick W.
;; APPLICANT: Schweikart, Vicki L.
;; TITLE OF INVENTION: Novel Seven Transmembrane Receptors
;; NUMBER OF SEQUENCES: 64
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
;; ADDRESSEE: Bicknell
;; STREET: 6300 Sears Tower, 233 South Wacker Drive
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60606

COMPUTER-READABLE-FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US93/11153
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/977,452
;; FILING DATE: 17-NOV-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Noland, Greta E.
;; REGISTRATION NUMBER: 35,302
;; REFERENCE/DOCKET NUMBER: 31794
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312) 474-6300
;; TELEFAX: (312) 474-0448
;; TELEX: 25-3856
;; INFORMATION FOR SEQ ID NO: 24:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 359 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; PCT-US93-11153-24

Query Match 61.5%; Score 48; DB 5; Length 359;
Best Local Similarity 56.2%; Pred. No. 0.62;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHKRAIR 16

Db 228 RTLLQARNFERKAIK 243
:||:||||:|:|:||||:

RESULT 7

US-08-902-294-2
; Sequence 2, Application US/08902294
; Patent No. 5874252
; GENERAL INFORMATION:
; APPLICANT: ZHU, YUAN
; TITLE OF INVENTION: A NOVEL SPLICING VARIANT OF
; TITLE OF INVENTION: THE EPSTEIN-BARR VIRUS-INDUCED G-PROTEIN COUPLED
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,294
; FILING DATE: 29-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-70177
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-902-294-2

Query Match 61.5%; Score 48; DB 2; Length 361;
Best Local Similarity 56.2%; Pred. No. 0.62;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHKAIK 16
:||:||||:|:|:||||:

Db 231 RTLLQARNFERKAIK 246

RESULT 8

US-09-178-637-2
; Sequence 2, Application US/09178637
; Patent No. 6001972
; GENERAL INFORMATION:
; APPLICANT: ZHU, YUAN
; TITLE OF INVENTION: A No. 6001972el Splicing Variant of
; TITLE OF INVENTION: the Epstein-Barr Virus-Induced G-Protein Coupled Receptor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/383,750
; FILING DATE: Herewith
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Fox, Samuel, L.
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 0627.3300001
; TELECOMMUNICATION INFORMATION:

STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/178,637
FILING DATE: 26-OCT-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/902,294
FILING DATE: 29-JUL-1998
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-70177-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-178-637-2

Query Match 61.5%; Score 48; DB 3; Length 361;
Best Local Similarity 56.2%; Pred. No. 0.62;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHKAIK 16
:||:||||:|:|:||||:

Db 231 RTLLQARNFERKAIK 246

RESULT 9

US-08-383-750-2
; Sequence 2, Application US/08383750
; Patent No. 5744301
; GENERAL INFORMATION:
; APPLICANT: Birkenbach, Mark
; TITLE OF INVENTION: Epstein Barr Virus Induced Genes
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W.,
; STREET: Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/383,750
; FILING DATE: Herewith
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Fox, Samuel, L.
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 0627.3300001
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-383-750-2

Query Match 61.5%; Score 48; DB 1; Length 378;
Best Local Similarity 56.2%; Pred. No. 0.65;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTLVQAQNSKRHKRAIR 16
:||:|:|:|:|:|:|:
Db 248 RTLLQARNFERNKAIR 263

RESULT 10
US-08-383-751A-2
Sequence 2, Application US/08383751A
Patent No. 5753516

GENERAL INFORMATION:
APPLICANT: Heagy, Wyrta E.
APPLICANT: Finberg, Robert W.
TITLE OF INVENTION: Identification and Uses of Opioid
TITLE OF INVENTION: Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: US
ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/383,751A
FILING DATE: 03-FEB-1995

ATTORNEY/AGENT INFORMATION:

NAME: Wilson, Mark B.

REGISTRATION NUMBER: 37,259

REFERENCE/DOCKET NUMBER: DFCI:001/WIM

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEFAX: (512) 474-7577

TELEX: 79-0924

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 378 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-383-751A-2

Query Match 61.5%; Score 48; DB 1; Length 378;
Best Local Similarity 56.2%; Pred. No. 0.65;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTLVQAQNSKRHKRAIR 16
:||:|:|:|:|:|:|:
Db 248 RTLLQARNFERNKAIR 263

RESULT 11
US-08-153-848-15
Sequence 15, Application US/08153848

Patent No. 5759804
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: NO. 5759804el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell,
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:

LENGTH: 378 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-153-848-15

Query Match 61.5%; Score 48; DB 1; Length 378;
Best Local Similarity 56.2%; Pred. No. 0.65;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTLVQAQNSKRHKRAIR 16
:||:|:|:|:|:|:|:
Db 248 RTLLQARNFERNKAIR 263

RESULT 12

US-08-352-678-2

Sequence 2, Application US/08352678

Patent No. 6043351

GENERAL INFORMATION:

APPLICANT: Birkenbach, Mark

APPLICANT: Kieff, Elliott

TITLE OF INVENTION: EPSTEIN BARR VIRUS INDUCED GENES

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

STREET: 600 Atlantic Avenue

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/352,678
FILING DATE: 30-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/980,518
FILING DATE: 25-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gates, Edward R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: B0801/7044
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-352-678-2

Query Match 61.5%; Score 48; DB 3; Length 378;
Best Local Similarity 56.2%; Pred. No. 0.65;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTLVQAQNSKRHKRAIR 16
DB 248 RTLLQARNFERNKAIRK 263

RESULT 13

US-09-299-843A-15
Sequence 15, Application US/09299843A
Patent No. 6107475
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Jill E. Uhl
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B

TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-299-843A-15

Query Match 61.5%; Score 48; DB 3; Length 378;
Best Local Similarity 56.2%; Pred. No. 0.65;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTLVQAQNSKRHKRAIR 16
DB 248 RTLLQARNFERNKAIRK 263

RESULT 14

US-09-299-843A-66
Sequence 66, Application US/09299843A
Patent No. 6107475
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Jill E. Uhl
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-299-843A-66

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:32:02 ; Search time 110.15 Seconds
(without alignments)
9.982 Million cell updates/sec

Title: US-08-887-977-10_COPY_230_245

Perfect score: 78

Sequence: 1 KTLVQAQNSKRHKAIR 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_67: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	100.0	369	2 JC5068	G protein-coupled
2	54	69.2	359	2 I49341	MIP-1 alpha recept
3	48	61.5	378	2 A45680	G protein-coupled
4	48	61.5	378	2 B55735	lymphocyte-specifi
5	48	61.5	378	2 A55735	G protein-coupled
6	44.5	57.1	352	2 A43113	chemokine (C-C) re
7	44.5	57.1	360	2 JC2443	chemokine (C-C) re
8	44.5	57.1	374	2 I38450	chemokine (C-C) re
9	43	55.1	355	2 G02436	chemokine (C-C) re
10	41	52.6	364	2 C83099	hypothetical prote
11	40	51.3	202	2 T52146	ribosomal protein
12	40	51.3	354	2 A23669	interleukin-8 rece
13	40	51.3	355	2 JQ1231	interleukin-8 rece
14	40	51.3	358	2 A53752	interleukin-8 rece
15	40	51.3	639	2 T24972	hypothetical prote
16	40	51.3	698	2 T24970	hypothetical prote
17	40	51.3	1217	2 T13996	pol protein - frui
18	39	50.0	139	2 S06568	finger protein (cl
19	39	50.0	235	2 H81276	N-acetylneuraminat
20	39	50.0	318	2 T26364	hypothetical prote
21	39	50.0	4568	2 T80830	dynamin beta heavy
22	38	48.7	150	2 F36809	hypothetical prote
23	38	48.7	360	2 A57160	chemokine (C-C) re
24	38	48.7	360	2 JC4587	chemokine (C-C) re
25	38	48.7	368	2 JC6081	proximal sequence
26	38	48.7	384	2 T19513	hypothetical prote
27	38	48.7	523	2 T05946	cytochrome P450 78
28	38	48.7	668	2 S49639	probable membrane
29	38	48.7	752	2 T16508	hypothetical prote

30 38 48.7 775 2 I49237
31 38 48.7 790 2 A35797
32 37 47.4 290 2 A70208
33 37 47.4 334 2 F83070
34 37 47.4 355 2 A45177
35 37 47.4 380 2 S49116
36 37 47.4 535 2 D75385
37 37 47.4 566 2 C81870
38 37 47.4 566 2 G81151
39 37 47.4 1570 2 T38792
40 37 47.4 1811 2 T39252
41 36 46.2 109 2 D81358
42 36 46.2 183 1 PWEG1
43 36 46.2 333 2 I65989
44 36 46.2 334 2 T02896
45 36 46.2 350 2 A39445

ALIGNMENTS

RESULT 1

JC5068

G protein-coupled receptor CKR-L3 - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000

C:Accession: JC5068

R:Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.

Biochem. Biophys. Res. Commun. 227, 846-853, 1996

A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-lik

A:Reference number: JC5067; MUID:97040707

A:Accession: JC5068

A:Molecule type: DNA

A:Residues: 1-369 <ZAB>

A:Cross-references: EMBL:Z79784; NID:gl668737; PIDN:CA802144.1; PID:gl668738

C:Comment: This protein belongs to the family of alpha chemokine receptors.

C:Genetics:

A:Gene: GDB:CMKBR6; SPTL22: GPR29; CC86; CKR-L3; GPR-CY4

A:Cross-references: GDB:5370639; OMIM:601835

A:Map-position: 6q27-6q27

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

F:42-68/Domain: transmembrane #status predicted <TM1>

F:79-99/Domain: transmembrane #status predicted <TM2>

F:115-136/Domain: transmembrane #status predicted <TM3>

F:160-180/Domain: transmembrane #status predicted <TM4>

F:212-233/Domain: transmembrane #status predicted <TM5>

F:250-271/Domain: transmembrane #status predicted <TM6>

F:292-315/Domain: transmembrane #status predicted <TM7>

Query Match 100.0%; Score 78; DB 2; Length 369;

Best Local Similarity 100.0%; Pred. No. 2e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHKAIR 16

Db 234 KTLVQAQNSKRHKAIR 249

RESULT 2

I49341

MIP-1 alpha receptor like-2 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 02-Jul-1998

C:Accession: I49341

R:Gao, J.L.; Murphy, P.M

J. Biol. Chem. 270, 17494-17501, 1995

A:Title: Cloning and differential tissue-specific expression of three mouse beta chem

A:Reference number: I49339; MUID:95340546

A:Accession: I49341

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A;Residues: 1-359 <RES>
A;Cross-references: EMBL:U28406; NID:g881551; PID:g881552
C;Superfamily: vertebrate rhodopsin

Query Match 69.2%; Score 54; DB 2; Length 359;
Best Local Similarity 62.5%; Pred. No. 0.043;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KTLVQAOQNSKRHKRAIR 16
||||:|:|:|||||
DB 228 KTLRCPCNKKRHKRAIR 243

RESULT 3

A45680
G protein-coupled peptide receptor EBI 1 - human
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C;Accession: A45680
R;Birkenbach, M.; Josefsen, K.; Yalamanchilli, R.; Lenoir, G.; Kieff, E.
J. Virol. 67, 2209-2220, 1993
A;Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-coupled p
A;Reference number: A45680; MUID:93188173
A;Accession: A45680
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-378 <BIR>
A;Cross-references: GB:L08176; NID:g183484; PID:g183485
A;Experimental source: B-lymphocytes
A;Note: sequence extracted from NCBI backbone (NCBIN:127094, NCBIPI:127095)
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 61.5%; Score 48; DB 2; Length 378;
Best Local Similarity 56.2%; Pred. No. 0.56;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTLVQAOQNSKRHKRAIR 16
||||:|:|:|||||
DB 248 RTLLQARNFERNKAIR 263

RESULT 4

B55735
Lymphocyte-specific G protein-coupled receptor EBII - human
N;Alternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 19-May-2000
C;Accession: B55735; S52443
R;Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.
Genomics 23, 643-650, 1994
A;Title: Cloning of human and mouse EBII, a lymphoid-specific G-protein-coupled receptor
A;Reference number: A55735; MUID:95154835
A;Accession: B55735
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-378 <SCH>
A;Cross-references: GB:L31581; NID:g468319; PIDN:AAA74231.1; PID:g468320
R;Burgstahler, R.; Kempkes, B.; Staube, K.; Lipp, M.
submitted to the EMBL Data Library, February 1995
A;Description: The expression of the chemokine receptor BLR2/EBII is specifically trans
A;Reference number: S52443
A;Accession: S52443
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 21-378 <BUR>
A;Cross-references: EMBL:X84702
C;Genetics:
A;Gene: GDB:CMKBR7; EBII; BLR2; CCR7
A;Cross-references: GDB:342065; OMIM:600242
A;Map position: 17q12-17q21.2

C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor

Query Match 61.5%; Score 48; DB 2; Length 378;
Best Local Similarity 56.2%; Pred. No. 0.56;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTLVQAOQNSKRHKRAIR 16
||||:|:|:|||||
DB 248 RTLLQARNFERNKAIR 263

RESULT 5

A55735
G protein-coupled receptor EBII - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 24-Nov-1999
C;Accession: A55735
R;Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.
Genomics 23, 643-650, 1994
A;Title: Cloning of human and mouse EBII, a lymphoid-specific G-protein-coupled recep
A;Reference number: A55735; MUID:95154835
A;Accession: A55735
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-378 <SCH>
A;Cross-references: GB:L31580; NID:g468340; PIDN:AAA74232.1; PID:g468341
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor

Query Match 61.5%; Score 48; DB 2; Length 378;
Best Local Similarity 56.2%; Pred. No. 0.56;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTLVQAOQNSKRHKRAIR 16
||||:|:~|:|:|||||
DB 248 RTLLQARNFERNKAIR 263

RESULT 6

A43113
chemokine (C-C) receptor 5 - human
N;Alternate names: C-C CKR-5; CCR5
C;Species: Homo sapiens (man)
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 20-Jun-2000
C;Accession: A43113; S71808; A58832; G02653; A58833
R;Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.
Biochemistry 35, 3362-3367, 1996
A;Title: Molecular cloning and functional expression of a new human CC-chemokine rece
A;Reference number: A43113; MUID:96241590
A;Accession: A43113
A;Molecule type: mRNA
A;Residues: 1-352 <SAM1>
A;Cross-references: GB:X91492; NID:g1262810; PIDN:CAA62796.1; PID:g1262811
R;Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Sarag
M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.;
Nature 382, 722-725, 1996
A;Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant allele
A;Reference number: S71808; MUID:96345670
A;Accession: S71808
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 182-206;207-230 <SAM2>
A;Accession: A58834
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-184, 'IKDSHLGAGPAACHGHLGNPKNSASVSK' <SAM3>
A;Cross-references: GB:X99393; NID:g1524062; PIDN:CAA67767.1; PID:g1524063
A;Note: this frameshift mutation results in a non-functional receptor but confers a d
nd may have had a selective advantage by conferring resistance to Yersinia plague inf
R;Combadiere, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.

J. Leukoc. Biol. 60, 147-152, 1996
A:Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine receptor
A:Reference number: A58832; MUID:96295970
A:Accession: A58832
A:Molecule type: mRNA
A:Residues: 1-352 <COM1>
A:Cross-references: GB:U57840; NID:gl502408; PIDN:AA1071.1; PID:gl502409
A:Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes
R:Combadiere, C.
submitted to the EMBL Data Library, May 1996
A:Reference number: H01541
A:Accession: G02653
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-89, 'L', 91-352 <COM2>
A:Cross-references: EMBL:U57840
R:Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
J. Biol. Chem. 271, 17161-17166, 1996
A:Title: Molecular cloning and functional characterization of a novel human CC chemokine receptor
A:Reference number: A58833; MUID:96291862
A:Accession: A58833
A:Molecule type: mRNA
A:Residues: 1-352 <RAP>
A:Cross-references: GB:U54994; NID:gl457945; PIDN:AA05098.1; PID:gl457946
C:Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-1beta (see PIR:A30575) and dual-tropic strains of HIV-1 bind to a complex of chemokine receptor and MIP-1.
C:Genetics:
A:Gene: GDB:CMKBR5; CCR5; CXR-5; CC-CXR-5; CXR5; ChemR13
A:Cross-references: GDB:1230510; OMIM:601373
A:Map position: 3p21-3p21
C:Function:
A:Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RANTES
A:Note: probably acts to control granulocyte proliferation and differentiation
C:Superfamily: vertebrate rhodopsin
C:Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
F:67-87/Domain: transmembrane #status predicted <TM1>
F:103-124/Domain: transmembrane #status predicted <TM2>
F:142-166/Domain: transmembrane #status predicted <TM4>
F:193-218/Domain: transmembrane #status predicted <TM5>
F:236-257/Domain: transmembrane #status predicted <TM6>
F:285-300/Domain: transmembrane #status predicted <TM7>
F:268/Binding site: disulfide bonds: #status predicted
F:336,337,342/Binding site: phosphate (Ser) (covalent) #status predicted
F:340,343/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 57.1%; Score 44.5; DB 2; Length 352;
Best Local Similarity 52.9%; Pred. No. 2.2;
Matches 9; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 KTLVQAQN-SKRHKAIR 16
||||:| |||:|
Db 219 KTLRCRNEKKRRAVR 235

RESULT 7
JC2443
chemokine (C-C) receptor 2, splice form B - human
N:Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chemoattractant protein 1
C:Species: Homo sapiens (man)
C:Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Jun-2000
C:Accession: JC2443; I38463
R:Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.
Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994
A:Title: cDNA cloning and functional expression of a human monocyte chemoattractant protein 1
A:Reference number: JC2443; MUID:94324942
A:Accession: JC2443
A:Molecule type: mRNA
A:Residues: 1-360 <YAM>
A:Cross-references: DDBJ:D29984; NID:g531246; PIDN:BA06253.1; PID:g531247
R:Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.

Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A:Title: Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors
A:Reference number: A53477; MUID:94195821
A:Accession: I38463
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-360 <RES>
A:Cross-references: EMBL:U03905; NID:g472557; PIDN:AA19120.1; PID:g472558
C:Genetics:
A:Gene: GDB:CMKBR2
A:Cross-references: GDB:337364; OMIM:601267
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein
F:81-100/Domain: transmembrane #status predicted <TM2>
F:115-136/Domain: transmembrane #status predicted <TM3>
F:154-178/Domain: transmembrane #status predicted <TM4>
F:207-226/Domain: transmembrane #status predicted <TM5>
F:244-268/Domain: transmembrane #status predicted <TM6>
F:287-309/Domain: transmembrane #status predicted <TM7>
F:14/Binding site: carboxylate (Asn) (covalent) #status predicted
F:113-190/Disulfide bonds: #status predicted

Query Match 57.1%; Score 44.5; DB 2; Length 360;
Best Local Similarity 52.9%; Pred. No. 2.3;
Matches 9; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 KTLVQAQN-SKRHKAIR 16
||||:| |||:|
Db 227 KTLRCRNEKKRRAVR 243

RESULT 8
I38450
chemokine (C-C) receptor 2, splice form A - human
N:Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chemoattractant protein 1
C:Species: Homo sapiens (man)
C:Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 13-Aug-1999
R:Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A:Title: Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors
A:Reference number: A53477; MUID:94195821
A:Accession: I38450
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <RES>
A:Cross-references: EMBL:U03882; NID:g472555; PIDN:AA19119.1; PID:g472556
C:Genetics:
A:Gene: GDB:CMKBR2
A:Cross-references: GDB:337364; OMIM:601267
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein
F:79-99/Domain: transmembrane #status predicted <TM2>
F:115-136/Domain: transmembrane #status predicted <TM3>
F:154-178/Domain: transmembrane #status predicted <TM4>
F:208-226/Domain: transmembrane #status predicted <TM5>
F:244-265/Domain: transmembrane #status predicted <TM6>
F:292-309/Domain: transmembrane #status predicted <TM7>
F:14/Binding site: carboxylate (Asn) (covalent) #status predicted
F:32-277,113-190/Disulfide bonds: #status predicted

Query Match 57.1%; Score 44.5; DB 2; Length 374;
Best Local Similarity 52.9%; Pred. No. 2.4;
Matches 9; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 KTLVQAQN-SKRHKAIR 16
||||:| |||:|

Db 227 KTLRCRNEKKRRRAVR 243

RESULT 9
G02436
chemokine (C-C) receptor 3 - human
N:Alternate names: C-C CKR-3
C:Species: Homo sapiens (man)
C>Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 04-Mar-2000
C:Accession: G02436; A57237
R:Ponath, P.D.
submitted to the EMBL Data Library, February 1996
A:Reference number: H01272
A:Accession: G02436
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-355 <PON>
A:Cross-references: EMBL:U49727; NID:g1477560; PIDN:RAB09726.1; PID:g1477561
R:Combadiere, C.; Ahuja, S.K.; Murphy, P.M.
J. Biol. Chem. 270, 16491-16494, 1995
A:Title: Cloning and functional expression of a human eosinophil CC chemokine receptor.
A:Reference number: A57237; MUID:95348056
A:Accession: A57237
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-106, 'N', 108-275, 'S', 277-280, 'R', 282-355 <COM>
A:Cross-references: GB:U28694; NID:g1199579; PIDN:AAC50469.1; PID:g1199580
A:Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN:AAC50469.
C:Genetics:
A:Gene: GDB:CMKBR3
A:Cross-references: GDB:579624; OMIM:601268
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
F:36-60/Domain: transmembrane #status predicted <TM1>
F:71-91/Domain: transmembrane #status predicted <TM2>
F:108-129/Domain: transmembrane #status predicted <TM3>
F:147-171/Domain: transmembrane #status predicted <TM4>
F:205-223/Domain: transmembrane #status predicted <TM5>
F:240-261/Domain: transmembrane #status predicted <TM6>
F:288-305/Domain: transmembrane #status predicted <TM7>
F:224-273,106-183/Disulfide bonds: #status predicted
F:345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 55.1%; Score 43; DB 2; Length 355;
Best Local Similarity 50.0%; Pred. No. 4.2;
Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHKAI 16
||||| : ||:||||
DB 224 KTLRCPSKKYKAIR 239

RESULT 10
C83099
hypothetical protein PA4373 [imported] - Pseudomonas aeruginosa (strain PAO1)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.
A:Reference number: A82950; MUID:20437337
A:Accession: C83099
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-364 <STO>
A:Cross-references: GB:AE004853; GB:AE004091; NID:g9950598; PIDN:AAG07761.1; GSPDB:GN001
A:Experimental source: strain PAO1
C:Genetics:

A:Gene: PA4373

Query Match 52.6%; Score 41; DB 2; Length 364;
Best Local Similarity 60.0%; Pred. No. 9.9;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHKAI 15
||| | ||| ||
DB 212 ETLAQMNNSVRHLAI 236

RESULT 11
T52146
ribosomal protein L13e [imported] - yeast (Candida albicans)
C:Species: Candida albicans
C>Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 03-Nov-2000
C:Accession: T52146
R:Taylor, K.; Harris, D.
submitted to the EMBL Data Library, November 1998
A:Reference number: Z25985
A:Accession: T52146
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-202 <TAY>
A:Cross-references: EMBL:AL033497; PIDN:CAA21966.1
A:Experimental source: strain 1161; cosmid Ca49C10
C:Genetics:
A:Gene: Ca49C10.02
A:Map position: 1
C:Superfamily: rat ribosomal protein L13
C:Keywords: protein biosynthesis; ribosome

Query Match 51.3%; Score 40; DB 2; Length 202;
Best Local Similarity 50.0%; Pred. No. 8.4;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHKAI 16
||| | ||: ||| ||
DB 170 RTLRLARNEKKYKGI 185

RESULT 12
A23669
interleukin-8 receptor, high affinity - rabbit
N:Alternate names: fMLP receptor
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 05-Nov-1999
C:Accession: A23669
R:Thomas, K.M.; Pyun, H.Y.; Navarito, J.
J. Biol. Chem. 265, 20061-20064, 1990
A:Title: Molecular cloning of the fMet-Leu-Phe receptor from neutrophils.
A:Reference number: A23669; MUID:91056034
A:Accession: A23669
A:Molecule type: mRNA
A:Residues: 1-354 <THO>
A:Cross-references: GB:W58021; GB:J05705; NID:g165442; PIDN:AAA31377.1; PID:g165443
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein; neutrophil

Query Match 51.3%; Score 40; DB 2; Length 354;
Best Local Similarity 43.8%; Pred. No. 15;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHKAI 16
||| | || : ||: ||
DB 231 RTLFQAHHGQKRRAMR 246

RESULT 13
J01231

interleukin-8 receptor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Nov-1999
C:Accession: J01231; A46483
R:Beckmann, M.P.; Munger, W.E.; Kozlosky, C.; VandenBos, T.; Price, V.; Lyman, S.; Gerard, B.; Biochem. Biophys. Res. Commun. 179, 784-789, 1991
A:Title: Molecular characterization of the interleukin-8 receptor.
A:Reference number: J01231; MUID:91378994
A:Accession: J01231
A:Molecule type: DNA
A:Residues: 1-355 <BEC>
A:Cross-references: GB:M74240; NID:q165438; PIDN:AAA31375.1; PID:g165439
R:Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.
J. Immunol. 148, 1261-1264, 1992
A:Title: Characterization of complementary DNA clones encoding the rabbit IL-8 receptor.
A:Reference number: A46483; MUID:92148149
A:Accession: A46483
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-355 <LEE>
A:Cross-references: GB:M82873; NID:q165440; PIDN:AAA31376.1; PID:g165441
A:Experimental source: neutrophils
A:Note: sequence extracted from NCBI backbone (NCBIN:81526, NCBI:P:81530)
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 51.3%; Score 40; DB 2; Length 355;
Best Local Similarity 43.8%; Pred. No. 15;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KTLVQAQNSKRHKRAIR 16
:|||:|:|:|:|:|:
Db 232 RTLFQAHMGQKRRAMR 247

RESULT 14

A53752
interleukin-8 receptor (clone 5Bla) - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: A53752
R:Prado, G.N.; Thomas, K.M.; Suzuki, H.; LaRosa, G.J.; Wilkinson, N.; Folco, E.; Navarro, J. Biol. Chem. 269, 12391-12394, 1994
A:Title: Molecular characterization of a novel rabbit interleukin-8 receptor isotype.
A:Reference number: A53752; MUID:94230294
A:Accession: A53752
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-358 <PRA>
A:Cross-references: GB:L24445; NID:q437661; PIDN:AAA31378.1; PID:g437662
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 51.3%; Score 40; DB 2; Length 358;
Best Local Similarity 43.8%; Pred. No. 15;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KTLVQAQNSKRHKRAIR 16
:|||:|:|:|:|:|:
Db 234 RTLFQAHMGQKRRAMR 249

RESULT 15

T24972
hypotheical protein T19A6.2b - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T24972
R:Clark, L.
submitted to the EMBL Data Library, January 1998
A:Reference number: Z19963

A:Accession: T24972
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-639 <WIL>
A:Cross-references: EMBL:AL021571; PIDN:CAA16514.1; GSPDB:GN00019; CESP:T19A6.2b
A:Experimental source: clone T19A6
C:Genetics:
A:Gene: CESP:T19A6.2b
A:Map position: 1
A:Introns: 9/2; 41/1; 85/3; 118/3; 186/3; 221/3; 458/3; 505/3; 609/3

Query Match 51.3%; Score 40; DB 2; Length 639;
Best Local Similarity 46.7%; Pred. No. 26;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KTLVQAQNSKRHKRAI 15
:|||:|:|:|:|:|:
Db 597 KTIVQAASEKKDKSV 611

Search completed: May 23, 2001, 15:32:02
Job time: 509 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:36:20 ; Search time 62.39 seconds
(without alignments)
8.785 Million cell updates/sec

Title: US-08-887-977-10_COPY_230_245

Perfect score: 78

Sequence: 1 KTLVQAQNSKRRAIR 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	78	100.0	374	1	CCR6_HUMAN
2	75	96.2	367	1	CCR6_MOUSE
3	54	69.2	359	1	CCR3_MOUSE
4	50	64.1	359	1	CCR3_RAT
5	50	64.1	369	1	CCR9_MOUSE
6	49	62.8	357	1	CCR9_HUMAN
7	48	61.5	378	1	CCR7_HUMAN
8	48	61.5	378	1	CCR7_MOUSE
9	44.5	57.1	352	1	CCR5_CERAE
10	44.5	57.1	352	1	CCR5_CERTO
11	44.5	57.1	352	1	CCR5_GORGO
12	44.5	57.1	352	1	CCR5_HUMAN
13	44.5	57.1	352	1	CCR5_HYLLE
14	44.5	57.1	352	1	CCR5_MACMU
15	44.5	57.1	352	1	CCR5_PANTR
16	44.5	57.1	352	1	CCR5_PAPHA
17	44.5	57.1	352	1	CCR5_PONPY
18	44.5	57.1	352	1	CCR5_PYGBI
19	44.5	57.1	352	1	CCR5_PYGNE
20	44.5	57.1	352	1	CCR5_TRAFH
21	44.5	57.1	352	1	CCR5_TRAPH
22	44.5	57.1	374	1	CCR2_HUMAN
23	43	55.1	355	1	CCR3_CERAE
24	43	55.1	355	1	CCR3_HUMAN
25	43	55.1	355	1	CCR3_MACMU
26	43	55.1	358	1	CCR3_CAVPO
27	40	51.3	202	1	RL13_CANAL
28	40	51.3	355	1	IL8A_RABIT
29	40	51.3	358	1	IL8B_RABIT
30	39	50.0	139	1	ZG29_XENLA
31	39	50.0	211	1	VNS3_RSVN
32	39	50.0	211	1	VNS3_RSVT
33	39	50.0	673	1	FOX3_HUMAN

RESULT 1

ID	CCR6_HUMAN	STANDARD;	PRT;	374 AA.
AC	P51684: Q92846; P78553;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CCR-6) (CCR-6) (LARC RECEPTOR) (GPR-CY4) (GPCY4) (CHEMOKINE RECEPTOR-LIKE 3) (CCR-L3) (DRY6).			
DE	CCR6 OR CMKBR6 OR STRL22 OR GPR29 OR CCR6L3.			
GN	Homo sapiens (Human).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND FUNCTION.			
RX	MEDLINE=97313465; PubMed=9169459;			
RA	Baba M., Imai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K., Nomiyama H., Yoshie O.;			
RA	"Identification of CCR6, the specific receptor for a novel lymphocyte-directed CC chemokine LARC.";			
RT	J--BioI--Chem--272:14893-14898(1997).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RP	Lautens L.L., Modi W., Bonner T.I.;			
RL	Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97040707; PubMed=8886020;			
RA	Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G.;			
RT	"Molecular cloning and RNA expression of two new human chemokine receptor-like genes.";			
RL	Biochem. Biophys. Res. Commun. 227:846-853(1996).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	McCoy R., Perlmutter D.H.;			
RL	Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97224503; PubMed=9070937;			
RA	Liao F., Lee H.-H., Farber J.M.;			
RT	"Cloning of STRL22, a new human gene encoding a G-protein-coupled receptor related to chemokine receptors and located on chromosome 6q27.";			
RL	Genomics 40:175-180(1997).			
CC	-!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-			
CC	ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.			
CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	-!- TISSUE SPECIFICITY: SPLEEN, LYMPH NODES, APPENDIX, AND FETAL LIVER. EXPRESSED IN LYMPHOCYTES, T CELLS AND B CELLS BUT NOT IN NATURAL KILLER CELLS, MONOCYTES, OR GRANULOCYTES.			
CC	-!- INDUCTION: INTERLEUKIN-2.			
CC	-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-6 IS THE INITIATOR.			

Q39565 chlamydomon
O54842 rattus norv
Q01024 herpesviro
P51679 homo sapien
Q28003 bos taurus
Q16533 homo sapien
O48927 glycine max
Q04511 saccharomyc
Q60769 mus musculu
P21580 homo sapien
P51682 mus musculu

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 CC EMBL; U45984; AAB62714.1; -
 DR EMBL; 279784; CAB02144.1; ALT_INIT.
 DR EMBL; U60000; AAB06949.1; -
 DR EMBL; U68030; AAC51124.1; -
 DR EMBL; U68032; AAC51125.1; -
 DR HSSP; P34996; 1DDO.
 DR GCRDB; GCR_1037; -
 DR GCRDB; GCR_1075; -
 DR GCRDB; GCR_1906; -
 DR GCRDB; GCR_1919; -
 DR GCRDB; GCR_1941; -
 DR GCRDB; GCR_2110; -
 DR MIM; 601835; -
 DR InterPro; IPR000276; -
 DR Pfam; PF00001; 7tm.1.1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECF_FL_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECF_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 47
 FT TRANSMEM 48 74
 FT DOMAIN 75 83
 FT TRANSMEM 84 104
 FT DOMAIN 105 119
 FT TRANSMEM 120 141
 FT DOMAIN 142 159
 FT TRANSMEM 160 180
 FT DOMAIN 181 211
 FT TRANSMEM 212 238
 FT DOMAIN 239 254
 FT TRANSMEM 255 279
 FT DOMAIN 280 303
 FT TRANSMEM 304 321
 FT DOMAIN 322 374
 FT DISULFID 118 197
 FT CARBOHYD 7 7
 FT CARBOHYD 23 23
 FT CONFLICT 60 60
 FT CONFLICT 74 74
 FT CONFLICT 86 86
 FT CONFLICT 164 164
 FT CONFLICT 182 182
 FT CONFLICT 192 192
 FT CONFLICT 206 206
 FT CONFLICT 225 225
 FT CONFLICT 370 374
 SQ SEQUENCE 374 AA; 42494 MW; D7F963534E990BC4 CRC64;

 Query Match 100.0%; Score 78; DB 1; Length 374;
 Best Local Similarity 100.0%; Pred. No. 2.9e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KTLVQAQNSKRHKRAIR 16
 |||||
 DB 239 KTLVQAQNSKRHKRAIR 254

 RESULT 2
 ID CKR6_MOUSE STANDARD; PRT; 367 AA.
 AC O54689;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CCR-6) (KY411).
 GN CCR6 OR CKMR6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RA Yanagihara S., Komura E., Yamaguchi Y.;
 RT "Mouse G protein-coupled receptor KY411.";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=99077268; PubMed=9862452;
 RA Varona R., Zaballos A., Gutierrez J., Martin P., Roncal F.,
 RA Albar J.P., Ardavin C., Marquez G.;
 RT "Molecular cloning, functional characterization and mRNA expression
 RT analysis of the murine chemokine receptor CCR6 and its specific ligand
 RT MIP-3alpha.";
 RL FEBS Lett. 440:188-194(1998).
 CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-
 CC ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE
 CC INTRACELLULAR CALCIUM IONS LEVEL.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC EMBL; AB009369; BAA23776.1; -
 DR EMBL; AJ222714; CAA10956.1; -
 DR MGD; MGI:133379; Cmkbr6.
 DR InterPro; IPR000276; -
 DR Pfam; PF00001; 7tm.1.1.
 DR PRINTS; PR00237; GPCRHHODOPSN
 DR PROSITE; PS00237; G_PROTEIN_RECF_FL_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECF_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 39
 FT TRANSMEM 40 66
 FT DOMAIN 67 75
 FT TRANSMEM 76 96
 FT DOMAIN 97 111
 FT TRANSMEM 112 133
 FT DOMAIN 134 151
 FT TRANSMEM 152 172
 FT DOMAIN 173 203
 FT TRANSMEM 204 230
 FT DOMAIN 231 246
 FT TRANSMEM 247 271
 FT DOMAIN 272 295
 FT TRANSMEM 296 313
 FT DOMAIN 314 367
 FT DISULFID 110 189
 FT CARBOHYD 2 2
 FT CARBOHYD 35 35
 SQ SEQUENCE 367 AA; 42102 MW; 6A309AF83B1117E CRC64;

 Query Match 96.2%; Score 75; DB 1; Length 367;
 Best Local Similarity 93.8%; Pred. No. 1e-06;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KTLVQAQNSKRHKRAIR 16
 |||||
 DB 231 KTLVQAQNSKRHKRAIR 246

RESULT 3
 CKR3_MOUSE
 ID CKR3_MOUSE STANDARD; PRT; 359 AA.
 AC P51678;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE PROBABLE C-C CHEMOKINE RECEPTOR TYPE 3 (C-C CKR-3) (CCR-3)
 DE (CCR3) (CCR3) (MACROPHAGE INFLAMMATORY PROTEIN-1 ALPHA RECEPTOR-LIKE
 DE 2) (MIP-1 ALPHA RL2)
 GN CCR3 OR CMKBR3 OR CMKBRIL2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV;
 RX MEDLINE=96072806; PubMed=7594543;
 RA Post T.W., Bozic C.R., Rothenberg M.E., Luster A.D., Gerard N.,
 RA Gerard C.;
 RT "Molecular characterization of two murine eosinophil beta chemokine
 RT receptors";
 RT J. Immunol. 155:5299-5305(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ;
 RX MEDLINE=95340546; PubMed=7542241;
 RA Gao J.-L., Murphy P.M.;
 RT "Cloning and differential tissue-specific expression of three mouse
 RT beta chemokine receptor-like genes, including the gene for a
 RT functional macrophage inflammatory protein-1 alpha receptor.";
 RL J. Biol. Chem. 270:17494-17501(1995).
 CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO EOTAXIN,
 CC MCP-3, MCP-4 AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: DETECTED IN SKELETAL MUSCLE AND IN TRACE
 CC AMOUNTS IN LEUKOCYTES.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC EMBL; U29677; AA86118.1; -
 CC EMBL; U28406; AA86155.1; -
 CC GCRDB; GCR_1673; -
 CC GCRDB; GCR_1695; -
 CC MGD; MGI:104616; Cmkbril2.
 CC InterPro; IPR000276; -
 CC InterPro; IPR000355; -
 CC Pfam; PF00001; 7tm1.1;
 CC PRINTS; PR00237; GPCRHHODOPSN.
 CC PRINTS; PR00657; CCHEMOKINER.
 CC PRINTS; PR01108; CHEMOKINER3.
 CC PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
 CC PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.
 CC KW G-protein coupled receptor; Transmembrane.
 CC FT DOMAIN 1 38 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 39 64 1 (POTENTIAL).
 CC FT DOMAIN 65 68 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 69 95 2 (POTENTIAL).
 CC FT DOMAIN 96 111 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 112 133 3 (POTENTIAL).
 CC FT DOMAIN 134 150 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 151 175 4 (POTENTIAL).
 CC

FT DOMAIN 176 201 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 202 227 5 (POTENTIAL).
 FT DOMAIN 228 243 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 244 268 6 (POTENTIAL).
 FT DOMAIN 269 285 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 286 309 7 (POTENTIAL).
 FT DOMAIN 310 359 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 110 187 BY SIMILARITY.
 FT CONFLICT 270 270 R -> S (IN REF. 2).
 SQ SEQUENCE 359 AA; 41825 MW; ACILED66E283CEAF CRC64;
 Query Match 69.2%; Score 54; DB 1; Length 359;
 Best Local Similarity 62.5%; Pred. No. 0.0095;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 KTLVQAQNSKRHKAIR 16
 DB 228 KTLRLCPNKKHKAIR 243
 |||:: | |::|
 |||:: | |::|
 RESULT 4
 CKR3_RAT
 ID CKR3_RAT STANDARD; PRT; 359 AA.
 AC O54814; O55169;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 3 (C-C CKR-3) (CCR-3) (CCR3)
 DE (CCR3).
 GN Rattus norvegicus (Rat).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. AND TISSUE SPECIFICITY.
 RC STRAIN=Wistar; TISSUE=Spleen;
 RX MEDLINE=98318173; PubMed=9853467;
 RA Jiang Y., Saifanica M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
 RA Defebvre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
 RT "Chemokine receptor expression in cultured glia and rat experimental
 RT allergic encephalomyelitis";
 RL J. Neuroimmunol. 86:1-12(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Spleen;
 RX Harrington P.M., Newton D.J., Coleman J.W., Flanagan B.F.;
 RA Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO EOTAXIN,
 CC MCP-3, MCP-4 AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN SPLEEN BUT NOT IN ASTROCYTES OR
 CC MICROGLIA.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC EMBL; Y13400; CAA73830.1; -
 CC InterPro; IPR000276; -
 CC InterPro; IPR000355; -
 CC InterPro; IPR002238; -
 CC Pfam; PF00001; 7tm1.1;
 CC PRINTS; PR00237; GPCRHHODOPSN.
 CC PRINTS; PR00657; CCHEMOKINER.
 CC

DR PRINTS; PRO1108; CHEMOKINER3.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
 DR PROSITE; PS0262; G-PROTEIN_RECEP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane.
 FT DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 44 64 POTENTIAL.
 FT DOMAIN 65 74 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 75 95 POTENTIAL.
 FT DOMAIN 96 112 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 113 133 POTENTIAL.
 FT DOMAIN 134 154 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 155 175 POTENTIAL.
 FT DOMAIN 176 206 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 207 227 POTENTIAL.
 FT DOMAIN 228 243 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 244 264 POTENTIAL.
 FT DOMAIN 265 288 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 289 309 POTENTIAL.
 FT DOMAIN 310 359 CYTOPLASMIC (POTENTIAL).
 FT CONFLICT 164 164 F -> L (IN REF. 2).
 SQ SEQUENCE 359 AA; 41643 MW; 880F682984F501DA CRC64;

Query Match 64.1%; Score 50; DB 1; Length 359;
 Best Local Similarity 56.2%; Pred. No. 0.054;
 Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 KTLVQAQNSRRHRAIR 16
 ||||: | | | | |
 DB 228 KILLRCPNKKKKRAIQ 243

RESULT 5

ID CKR9_MOUSE STANDARD; PRT; 369 AA.
 AC Q9WUT7;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 9 (C-C CKR-9) (CC-CKR-9) (CCR-9)
 DE (CHEMOKINE C-C RECEPTOR 10).
 GN CKR9 OR CMKBR10.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thymus;
 RX MEDLINE=99248139; PubMed=10229797;
 RA Zaballios A., Gutierrez J., Varona R., Ardavin C., Marquez G.;
 RT "Cutting edge: identification of the orphan chemokine receptor GPR-9-6
 RT as CCR9, the receptor for the chemokine TECK.";
 RL J. Immunol. 162:5671-5675(1999).
 CC -!- FUNCTION: RECEPTOR FOR CHEMOKINE SCYA25/TECK. SUBSEQUENTLY
 CC TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS
 CC LEVEL.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE THYMUS AND LOW IN
 CC LYMPH NODES AND SPLEEN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL; AJ132336; CAB43480.1;
 CC MGD; MGI:1341902; Cmkbr10.
 DR InterPro; IPR000174; -.

DR InterPro; IPR000248; -.
 DR InterPro; IPR000276; -.
 DR InterPro; IPR000355; -.
 DR InterPro; IPR000496; -.
 DR InterPro; IPR001277; -.
 DR InterPro; IPR001718; -.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PRO0237; GPCRHHODPSN.
 DR PRINTS; PRO0241; ANGIOTENSINR.
 DR PRINTS; PRO0425; BRADYKININR.
 DR PRINTS; PRO0427; INTRLEUKINR.
 DR PRINTS; PRO0641; CHEMOKINER7.
 DR PRINTS; PRO0645; LCRIORPHANR.
 DR PRINTS; PRO0657; CCHEMOKINER.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
 DR PROSITE; PS0262; G-PROTEIN_RECEP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 49 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 50 76 1 (POTENTIAL).
 FT DOMAIN 77 85 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 86 106 2 (POTENTIAL).
 FT DOMAIN 107 120 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 121 142 3 (POTENTIAL).
 FT DOMAIN 143 160 4 (POTENTIAL).
 FT TRANSMEM 161 181 5 (POTENTIAL).
 FT DOMAIN 182 210 6 (POTENTIAL).
 FT TRANSMEM 211 238 7 (POTENTIAL).
 FT DOMAIN 239 254 8 (POTENTIAL).
 FT TRANSMEM 255 280 9 (POTENTIAL).
 FT DOMAIN 281 304 10 (POTENTIAL).
 FT TRANSMEM 305 322 11 (POTENTIAL).
 FT DOMAIN 323 369 12 (POTENTIAL).
 FT CARBOHYD 32 32 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 119 198 BY SIMILARITY.
 SQ SEQUENCE 369 AA; 41913 MW; 6971F76F0A24B4AE CRC64;

Query Match 64.1%; Score 50; DB 1; Length 369;
 Best Local Similarity 60.0%; Pred. No. 0.056;
 Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 TLVQAQNSRRHRAIR 16
 ||||: | | | | |
 DB 240 TLVQAQNSRRHRAIR 254

RESULT 6

ID CKR9_HUMAN STANDARD; PRT; 357 AA.
 AC P51686;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 9 (C-C CKR-9) (CC-CKR-9) (CCR-9) (GPR-9-6)
 DE 6).
 GN CKR9 OR CMKBR9.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lautens L.L., Tiffany H.L., Gao J.-L., Modi W., Murphy P.M.,
 RA Bonner T.I.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE=99248139; PubMed=10229797;
 RA Zaballios A., Gutierrez J., Varona R., Ardavin C., Marquez G.;
 RT "Cutting edge: identification of the orphan chemokine receptor GPR-9-6
 RT as CCR9, the receptor for the chemokine TECK.";
 RL J. Immunol. 162:5671-5675(1999).
 CC -!- FUNCTION: RECEPTOR FOR CHEMOKINE SCYA25/TECK. SUBSEQUENTLY

CC TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS
 CC LEVEL.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE THYMUS AND LOW IN
 CC LYMPH NODES AND SPLEEN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 CC EMBL; U45982; AAA93319.1; --
 CC MIM; 604738; --
 CC GCRDB; GCR_1943; --
 CC InterPro; IPR000276; --
 CC Pfam; PF00001; 7tm_1; 1.
 CC PRINTS; PR00237; GPCRHHODOPSN.
 CC PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
 CC PROSITE; PS0262; G-PROTEIN_RECEP_FL_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein.
 CC DOMAIN 1 37
 CC TRANSMEM 38 64
 CC DOMAIN 65 73
 CC TRANSMEM 74 94
 CC DOMAIN 95 108
 CC TRANSMEM 109 130
 CC DOMAIN 131 148
 CC TRANSMEM 149 169
 CC DOMAIN 170 198
 CC TRANSMEM 199 226
 CC DOMAIN 227 242
 CC TRANSMEM 243 268
 CC DOMAIN 269 292
 CC TRANSMEM 293 310
 CC DOMAIN 311 357
 CC CARBOHYD 20 20 -- N-LINKED (GLCNAC...) (POTENTIAL).
 CC DISULFID 107 186 BY SIMILARITY.
 CC SEQUENCE 357 AA; 40713 MW; 96982E0B922F6B31 CRC64;
 SQ

Query Match 62.8%; Score 49; DB 1; Length 357;
 Best Local Similarity 53.3%; Score No. 0.083;
 Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Oy 2 TLVQAKSKRKAIR 16
 Db 228 TLVQAKSKRKAIR 242
 |||||:|:|:|:|:
 |||||:|:|:|:|:

RESULT 7
 ID CKR7_HUMAN STANDARD; PRT; 378 AA.
 AC P32248;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 7 PRECURSOR (C-C CKR-7) (CCR-7)
 DE (MIP-3 BETA RECEPTOR) (EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 1)
 DE (EB1) (BLR2).
 GN CCR7 OR CMKBR7 OR EB1 OR EVIL.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93188173; PubMed=8832338;
 RA Birkenbach M.P., Josefsen K., Valamanchili R.R., Lenoir G.M.,
 RA Elliott K.;

RT "Epstein-Barr virus-induced genes: first lymphocyte-specific G
 RL protein-coupled peptide receptors."; J. Virol. 67:2209-2220(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Placenta;
 RA MEDLINE=95154835; PubMed=7851893;
 RA Schweickart V.L., Raport C.J., Godiska R., Byers M.G., Eddy R.L. Jr.,
 RA Shows T.B., Gray P.W.;
 RT "Cloning of human and mouse EB1, a lymphoid-specific
 RT G-protein-coupled receptor encoded on human chromosome 17q12-q21.2.";
 RL Genomics 23:643-650(1994).
 CC -!- FUNCTION: RECEPTOR FOR THE MIP-3-BETA CHEMOKINE. PROBABLE MEDIATOR
 CC OF EBV EFFECTS ON B LYMPHOCYTES OR OF NORMAL LYMPHOCYTE FUNCTIONS.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN VARIOUS LYMPHOID TISSUES AND
 CC ACTIVATED B AND T LYMPHOCYTES, STRONGLY UPREGULATED IN B CELLS
 CC INFECTED WITH EPSTEIN-BARR VIRUS AND T CELLS INFECTED WITH
 CC HERPESVIRUS 6 OR 7.
 CC -!- INDUCTION: BY EBV.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 CC EMBL; L08176; AAA58615.1; --
 CC EMBL; L31584; AAA74230.1; --
 CC EMBL; L31582; AAA74230.1; JOINED.
 CC EMBL; L31583; AAA74230.1; JOINED.
 CC EMBL; L31581; AAA74231.1; --
 CC PIR; A45680; A45680.
 CC HSPP; P34996; 1DDD.
 CC GCRDB; GCR_0492; --
 CC GCRDB; GCR_0958; --
 CC MIM; 600242; --
 CC InterPro; IPR000276; --
 CC InterPro; IPR001718; --
 CC Pfam; PF00001; 7tm_1; 1.
 CC PRINTS; PR00237; GPCRHHODOPSN.
 CC PRINTS; PR00641; CHEMOKINER7
 CC PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
 CC PROSITE; PS0262; G-PROTEIN_RECEP_FL_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
 CC SIGNAL 1 24
 CC CHAIN 25 378
 CC C-C CHEMOKINE RECEPTOR TYPE 7.
 CC DOMAIN 25 59
 CC TRANSMEM 60 86
 CC TRANSMEM 87 95
 CC DOMAIN 96 116
 CC TRANSMEM 117 130
 CC DOMAIN 131 152
 CC TRANSMEM 153 170
 CC DOMAIN 171 191
 CC TRANSMEM 192 219
 CC DOMAIN 220 247
 CC TRANSMEM 248 263
 CC DOMAIN 264 289
 CC TRANSMEM 290 313
 CC DOMAIN 314 331
 CC TRANSMEM 332 378
 CC DOMAIN 36 36
 CC CARBOHYD 129 210
 CC DISULFID 182 183
 CC CONFLICT 337 337
 CC SEQUENCE 378 AA; 42874 MW; D4CB4213841A1BD4 CRC64;
 SQ

Query Match 61.5%; Score 48; DB 1; Length 378;

FT DISULFID 129 210 BY SIMILARITY:
SQ SEQUENCE 378 AA; 42941 MW; ACBIA422CF54AA54 CRC64;

Query Match 61.5%; Score 48; DB 1; Length 378;
Best Local Similarity 56.2%; Pred. No. 0.14;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTLVQAQNSKRHRKAIR 16
:||:||||:|:|:|:
Db 248 RTLQARNFERNKAIR 263

RESULT 8
CKR7_MOUSE STANDARD; PRT; 378 AA.
AC P4774;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 7 PRECURSOR (C-C CKR-7) (CCR-7)
DE (MIP-3 BETA RECEPTOR) (EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 1)
DE (EBI1).
GN CCR7 OR CMKBR7 OR EBI1 OR EBILH.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=B6/CBA; TISSUE=Thymus;
RC MEDLINE=95154835; PubMed=7851893;
RA Schweickart V.L., Raport C.J., Godiska R., Byers M.G., Eddy R.L. Jr.,
RA Shows T.B., Gray P.W.;
RT "Cloning of human and mouse EBI1, a lymphoid-specific
RT G-protein-coupled receptor encoded on human chromosome 17q12-q21.2.";
RL Genomics 23:643-650(1994).
CC -!- FUNCTION: RECEPTOR FOR THE MIP-3-BETA CHEMOKINE. PROBABLE MEDIATOR
CC OF EBV EFFECTS ON B LYMPHOCYTES OR OF NORMAL LYMPHOCYTE FUNCTIONS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC
CC EMBL: L31580; AAA74232.1; -;
CC MGD; MGI:103011; Cmkdr7.
CC InterPro: IPR000276; -;
CC InterPro: IPR001718; -;
CC Pfam: PF00001; 7tm.1; 1.
CC PRINTS: PR00237; GPCRHHODPSN.
CC PRINTS: PR00641; CHEMOKINER7.
CC PROSITE: PS00237; G_PROTEIN_RECEP_FL_1; 1.
CC PROSITE: PS00262; G_PROTEIN_RECEP_FL_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
CC SIGNAL 1 24
CC CHAIN 25 378
CC FT CHAIN 25 378 C-C CHEMOKINE RECEPTOR TYPE 7.
CC FT DOMAIN 25 59 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 60 86
CC FT TRANSMEM 87 95
CC FT TRANSMEM 96 116 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 117 130
CC FT TRANSMEM 131 152 EXTRACELLULAR (POTENTIAL).
CC FT DOMAIN 153 170
CC FT TRANSMEM 171 191 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 192 219
CC FT TRANSMEM 220 247 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 248 263
CC FT DOMAIN 264 289
CC FT TRANSMEM 290 313
CC FT TRANSMEM 314 331
CC FT TRANSMEM 332 378
CC FT CARBOHYD 36
CC N-LINKED (GLCNAC...) (POTENTIAL).
CC

FT DISULFID 129 210 BY SIMILARITY:
SQ SEQUENCE 378 AA; 42941 MW; ACBIA422CF54AA54 CRC64;

Query Match 61.5%; Score 48; DB 1; Length 378;
Best Local Similarity 56.2%; Pred. No. 0.14;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTLVQAQNSKRHRKAIR 16
:||:||||:|:|:|:
Db 248 RTLQARNFERNKAIR 263

RESULT 9
CKR5_CERAE STANDARD; PRT; 352 AA.
AC P56493;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CCR-5) (CCR5).
DE CCR5 OR CMKBR5.
GN Cercopithecus aethiops (Green monkey) (Grivet).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Kidney;
RC MEDLINE=98001387; PubMed=9343222;
RA Kuhlmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RA "Polymorphisms in the CCR5 genes of African green monkeys and mice
RT implicate specific amino acids in infections by simian and human
RT immunodeficiency viruses.";
RL J. Virol. 71:8642-8656(1997).
RN [2]
SEQUENCE FROM N.A.
RA Murayama Y., Matsunaga S., Inoue-Murayama M.;
RA "CDNA sequence of African green monkey CCR-5 chemokine receptor
RT gene.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC
CC EMBL: U83324; AAC51795.1; -;
CC EMBL: AB03325; AAC51796.1; -;
CC EMBL: AB015944; BAA31328.1; -;
CC GCRDB; GCR_2465; -;
CC GCRDB; GCR_2466; -;
CC InterPro: IPR000276; -;
CC InterPro: IPR000355; -;
CC InterPro: IPR002240; -;
CC Pfam: PF00001; 7tm.1; 1.
CC PRINTS: PR00237; GPCRHHODPSN.
CC PRINTS: PR00657; CCHEMOKINER.
CC PRINTS: PR01110; CHEMOKINER5.
CC PROSITE: PS00237; G_PROTEIN_RECEP_FL_1; 1.
CC PROSITE: PS00262; G_PROTEIN_RECEP_FL_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.
CC

```

FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT VARIANT 14 14 N -> Y.
FT VARIANT 352 352 F -> L.
SQ SEQUENCE 352 AA; 40561 MW; 7F52E690C72EC29A CRC64;

Query Match 57.1%; Score 44.5; DB 1; Length 352;
Best Local Similarity 52.9%; Pred. No. 0.58;
Matches 9; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 KTLVQAQN-SKRHKAIR 16
DB 219 KTLRCRNEKRRHRAVR 235
||||: :| |||:|

RESULT 10
ID CKR5_CERTO STANDARD; PRT; 352 AA.
AC 062743; 062744; 062745; 062746;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKBR5.
OS -Cercopithecus torquatus-atys-(Red-crowned-mangabey)-(Sooty-mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ISOLATE 079, 085, 087 AND 089;
RX MEDLINE=98321155; PubMed=9656999;
RA Chen Z., Gettle A., Ho D.D., Marx P.A.;
RT "Primary SIVsm isolates use the CCR5 coreceptor from sooty mangabeys
RT naturally infected in west Africa: a comparison of coreceptor usage
RT of primary SIVsm, HIV-2, and SIVmac.";
RL Virology 246:113-124(1998).
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL; AF051902; AAC39830.1; -
CC DR EMBL; AF051903; AAC39831.1; -
CC DR EMBL; AF051904; AAC39832.1; -
CC DR EMBL; AF051905; AAC39833.1; -

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DR InterPro; IPR000276; -
DR InterPro; IPR000355; -
DR InterPro; IPR002240; -
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PRO0237; GPCRHHODOPSN.
DR PRINTS; PRO0657; CCHEMOKINER.
DR PRINTS; PRO1110; CHEMOKINER5.
DR PROSITE; PS00237; G-PROTEIN_RECF_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECF_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT VARIANT 2 2 D -> E (IN ISOLATE 087).
FT VARIANT 3 3 Y -> D (IN ISOLATE 079).
FT VARIANT 25 25 V -> G (IN ISOLATE 087).
FT VARIANT 100 100 M -> K (IN ISOLATE 079).
FT VARIANT 107 107 L -> V (IN ISOLATE 089).
FT VARIANT 134 134 V -> G (IN ISOLATE 079).
FT VARIANT 146 146 T -> L (IN ISOLATES 085 AND 089).
FT VARIANT 340 340 T -> I (IN ISOLATE 079).
SQ SEQUENCE 352 AA; 40489 MW; 20A196E2D47E49CA CRC64;

Query Match 57.1%; Score 44.5; DB 1; Length 352;
Best Local Similarity 52.9%; Pred. No. 0.58;
Matches 9; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 KTLVQAQN-SKRHKAIR 16
DB 219 KTLRCRNEKRRHRAVR 235
||||: :| |||:|

RESULT 11
ID CKR5_GORGO STANDARD; PRT; 352 AA.
AC P56439;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKBR5.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amodee A., Miller K., Doranz B.J., Endres M.,
RA Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
CC

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CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF005659; AAB62553.1; -
DR GCRDB; GCR_1372; -
DR InterPro; IPR000276; -
DR InterPro; IPR000355; -
DR InterPro; IPR002240; -
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR00657; CCEMOKINER.
DR PRINTS; PR01110; CHEMOKINERS.
DR PROSITE; PS00237; G_PROTEIN_RECP_FL_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
SQ SEQUENCE 352 AA; 40515 MW; D0E6FCB9FE5EAC84 CRC64;

Query Match 57.1%; Score 44.5; DB 1; Length 352;
Best Local Similarity 52.9%; Pred. No. 0.58;
Matches 9; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 KILVQAN-SKRHKAIR 16
DB 219 KTLRCRNEKKHRAVR 235

RESULT 12
CKR5_HUMAN
ID CKR5_HUMAN STANDARD; PRT; 352 AA.
AC P51681; O14692; O14693; O14695; O14696; O14697; O14698; O14699;
AC O14700; O14701; O14702; O14703; O14704; O14705; O14706; O14707;
AC O14708;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CC-CKR-5) (CCR5)
DE (HIV-1 FUSION CO-RECEPTOR) (CHEMR13).
GN CKR5 OR CKR5
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-96241590; PubMed-8639485;
RA Samson M., Labbe O., Mollereau C., Vassart G., Parmentier M.;
RT "Molecular cloning and functional expression of a new human
CC-chemokine receptor gene.";

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RL Biochemistry 35:3362-3367(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-96291862; PubMed-8663314;
RA Raport C.J., Gosling J., Schweichart V.L., Gray P.W., Charo I.F.;
RT "Molecular cloning and functional characterization of a novel human
CC chemokine receptor (CCR5) for RANTES, MIP-1beta, and MIP-1alpha.";
RL J. Biol. Chem. 271:17161-17166(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-96295970; PubMed-8699119;
RA Combadiere C., Ahuja S.K., Tiffany H.L., Murphy P.M.;
RT "Cloning and functional expression of CC CKR5, a human monocyte CC
chemokine receptor selective for MIP-1(alpha), MIP-1(beta), and
RANTES.";
RL J. Leukoc. Biol. 60:147-152(1996).
RN [4]
RP SEQUENCE FROM N.A.
RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
RA Nham M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
RA Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J.,
RA Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,
RA Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E.,
RA Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,
RA Watanabe M., Doggett N., Garcia D., Sagripanti J.L.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE-98001387; PubMed-9343222;
RA Kuhnmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
implicate specific amino acids in infections by simian and human
immunodeficiency viruses.";
RL J. Virol. 71:8642-8656(1997).
RN [6]
RP SEQUENCE FROM N.A., AND POLYMORPHISMS.
RX MEDLINE-98022612; PubMed-9359654;
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA Ho D.D.;
RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";
RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE-98049523; PubMed-9388201;
RA Mummidi S., Ahuja S.S., McDaniel B.L., Ahuja S.K.;
RT "The human CC chemokine receptor 5 (CCR5) gene. Multiple transcripts
with 5'-end heterogeneity, dual promoter usage, and evidence for
polymorphisms within the regulatory regions and noncoding exons.";
RL J. Biol. Chem. 272:30662-30671(1997).
RN [8]
RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
RX MEDLINE-96260017; PubMed-8649511;
RA Deng H., Liu R., Elmeier W., Choe S., Unutmaz D., Burkhardt M.,
RA di Marzio P., Marmon S., Sutton R.E., Hill C.M., Davis C.B.,
RA Peiper S.C., Schall T.J., Littman D.R., Landau N.R.;
RT "Identification of a major co-receptor for primary isolates of
HIV-1.";
RL Nature 381:661-666(1996).
RN [9]
RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
RX MEDLINE-96260018; PubMed-8649512;
RA Dragic T., Litwin V., Allaway G.P., Martin S.R., Huang Y.,
RA Nagashima K.A., Cayanan C., Maddon P.J., Koup R.A., Moore J.P.,
RA Paxton W.A.;
RT "HIV-1 entry into CD4+ cells is mediated by the chemokine receptor
CC-CKR-5.";
RL Nature 381:667-673(1996).
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION. ACTS AS CO-RECEPTOR WITH CD4 FOR PRIMARY NON-
CC SYNCYTIIUM-INDUCING STRAINS (NSI) (MACROPHAGE-TROPIC) OF HIV-1

```

VIRUS. IT PROMOTES ENV-MEDIATED FUSION OF THE VIRUS.
 -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 -!- TISSUE SPECIFICITY: FOUND IN PROMYELOCYTIC CELLS.
 -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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 DR EMBL; X91492; CAA62796.1; -
 DR EMBL; U54994; AAC50598.1; -
 DR EMBL; U57840; AAB17071.1; -
 DR EMBL; U56626; AAB57793.1; -
 DR EMBL; U83326; AAC51797.1; -
 DR EMBL; AF011500; AAB65700.1; -
 DR EMBL; AF011501; AAB65701.1; -
 DR EMBL; AF011502; AAB65702.1; -
 DR EMBL; AF011503; AAB65703.1; -
 DR EMBL; AF011505; AAB65705.1; -
 DR EMBL; AF011506; AAB65706.1; -
 DR EMBL; AF011507; AAB65707.1; -
 DR EMBL; AF011508; AAB65708.1; -
 DR EMBL; AF011509; AAB65709.1; -
 DR EMBL; AF011510; AAB65710.1; -
 DR EMBL; AF011511; AAB65711.1; -
 DR EMBL; AF011512; AAB65712.1; -
 DR EMBL; AF011513; AAB65713.1; -
 DR EMBL; AF011514; AAB65714.1; -
 DR EMBL; AF011515; AAB65715.1; -
 DR EMBL; AF011517; AAB65717.1; -
 DR EMBL; AF011518; AAB65718.1; -
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 DR EMBL; AF011524; AAB65724.1; -
 DR EMBL; AF011525; AAB65725.1; -
 DR EMBL; AF011526; AAB65726.1; -
 DR EMBL; AF011527; AAB65727.1; -
 DR EMBL; AF011528; AAB65728.1; -
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 DR EMBL; AF011531; AAB65731.1; -
 DR EMBL; AF011532; AAB65732.1; -
 DR EMBL; AF011533; AAB65733.1; -
 DR EMBL; AF011535; AAB65735.1; -
 DR EMBL; AF011537; AAB65737.1; -
 DR EMBL; AF011538; AAB65738.1; -
 DR GCRDb; GCR_1923; -
 DR GCRDb; GCR_1927; -
 DR GCRDb; GCR_2116; -
 DR GCRDb; GCR_2454; -
 DR GCRDb; GCR_2497; -
 DR MIN; 601373; -
 DR InterPro; IPR000276; -
 DR InterPro; IPR000355; -
 DR InterPro; IPR002240; -
 DR Pfam; PF00001; 7un_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01110; CHEMOKINER5.
 DR PROSITE; PS00237; G-PROTEIN RECF_F1_1; 1.
 DR PROSITE; PS0262; G-PROTEIN RECF_F2_1; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.
 KW DOMAIN 1 30
 FT TRANSMEM 31 58
 FT DOMAIN 59 68
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89
 FT 2 (POTENTIAL).

FT DOMAIN 90 102
 FT TRANSMEM 103 124
 FT DOMAIN 125 141
 FT TRANSMEM 142 166
 FT DOMAIN 167 198
 FT TRANSMEM 199 218
 FT DOMAIN 219 235
 FT TRANSMEM 236 260
 FT DOMAIN 261 277
 FT TRANSMEM 278 301
 FT DOMAIN 302 352
 FT DISULFID 101 178
 FT CARBOHYD 268 268
 FT VARIANT 10 10
 FT VARIANT 31 31
 FT VARIANT 34 34
 FT VARIANT 62 62
 FT VARIANT 68 68
 FT VARIANT 95 95
 FT VARIANT 97 97
 FT VARIANT 122 122
 FT VARIANT 158 158
 FT VARIANT 176 176
 FT VARIANT 177 177
 Query Match 57.1%; Score 44.5; DB 1; Length 352;
 Best Local Similarity 52.9%; Pred. No. 0.58;
 Matches 9; Conservative 5; Mismatches 2; Indels 1; Gaps 1;
 QY 1 KTLVQAOON-SRRHRAIR 16
 Db 219 KTLRCRCNKRHRAVR 235
 RESULT 13
 CCR5_HYLL
 ID CCR5_HYLL STANDARD; PRT; 352 AA.
 AC 097883;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CCR-5) (CCR5).
 GN CCR5 OR CMKBR5.
 OS Hylobates leucogenys (White-cheeked gibbon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
 OX NCBI_TaxID=61853;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang Y.-W., Zhang Y.-P.;
 RT "Sequence evolution of chemokine receptor CCR5 gene in primates."; Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA, MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR DIFFERENTIATION.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT CARBOHYD 268 268 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 241 241 M -> I (IN REF. 3).
FT CONFLICT 292 292 I -> M (IN REF. 3).
SQ SEQUENCE 352 AA; 58B96C85909FACB2 CRC64;

Query Match 57.1%; Score 44.5; DB 1; Length 352;
Best Local Similarity 52.9%; Pred. No. 0.58;
Matches 9; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 KTLVQAOQN-SKRHKAIR 16
| | | | | | | | | |
Db 219 KTLRCRNEKKRHRAVR 235

RESULT 15
CKR5_PANTR STANDARD; PRT; 352 AA.
AC P56440; O02778;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-CR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKBR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RX SEQUENCE FROM N.A.
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharron M., Samson M., Lu Z.H.; Clements J.E.; Murphy-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains."
RT Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
RN [2]
RX SEQUENCE FROM N.A.
RA Zimmerman P.A., Buckler-White A., Alkhatib G.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RX SEQUENCE FROM N.A.
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA Ho D.D.;
RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism."
RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
RN [4]
RX SEQUENCE FROM N.A.
RA MEDLINE=97426118; PubMed=9282822;
RA Zacharova V., Zachar V., Goustin A.S.;
RT "Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural
RT HIV type 1 host."
RL AIDS Res. Hum. Retroviruses 13:1159-1161(1997).
RN [5]
RX SEQUENCE FROM N.A.
RA MEDLINE=98090115; PubMed=9430250;
RA Pretet J.-L., Zerbib A., Girard J.-G., Butor C.;
RT "Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1."
RL AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
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CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; AF005663; AAB62557.1; -
DR EMBL; U94329; AAB58446.1; -
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DR EMBL; U89797; AAC03717.1; -
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DR GCRDB; GCR_2432; -
DR InterPro; IPR000276; -
DR InterPro; IPR000355; -
DR InterPro; IPR002240; -
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01110; CHEMOKINER5.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT CARBOHYD 268 268 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 123 123 T -> S (IN REF. 1).
SQ SEQUENCE 352 AA; 40539 MW; 4A33E698B80FE34C CRC64;

Query Match 57.1%; Score 44.5; DB 1; Length 352;
Best Local Similarity 52.9%; Pred. No. 0.58;
Matches 9; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 KTLVQAOQN-SKRHKAIR 16
| | | | | | | | | |
Db 219 KTLRCRNEKKRHRAVR 235

Search completed: May 23, 2001, 15:36:20
Job time: 651 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:35:16 ; Search time 189.03 Seconds
(without alignments)
9.921 Million cell updates/sec

Title: US-08-887-977-10_COPY_230_245

Perfect score: 78

Sequence: 1 KTLVQAQNSKRHKRAIR 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_15:*

- 1: sp.archaea:*
- 2: sp.bacteria:*
- 3: sp.fungi:*
- 4: sp.human:*
- 5: sp.invertebrate:*
- 6: sp.mammal:*
- 7: sp.mhc:*
- 8: sp.organelle:*
- 9: sp.phase:*
- 10: sp.plant:*
- 11: sp.rodent:*
- 12: sp.unclassified:*
- 13: sp.vertebrate:*
- 14: sp.virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	75	96.2	367	11	Q9R1V0	Q9rlv0 mus musculu
2	49	62.8	369	4	Q9U0Q6	Q9uqg6 homo sapien
3	48.5	62.2	339	6	Q9TQU7	Q9tqu7 cercopithec
4	47.5	60.9	339	6	Q9TUS4	Q9tus4 lemur varie
5	47.5	60.9	339	6	Q9TUS3	Q9tus3 lemur catia
6	47.5	60.9	339	6	Q9TUS2	Q9tus2 lemur catia
7	47.5	60.9	339	6	Q9TUS1	Q9tus1 lemur varie
8	47.5	60.9	339	6	Q9TQU3	Q9tqu3 lemur catia
9	44.5	57.1	140	4	Q9S9S0	Q9s9s0 homo sapien
10	44.5	57.1	316	6	Q9TUV7	Q9tuv7 saguinus sp
11	44.5	57.1	333	4	O14694	O14694 homo sapien
12	44.5	57.1	334	6	Q9TU07	Q9tuq7 erythrocebu
13	44.5	57.1	339	4	Q9UN28	Q9un28 homo sapien
14	44.5	57.1	339	4	Q9UN27	Q9un27 homo sapien
15	44.5	57.1	339	4	Q9UN26	Q9un26 homo sapien
16	44.5	57.1	339	4	Q9UN25	Q9un25 homo sapien
17	44.5	57.1	339	4	Q9UN24	Q9un24 homo sapien
18	44.5	57.1	339	4	Q9UN23	Q9un23 homo sapien
19	44.5	57.1	339	4	Q9UBT9	Q9ubt9 homo sapien

20	44.5	57.1	339	4	Q9UBJ7	Q9ubj7 homo sapien
21	44.5	57.1	339	6	Q9TUX1	Q9tux1 hyllobates c
22	44.5	57.1	339	6	Q9TUX0	Q9tux0 hyllobates c
23	44.5	57.1	339	6	Q9TUN9	Q9tun9 hyllobates c
24	44.5	57.1	339	6	Q9TUN8	Q9tun8 gorilla gor
25	44.5	57.1	339	6	Q9TUN7	Q9tun7 pan troglod
26	44.5	57.1	339	6	Q9TUN6	Q9tun6 pan troglod
27	44.5	57.1	339	6	Q9TUN5	Q9tun5 pan troglod
28	44.5	57.1	339	6	Q9TUN4	Q9tun4 pan troglod
29	44.5	57.1	339	6	Q9TUN3	Q9tun3 pongo pygma
30	44.5	57.1	339	6	Q9TUN2	Q9tun2 saguinus sp
31	44.5	57.1	339	6	Q9TUN1	Q9tun1 saguinus sp
32	44.5	57.1	339	6	Q9TUW0	Q9tuw0 saguinus sp
33	44.5	57.1	339	6	Q9TUV9	Q9tuv9 saguinus sp
34	44.5	57.1	339	6	Q9TUV8	Q9tuv8 saguinus sp
35	44.5	57.1	339	6	Q9TUV6	Q9tuv6 saguinus sp
36	44.5	57.1	339	6	Q9TUV5	Q9tuv5 saguinus sp
37	44.5	57.1	339	6	Q9TUV2	Q9tuv2 alouatta ca
38	44.5	57.1	339	6	Q9TUV1	Q9tuv1 aotus trivi
39	44.5	57.1	339	6	Q9TUV0	Q9tuv0 aotus trivi
40	44.5	57.1	339	6	Q9TUU9	Q9tuu9 cercopithec
41	44.5	57.1	339	6	Q9TUU8	Q9tuu8 cercopithec
42	44.5	57.1	339	6	Q9TUU7	Q9tuu7 macaca fusc
43	44.5	57.1	339	6	Q9TUU6	Q9tuu6 macaca fusc
44	44.5	57.1	339	6	Q9TUU5	Q9tuu5 macaca fusc
45	44.5	57.1	339	6	Q9TUU4	Q9tuu4 macaca mula

ALIGNMENTS

RESULT 1

Q9R1V0 ID Q9R1V0 PRELIMINARY; PRT; 367 AA.

AC Q9R1V0; 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)

DE CC CHEMOKINE LARC SPECIFIC RECEPTOR.

GN MCCR6.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Tanaka Y.;

RT "Molecular Cloning of Murine Homologue of CCR6, the Specific Receptor for CC Chemokine LARC."

RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB016031; BAA82443.1; -

DR INTERPRO; IPR000190; -

DR INTERPRO; IPR000276; -

DR INTERPRO; IPR000355; -

DR PFAM; PF000001; 7tm.1; 1.

DR PRINTS; PR00237; GPCRHDOPSN.

DR PRINTS; PR00635; ANGIOTENSINR.

DR PRINTS; PR00657; CCHEMOKINR.

DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.

KW Receptor.

SQ SEQUENCE 367 AA; 42082 MW; 207FD98B2F7A6DD3 CRC64;

Query Match 96.2%; Score 75; DB 11; Length 367;

Best Local Similarity 93.8%; Pred. No. 6.8e-06;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHKRAIR 16

|||||

Db 231 KTLVQAQNSKRHKRAIR 246

RESULT 2

FT NON_TER 1 1
 FT NON_TER 339 339
 SQ SEQUENCE 339 AA; 38664 MW; B53CFB4F66B09E1A CRC64;

Query Match 60.9%; Score 47.5; DB 6; Length 339;
 Best Local Similarity 58.8%; Pred. No. 0.73;
 Matches 10; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

OY 1 KTLVQAQN-SKHKRAIR 16
 ||||:| |||||:
 Db 212 KTLRCRNEKKRHKAVR 228

RESULT 5

O9TUS3 PRELIMINARY; PRT; 339 AA.

AC O9TUS3;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
 GN CCR5.

OS Lemur catta (Ring-tailed lemur).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Strepsirrhini; Lemnridae; Lemur.
 OX NCBI_TaxID=9447;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF162010; AAD47765.1; -

DR INTERPRO; IPR000248; -

DR INTERPRO; IPR000276; -

DR INTERPRO; IPR000355; -

DR INTERPRO; IPR001277; -

DR INTERPRO; IPR002236; -

DR INTERPRO; IPR002237; -

DR INTERPRO; IPR002238; -

DR INTERPRO; IPR002240; -

DR PFAM; PF00001; 7tm1.1;

DR PRINTS; PR00237; GPCRHHODPSN.

DR PRINTS; PR00241; ANGIOTENSINR.

DR PRINTS; PR00645; LCRIORPHANR.

DR PRINTS; PR00657; CCHEMOKINER.

DR PRINTS; PR01106; CHEMOKINER1.

DR PRINTS; PR01107; CHEMOKINER2.

DR PRINTS; PR01108; CHEMOKINER3.

DR PRINTS; PR01110; CHEMOKINER5.

DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.

KW Receptor.

FT NON_TER 1 1

FT NON_TER 339 339

SQ SEQUENCE 339 AA; 38678 MW; 4CF660C5648C8DC1 CRC64;

Query Match 60.9%; Score 47.5; DB 6; Length 339;
 Best Local Similarity 58.8%; Pred. No. 0.73;
 Matches 10; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

OY 1 KTLVQAQN-SKHKRAIR 16
 ||||:| |||||:
 Db 212 KTLRCRNEKKRHKAVR 228

RESULT 6

O9TUS2 PRELIMINARY; PRT; 339 AA.

AC O9TUS2;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)

DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
 GN CCR5.

OS Lemur catta (Ring-tailed lemur).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Strepsirrhini; Lemnridae; Lemur.

OX NCBI_TaxID=9447;
 RN [1]

RP SEQUENCE FROM N.A.

RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF162012; AAD47767.1; -

DR INTERPRO; IPR000248; -

DR INTERPRO; IPR000276; -

DR INTERPRO; IPR000355; -

DR INTERPRO; IPR001277; -

DR INTERPRO; IPR002236; -

DR INTERPRO; IPR002237; -

DR INTERPRO; IPR002238; -

DR INTERPRO; IPR002240; -

DR PFAM; PF00001; 7tm1.1;

DR PRINTS; PR00237; GPCRHHODPSN.

DR PRINTS; PR00241; ANGIOTENSINR.

DR PRINTS; PR00645; LCRIORPHANR.

DR PRINTS; PR00657; CCHEMOKINER.

DR PRINTS; PR01106; CHEMOKINER1.

DR PRINTS; PR01107; CHEMOKINER2.

DR PRINTS; PR01108; CHEMOKINER3.

DR PRINTS; PR01110; CHEMOKINER5.

DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.

KW Receptor.

FT NON_TER 1 1

FT NON_TER 339 339

SQ SEQUENCE 339 AA; 38646 MW; BA7E73C6F05E2CA4 CRC64;

Query Match 60.9%; Score 47.5; DB 6; Length 339;
 Best Local Similarity 58.8%; Pred. No. 0.73;
 Matches 10; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

OY 1 KTLVQAQN-SKHKRAIR 16
 ||||:| |||||:
 Db 212 KTLRCRNEKKRHKAVR 228

RESULT 7

O9TUS1 PRELIMINARY; PRT; 339 AA.

AC O9TUS1;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
 GN CCR5.

OS Lemur variegatus (Ruffed lemur) (Varecia variegata).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Strepsirrhini; Lemnridae; Varecia.

OX NCBI_TaxID=9455;
 RN [1]

RP SEQUENCE FROM N.A.

RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF162013; AAD47768.1; -

DR INTERPRO; IPR000248; -

DR INTERPRO; IPR000276; -

DR INTERPRO; IPR000355; -

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DR INTERPRO: IPR001277; -
DR INTERPRO: IPR002236; -
DR INTERPRO: IPR002237; -
DR INTERPRO: IPR002238; -
DR INTERPRO: IPR002240; -
DR PFAM: PF00001; 7tm1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PRINTS: PR00241; ANGIOTENSINR.
DR PRINTS: PR00645; LCLORPHANR.
DR PRINTS: PR00657; CCHEMOKINER.
DR PRINTS: PR01106; CHEMOKINER1.
DR PRINTS: PR01107; CHEMOKINER2.
DR PRINTS: PR01108; CHEMOKINER3.
DR PRINTS: PR01110; CHEMOKINER5.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 38682 MW; 6A770AFCAF7E02F6 CRC64;

Query Match 60.9%; Score 47.5; DB 6; Length 339;
Best Local Similarity 58.8%; Pred. No. 0.73; Mismatches 4; Indels 1; Gaps 1;
Matches 10; Conservative 4;

OY 1 KTLVQAQN-SKRHKAIR 16
DB 212 KTLRCRNEKRRHKAVR 228
||||: :| |||||:|

RESULT 8
O9TQU3 PRELIMINARY; PRT; 339 AA.
AC O9TQU3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN CCR5.
OS Lemur catta (Ring-tailed lemur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Lemuridae; Lemur.
OX NCBI_TaxID=9447;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF162011; AAD47766.1; -
DR EMBL: AF162008; AAD47763.1; -
DR INTERPRO: IPR000248; -
DR INTERPRO: IPR000276; -
DR INTERPRO: IPR000355; -
DR INTERPRO: IPR001277; -
DR INTERPRO: IPR002236; -
DR INTERPRO: IPR002237; -
DR INTERPRO: IPR002238; -
DR PFAM: PF00001; 7tm1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PRINTS: PR00241; ANGIOTENSINR.
DR PRINTS: PR00645; LCLORPHANR.
DR PRINTS: PR00657; CCHEMOKINER.
DR PRINTS: PR01106; CHEMOKINER1.
DR PRINTS: PR01107; CHEMOKINER2.
DR PRINTS: PR01108; CHEMOKINER3.
DR PRINTS: PR01110; CHEMOKINER5.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 38682 MW; 6A770AFCAF7E02F6 CRC64;

Query Match 60.9%; Score 47.5; DB 6; Length 339;
Best Local Similarity 58.8%; Pred. No. 0.73; Mismatches 4; Indels 1; Gaps 1;
Matches 10; Conservative 4;

OY 1 KTLVQAQN-SKRHKAIR 16
DB 212 KTLRCRNEKRRHKAVR 228
||||: :| |||||:|

RESULT 8
O9TQU3 PRELIMINARY; PRT; 339 AA.
AC O9TQU3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN CCR5.
OS Lemur catta (Ring-tailed lemur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Lemuridae; Lemur.
OX NCBI_TaxID=9447;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF162011; AAD47766.1; -
DR EMBL: AF162008; AAD47763.1; -
DR INTERPRO: IPR000248; -
DR INTERPRO: IPR000276; -
DR INTERPRO: IPR000355; -
DR INTERPRO: IPR001277; -
DR INTERPRO: IPR002236; -
DR INTERPRO: IPR002237; -
DR INTERPRO: IPR002238; -
DR PFAM: PF00001; 7tm1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PRINTS: PR00241; ANGIOTENSINR.
DR PRINTS: PR00645; LCLORPHANR.
DR PRINTS: PR00657; CCHEMOKINER.
DR PRINTS: PR01106; CHEMOKINER1.
DR PRINTS: PR01107; CHEMOKINER2.
DR PRINTS: PR01108; CHEMOKINER3.
DR PRINTS: PR01110; CHEMOKINER5.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 38682 MW; 6A770AFCAF7E02F6 CRC64;

Query Match 60.9%; Score 47.5; DB 6; Length 339;
Best Local Similarity 58.8%; Pred. No. 0.73; Mismatches 4; Indels 1; Gaps 1;
Matches 10; Conservative 4;

OY 1 KTLVQAQN-SKRHKAIR 16
DB 212 KTLRCRNEKRRHKAVR 228
||||: :| |||||:|

RESULT 9
O95950 PRELIMINARY; PRT; 140 AA.
AC O95950;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE MCP-1 RECEPTOR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-MONOCYTIC LINE;
RX MEDLINE-97211835; PubMed-9058802;
RA Polentarutti N., Allavena P., Bianchi G., Giardina G., Basile A.,
RA Sozzani S., Mantovani A., Introna M.;
RT "IL-2-regulated expression of the monocyte chemotactic protein-1
RT receptor (CCR2) in human NK cells: characterization of a predominant
RT 3.4-kilobase transcript containing CCR2B and CCR2A sequences.";
RL J. Immunol. 158:2689-2694 (1997).
DR EMBL: X95583; CAA64835.1; -
DR INTERPRO: IPR000276; -
DR INTERPRO: IPR002238; -
DR PFAM: PF00001; 7tm1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PRINTS: PR01108; CHEMOKINER3.
KW Receptor.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 140 AA; 16273 MW; 63BE2A527757D8C2 CRC64;

Query Match 57.1%; Score 44.5; DB 4; Length 140;
Best Local Similarity 52.9%; Pred. No. 1.1; Mismatches 5; Indels 1; Gaps 1;
Matches 9; Conservative 5;

OY 1 KTLVQAQN-SKRHKAIR 16
DB 7 KTLRCRNEKRRHKAVR 23
||||: :| ||||:|

RESULT 10
O9TUV7 PRELIMINARY; PRT; 316 AA.
AC O9TUV7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN CCR5.
OS Saginus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saginus.
OX NCBI_TaxID=100754;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF162011; AAD47766.1; -
DR EMBL: AF162008; AAD47763.1; -
DR INTERPRO: IPR000248; -
DR INTERPRO: IPR000276; -
DR INTERPRO: IPR000355; -
DR INTERPRO: IPR001277; -
DR INTERPRO: IPR002236; -
DR INTERPRO: IPR002237; -
DR INTERPRO: IPR002238; -
DR PFAM: PF00001; 7tm1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PRINTS: PR00241; ANGIOTENSINR.
DR PRINTS: PR00645; LCLORPHANR.
DR PRINTS: PR00657; CCHEMOKINER.
DR PRINTS: PR01106; CHEMOKINER1.
DR PRINTS: PR01107; CHEMOKINER2.
DR PRINTS: PR01108; CHEMOKINER3.
DR PRINTS: PR01110; CHEMOKINER5.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 38682 MW; 6A770AFCAF7E02F6 CRC64;
```

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161930; AAD47687.1; -
DR INTERPRO; IPR000248; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR000355; -
DR INTERPRO; IPR000923; -
DR INTERPRO; IPR002236; -
DR INTERPRO; IPR002237; -
DR INTERPRO; IPR002240; -
DR PFAM; PF00001; 7tm.1.1;
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00241; ANGIOTENSINR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01106; CHEMOKINER1.
DR PRINTS; PR01107; CHEMOKINER2.
DR PRINTS; PR01110; CHEMOKINER5.
DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 1
FT NON_TER 316
SQ SEQUENCE 316 AA; 4DAD95C3848F04EA CRC64;

Query Match 57.1%; Score 44.5; DB 6; Length 316;
Best Local Similarity 52.9%; Pred. No. 2.4;
Matches 9; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 KTLVQAQN-SKRHKAIR 16
| | | | : : | | | | : :
Db 189 KTLRCRNEKKRRAVR 205

RESULT 11

OL14694 ID O14694 PRELIMINARY; PRT; 333 AA.
AC O14694;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CCR5 RECEPTOR (FRAGMENT).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA Ho D.D.;
RL AIDS Res. Hum. Retroviruses 0:0-0(1997).
DR EMBL; AF011504; AAB65704.1; -
DR INTERPRO; IPR000190; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR000355; -
DR INTERPRO; IPR000127; -
DR INTERPRO; IPR002236; -
DR INTERPRO; IPR002237; -
DR INTERPRO; IPR002238; -
DR INTERPRO; IPR002240; -
DR PFAM; PF00001; 7tm.1.1;
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00635; ANGIOTENSINR.
DR PRINTS; PR00645; LCR1ORPHANR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01106; CHEMOKINER1.
DR PRINTS; PR01107; CHEMOKINER2.
DR PRINTS; PR01108; CHEMOKINER3.
DR PRINTS; PR01110; CHEMOKINER5.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
FT NON_TER 333
SQ SEQUENCE 333 AA; 38174 MW; AEFBA07A67893AEB CRC64;

Query Match 57.1%; Score 44.5; DB 4; Length 333;
Best Local Similarity 52.9%; Pred. No. 2.6;
Matches 9; Conservative 5; Mismatches 2; Indels 1; Gaps 1;
QY 1 KTLVQAQN-SKRHKAIR 16
| | | | : : | | | | : :
Db 200 KTLRCRNEKKRRAVR 216
RESULT 12
Q9TUQ7 ID Q9TUQ7 PRELIMINARY; PRT; 334 AA.
AC Q9TUQ7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN CCR5.
OS Erythrocebus patas (Red quonon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Erythrocebus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162049; AAD47804.1; -
DR INTERPRO; IPR000248; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR000355; -
DR INTERPRO; IPR001277; -
DR INTERPRO; IPR002236; -
DR INTERPRO; IPR002237; -
DR INTERPRO; IPR002240; -
DR PFAM; PF00001; 7tm.1.1;
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00241; ANGIOTENSINR.
DR PRINTS; PR00645; LCR1ORPHANR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01106; CHEMOKINER1.
DR PRINTS; PR01107; CHEMOKINER2.
DR PRINTS; PR01110; CHEMOKINER5.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 1
FT NON_TER 334
SQ SEQUENCE 334 AA; 38460 MW; B19D0CEC667B69F0 CRC64;

Query Match 57.1%; Score 44.5; DB 6; Length 334;
Best Local Similarity 52.9%; Pred. No. 2.6;
Matches 9; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 KTLVQAQN-SKRHKAIR 16
| | | | : : | | | | : :
Db 207 KTLRCRNEKKRRAVR 223

RESULT 13

Q9UN28 ID Q9UN28 PRELIMINARY; PRT; 339 AA.
AC Q9UN28;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN CCR5.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF161913; RAD47670.1; -
DR INTERPRO: IPR000190; -
DR INTERPRO: IPR000248; -
DR INTERPRO: IPR000276; -
DR INTERPRO: IPR000355; -
DR INTERPRO: IPR001277; -
DR INTERPRO: IPR002236; -
DR INTERPRO: IPR002237; -
DR INTERPRO: IPR002240; -
DR PFAM: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODOPS.
DR PRINTS: PR00241; ANGIOTENSINR.
DR PRINTS: PR00635; ANGIOTENSINR.
DR PRINTS: PR00645; LCR1ORPHANR.
DR PRINTS: PR00657; CCHEMOKINER.
DR PRINTS: PR01106; CHEMOKINER1.
DR PRINTS: PR01107; CHEMOKINER2.
DR PRINTS: PR01110; CHEMOKINER5.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39183 MW; 56C819F92D6DB1A6 CRC64;

Query Match 57.1%; Score 44.5; DB 4; Length 339;
Best Local Similarity 52.9%; Pred. No. 2.6;
Matches 9; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 KTLVQAOON-SKRHKAIR 16
||||:| |||:|
DB 212 KTLRCRNEKRRRAVR 228

RESULT 14
Q9UN27
ID Q9UN27 PRELIMINARY; PRT; 339 AA.
AC Q9UN27;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF161914; AAD47671.1; -
DR INTERPRO: IPR000190; -
DR INTERPRO: IPR000248; -
DR INTERPRO: IPR000276; -
DR INTERPRO: IPR000355; -
DR INTERPRO: IPR001277; -
DR INTERPRO: IPR002236; -
DR INTERPRO: IPR002237; -
DR PFAM: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODOPS.
DR PRINTS: PR00241; ANGIOTENSINR.
DR PRINTS: PR00635; ANGIOTENSINR.
DR PRINTS: PR00645; LCR1ORPHANR.
DR PRINTS: PR00657; CCHEMOKINER.
DR PRINTS: PR01106; CHEMOKINER1.
DR PRINTS: PR01107; CHEMOKINER2.
DR PRINTS: PR01110; CHEMOKINER5.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39162 MW; A56369FE0529F4AB CRC64;

Query Match 57.1%; Score 44.5; DB 4; Length 339;
Best Local Similarity 52.9%; Pred. No. 2.6;
Matches 9; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 KTLVQAOON-SKRHKAIR 16
||||:| |||:|
DB 212 KTLRCRNEKRRRAVR 228

RESULT 14
Q9UN27
ID Q9UN27 PRELIMINARY; PRT; 339 AA.
AC Q9UN27;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF161914; AAD47671.1; -
DR INTERPRO: IPR000190; -
DR INTERPRO: IPR000248; -
DR INTERPRO: IPR000276; -
DR INTERPRO: IPR000355; -
DR INTERPRO: IPR001277; -
DR INTERPRO: IPR002236; -
DR INTERPRO: IPR002237; -
DR PFAM: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODOPS.
DR PRINTS: PR00241; ANGIOTENSINR.
DR PRINTS: PR00635; ANGIOTENSINR.
DR PRINTS: PR00645; LCR1ORPHANR.
DR PRINTS: PR00657; CCHEMOKINER.
DR PRINTS: PR01106; CHEMOKINER1.
DR PRINTS: PR01107; CHEMOKINER2.
DR PRINTS: PR01110; CHEMOKINER5.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39162 MW; A56369FE0529F4AB CRC64;

Query Match 57.1%; Score 44.5; DB 4; Length 339;
Best Local Similarity 52.9%; Pred. No. 2.6;
Matches 9; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 KTLVQON-SRRKAIR 16
| | | : : | | | : | |
Db 212 KTLRCRNEKKRRRAVR 228

Search completed: May 23, 2001, 15:35:16
Job time: 622 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:28:32 ; Search time 184.73 Seconds
(without alignments)
7.736 Million cell updates/sec

Title: US-08-887-977-10_COPY_246_270

Perfect score: 119

Sequence: 1 VIIAVVFLACQIPHNMLVTA 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A_Geneseq_0401.*
1: /SID56/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID56/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID56/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SID56/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SID56/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SID56/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SID56/gcgdata/geneseq/geneseq/AA1986.DAT.*
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20: /SID56/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID56/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID56/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	119	100.0	365	19 W48086	Human dendritic ce
2	119	100.0	365	21 Y97077	Primate (human) ch
3	74	62.2	350	13 R27791	Interleukin-8 rece
4	74	62.2	350	16 R68811	Interleukin-8 rece
5	74	62.2	350	16 R80756	Interleukin 8 rece
6	74	62.2	350	16 R80951	Recombinant high a
7	74	62.2	350	17 B09389	Human IL-8 recepto
8	74	62.2	354	15 R53932	Interleukin 8 (IL
9	74	62.2	355	13 R28272	Sequence in a high
10	74	62.2	355	14 R33420	Human IL-8 recepto
11	74	62.2	355	16 R80950	Recombinant high a

12	74	62.2	355	17 B09990	Human IL-8 recepto
13	74	62.2	358	16 R80952	Recombinant high a
14	74	62.2	360	13 R28273	Sequence in a low
15	74	62.2	360	16 R80758	Interleukin 8 rece
16	74	62.2	360	16 R80953	Recombinant high a
17	74	62.2	1060	16 R70123	IL8-R type 1-GBP 1
18	74	62.2	1064	16 R70124	IL8-R type 2-GBP 1
19	73	61.3	358	13 R28274	Sequence in a lowh
20	72	60.5	312	15 R48717	G-protein coupled
21	72	60.5	312	17 W02689	G-protein coupled
22	70	58.8	371	19 W69599	Human G-protein co
23	70	58.8	371	19 W69970	Human 7-transmembr
24	70	58.8	371	21 Y11302	Human orphan G pro
25	70	58.8	371	21 B02836	Human G protein co
26	70	58.8	380	20 Y06215	Human G protein co
27	67	56.3	382	20 Y06214	Mouse G protein co
28	63	52.9	358	15 R53745	Partial sequence o
29	63	52.9	358	21 B21689	Human 7TM receptor
30	63	52.9	359	15 R53747	Seven transmembran
31	63	52.9	359	19 W48728	Murine V31 seven t
32	63	52.9	359	21 B21691	Murine 7TM recepto
33	63	52.9	361	20 W97348	An Epstein-Barr vi
34	63	52.9	378	15 R54079	Epstein Barr virus
35	63	52.9	378	15 R53744	Putative seven tra
36	63	52.9	378	19 W48724	Human V31 seven tr
37	63	52.9	378	19 W56164	G-protein coupled
38	63	52.9	378	19 W53622	Epstein Barr virus
39	63	52.9	378	21 B21688	Human 7TM receptor
40	63	52.9	378	21 B21699	7TM receptor prote
41	63	52.9	378	21 Y90629	Human G protein-co
42	63	52.9	378	21 Y90663	Human mutant G pro
43	63	52.9	378	22 B50859	Human CCR7, Homo
44	63	52.9	410	15 R53743	Putative seven tra
45	63	52.9	410	19 W48723	Polypeptide sequen

ALIGNMENTS

RESULT 1

ID	W48086	standard; Protein; 365 AA.
XX	XX	
AC	W48086;	
XX	XX	
DT	11-JUN-1998	(first entry)
XX	XX	Human dendritic cell chemokine receptor.
DE	DE	
XX	XX	Human; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta;
KW	KW	receptor; dendritic cell; macrophage; inflammation; asthma.
XX	XX	
OS	OS	Homo sapiens.
XX	XX	
FH	FH	Key Location/Qualifiers
FT	FT	Misc-difference 193
FT	FT	/note= "encoded by CAN"
XX	XX	
PN	PN	W09801557-A2.
XX	XX	
PD	PD	15-JAN-1998.
XX	XX	
PF	PF	02-JUL-1997; 97WO-US10819.
XX	XX	
PR	PR	04-JUN-1997; 97US-Q048593.
PR	PR	05-JUL-1996; 96US-0675814.
PR	PR	11-OCT-1996; 96US-0028329.
XX	XX	
PA	PA	(SCHE) SCHERING CORP.
XX	XX	
PI	PI	Gish KC, Schall TJ, Vicari A, Wang W, Zlotnik A;
XX	XX	WPI; 1998-101054/09.
DR	DR	

PT polypeptide and corresp. antibodies and DNA - useful as
 PT diagnostic and screening agents, and for treating inflammation or
 PS PF4AR-mediated disorders

XX Claim 7; Fig 2; 78pp; English.

XX A cDNA library constructed from human neutrophil mRNA in the mammalian
 CC expression vector pRK5B was transfected into COS-7 cells as pools of
 CC 2500 clones. One positive pool from the first 58 transfections was
 CC partitioned into smaller pools until a pure clone (pRK5B.il8r1.1)
 CC was obtained. The ORF encodes a protein of 350 amino acids which
 CC shares several features with the G-protein coupled receptors of the
 CC rhodopsin superfamily, including 7 hydrophobic (transmembrane)
 CC domains. The IL-8 receptor is a preferred PF4AR superfamily member
 CC of the invention. See also Q29506 and Q37107.

XX Sequence 350 AA;

Query Match 62.2%; Score 74; DB 13; Length 350;
 Best Local Similarity 66.7%; Pred. No. 0.00047;
 Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VIIAVLVFLACQIPHNWLL 21
 || ||||| || | : ||: |||
 Db 243 vifavvlflcwpynlavl 263

RESULT 4

R68811 ID R68811 standard; Protein; 350 AA.

XX AC R68811;

DT 18-JUL-1995 (first entry)

XX Interleukin-8 receptor.

XX Interleukin-8 receptor; IL-8 receptor; PF4AR;

KW--platelet factor-superfamily receptor; neutrophil; chemotactic;
 KW inflammation; inflammatory disease; arthritis; emphysema; cystic;
 KW fibrosis; colitis; bronchitis; meningitis; therapeutic.

XX OS Homo sapiens.

XX PN W09428931-A.

XX PD 22-DEC-1994.

XX 07-JUN-1994; 94WO-US06380.

XX 11-JUN-1993; 93US-0076093.

XX (GETH) GENENTECH INC.

XX Chuntharapai A, Hebert C, Kim KJ, Lee J;

XX WPI; 1995-036114/05.

DR N-PSDB; Q80520.

XX Treatment of inflammatory disorders - by administering an
 PT antibody capable of binding a platelet factor 4 superfamily
 PT receptor polypeptide

XX Disclosure; Page 51-54; 83pp; English.

XX A cDNA library constructed from human neutrophil mRNA in pRK5B was
 CC transfected into COS-7 cells, and the cells were screened with 125I-
 CC IL-8. The DNA sequence of isolated cDNA clone pRK5B.il8r1.1,
 CC encoding human IL-8 receptor, is given in Q80520 and the predicted
 CC amino acid sequence in R68811. The receptor is used to raise
 CC antibodies that neutralize the activity of PF4AR, e.g. IL-8 receptor.

XX

SQ Sequence 350 AA;

Query Match 62.2%; Score 74; DB 16; Length 350;
 Best Local Similarity 66.7%; Pred. No. 0.00047;
 Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VIIAVLVFLACQIPHNWLL 21
 || ||||| || | : ||: |||
 Db 243 vifavvlflcwpynlavl 263

RESULT 5

R80756 ID R80756 standard; Protein; 350 AA.

XX AC R80756;

XX 26-MAR-1996 (first entry)

DT Interleukin 8 receptor A partial sequence.

XX Interleukin; IL-8; inflammation; psoriasis; dermatitis;

KW rheumatoid arthritis; inflammatory bowel disease;

KW chronic lung inflammation; treatment; antibody;

XX affinity purification; detection.

XX OS Homo sapiens.

XX PN US5440021-A.

XX 08-AUG-1995.

XX 29-MAR-1991; 91US-0677211.

XX 25-FEB-1994; 94US-0202056.

XX 29-MAR-1991; 91US-0677211.

XX (CHUN/) CHUNTHARAPAI A.

XX (HEBE/) HEBERT C.

XX (KIMK/) KIM K J.

XX (LEEJ/) LEE J.

XX Chuntharapai A, Hebert C, Kim KJ, Lee J;

XX WPI; 1995-283151/37.

DR N-PSDB; Q99006.

XX New antibodies against interleukin 8 type B receptor - used to treat
 PT or prevent inflammation, also for detecting receptor expression and
 PT purification.

XX Example 2; Columns 41-44; 62pp; English.

XX Antibodies directed against the interleukin-8 receptor B can be used
 CC to treat or prevent inflammation e.g. psoriasis, dermatitis,
 CC rheumatoid arthritis and particularly inflammatory bowel disease and
 CC chronic lung inflammation. When immobilised, these antibodies may
 CC be used to detect interleukin-8 receptor B expression in cells and
 CC tissues and for affinity purification of interleukin-8 receptor B
 CC from cells. A sequence encoding amino acids 23-314 of this fragment
 CC of the high affinity interleukin-8 receptor, was used to probe lambda
 CC gt10 cDNA libraries for the human interleukin-8 type B receptor.

XX Sequence 350 AA;

Query Match 62.2%; Score 74; DB 16; Length 350;
 Best Local Similarity 66.7%; Pred. No. 0.00047;
 Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VIIAVLVFLACQIPHNWLL 21
 || ||||| || | : ||: |||

Db 243 vifavvlflclwlpynlvll 263

RESULT 6
R80951
ID R80951 standard; Protein; 350 AA.

XX AC R80951;

XX DT 24-APR-1996 (first entry)

XX DE Recombinant high affinity interleukin-8 receptor subtype A.

XX KW IL-8A; IL-8B; receptor; monoclonal antibody; inflammatory disorder;
KW anaphylaxis; systemic lupus erythematosus; rheumatoid arthritis;
KW systemic necrotising vasculitis; psoriasis; asthma; allergy; ARDS;
KW adult respiratory distress syndrome; neutrophil detection.

XX OS Homo sapiens.

XX PN W09525126-A1.

XX PD 21-SEP-1995.

XX PF 09-MAR-1995; 95WO-US03032.

XX PR 02-MAY-1994; 94US-0237937.

XX PR 15-MAR-1994; 94US-0210250.

XX PA (REPK) REPLIGEN CORP.

XX PA (UYBO-) UNIV BOSTON.

XX PI Greenfield EA, Larosa GJ, Navarro J, Thomas KM;

XX PI Witt DT;

XX DR WPI; 1995-336945/43.

XX DR N-PSDB; Q99950.

XX PT Monoclonal antibody against recombinant IL-8 receptor polypeptide -

XX PT useful for treating inflammatory disorders, for detecting

XX PT neutrophil(s) and for isolating IL-8 receptor from liq.mixt.

XX PS Disclosure; Fig 2A-B; 74pp; English.

XX CC Monoclonal antibodies were raised against recombinant interleukin-8
XX CC (IL-8) receptor subtypes A and B from both human and rabbit sources
XX CC (R80950-53 encoded by Q9949-52). The A subtype receptor (IL-8rA) is
XX CC a high affinity receptor and the B subtype receptor (IL-8rB) is a
XX CC low affinity receptor. The monoclonal antibody (mAb) pref. binds to
XX CC the IL-8 binding domain thus blocking its activation. The mAbs are
XX CC useful for treating inflammatory disorders (see key words) and for
XX CC detecting the presence of neutrophils in a biological sample. The
XX CC mAbs are also useful in the isolation of IL-8 receptors from a mixture.

XX SQ Sequence 350 AA;

Query Match 62.2%; Score 74; DB 16; Length 350;
Best Local Similarity 66.7%; Pred. No. 0.00047;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VIIAVVLFLACQIPHNWLL 21

II IIII:II I:I:I:III

Db 243 vifavvlflclwlpynlvll 263

RESULT 7

B09989

ID B09989 standard; Protein; 350 AA.

XX AC B09989;

XX DT 20-OCT-2000 (first entry)

XX Human IL-8 receptor protein hIL8RA.

XX DE IL-8 receptor protein; hIL8RA; hIL8RB; human; interleukin-8; drug;
XX KW treatment; inflammatory disease; anti-tumor.

XX OS Homo sapiens.

XX PN JP08103276-A.

XX PD 23-APR-1996.

XX PF 06-OCT-1994; 94JP-0242534.

XX PR 06-OCT-1994; 94JP-0242534.

XX PA (TAKE) TAKEDA CHEM IND LTD.

XX WPI; 1996-253878/26.

XX DR N-PSDB; A40127.

XX Recombinant human interleukin 8 receptor protein, - its prepn. and
XX PT application.

XX Example 1; Fig 2; 22pp; Japanese.

XX CC This invention describes a novel expression vector which carries a DNA
XX CC encoding human interleukin 8 receptor protein and is expressed by
XX CC pAKKOL.11/hIL8RA or pAKKOL.11/hIL8RB. Also claimed are (I) CHO cell
XX CC containing the above expression vector, (II) the preparation of a
XX CC recombinant human interleukin 8 receptor protein in which the above CHO
XX CC cell is cultured under a condition enabling the expression of a DNA
XX CC coding human interleukin 8 receptor protein, (III) a CHO cell
XX CC containing a recombinant human interleukin 8 receptor protein which can
XX CC be prepared, by culturing the above CHO cell under a condition enabling
XX CC the expression of a DNA coding human interleukin 8 receptor protein or
XX CC its cell membrane fraction, (IV) a recombinant human interleukin 8
XX CC receptor protein isolated from a CHO cell containing the above
XX CC recombinant human interleukin 8 receptor protein, its partial peptide or
XX CC their salt, (V) the screening of human interleukin 8 receptor agonist or
XX CC antagonist in which the above CHO cell or its cell membrane fraction is
XX CC used or the above recombinant human interleukin 8 receptor protein, its
XX CC partial peptide or their salt is used (VI) a kit for screening the human
XX CC interleukin 8 receptor agonist or antagonist containing the above CHO
XX CC cell or its cell membrane fraction or the above recombinant human
XX CC interleukin 8 receptor protein, its partial peptide or their salt, (VII)
XX CC a human interleukin 8 receptor agonist or antagonist prepared by using
XX CC the above screening method or the above screening kit or its salt, (VII)
XX CC an activation promoter or a migration promoter of neutrophils containing
XX CC the above agonist or its salt, and an activation inhibitor or a migration
XX CC inhibitor containing the above antagonist or its salt. The agonist or the
XX CC antagonist can be used in drug compositions for the prevention and
XX CC treatment of inflammatory diseases and anti-tumor agents. The screening
XX CC method can select an agonist or an antagonist advantageously. This
XX CC sequence represents the human IL-8 receptor protein hIL8RA which is
XX CC described in the method of the invention.

XX SQ Sequence 350 AA;

Query Match 62.2%; Score 74; DB 17; Length 350;
Best Local Similarity 66.7%; Pred. No. 0.00047;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VIIAVVLFLACQIPHNWLL 21

II IIII:II I:I:I:III

Db 243 vifavvlflclwlpynlvll 263

RESULT 8

R53932

ID R53932 standard; Protein; 354 AA.

XX

AC R53932;
 XX 23-FEB-1995 (first entry)
 XX Interleukin 8 (IL-8) receptor.
 DE Interleukin; receptor; antiinflammatory; psoriasis; reperfusion;
 XX rheumatoid arthritis; allograft; graft rejection.
 KW Homo sapiens.
 XX
 XX JP06100595-A.
 PN 12-APR-1994.
 XX 27-MAY-1991; 91JP-0149245.
 XX 27-MAY-1991; 91JP-0149245.
 PR (UYBO-) UNIV BOSTON.
 XX WPI: 1994-156656/19.
 XX N-PSDB; Q63919.
 XX Recombinant interleukin-8 receptor polypeptide - having
 PT antiinflammatory properties
 XX
 XX Claim 1; Figure 1; 13pp; Japanese.
 PS
 XX Anti-inflammatory agents containing the interleukin-8 receptor
 CC polypeptide can be used for the treatment of psoriasis, rheumatoid
 CC arthritis and other acute and chronic inflammatory diseases,
 CC including reperfusion and allograft rejection.
 XX
 XX Sequence 354 AA;
 SQ

Query Match 62.2%; Score 74; DB 15; Length 354;
 Best Local Similarity 66.7%; Pred. No. 0.00048;
 Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 1 VIIAVLVFLACQIPHNMLL 21
 II IIII:II I :I:IIII
 Db 247 vifavvlflclwlpynlavl 267

RESULT 9
 R28272
 ID R28272 standard; Protein; 355 AA.
 XX AC R28272;
 XX 04-APR-1993 (first entry)
 XX Sequence in a high affinity recombinant rabbit interleukin-8
 DE (IL-8) receptor polypeptide in FR.
 XX IL-8 receptor polypeptide; G-protein-coupled receptor.
 KW Oryctolagus cuniculus.
 XX
 XX WO9218641-A.
 PN 29-OCT-1992.
 XX 10-APR-1992; 92WO-US02977.
 XX 10-APR-1991; 91US-0685101.
 PR 09-JUL-1991; 91US-0726608.
 PR 09-DEC-1991; 91US-0803842.
 XX (REPK) REPLIGEN CORP.
 PA (UYBO-) UNIV BOSTON.

XX Navarro J, Thomas KM, Witt DP;
 XX WPI: 1992-382123/46.
 DR N-PSDB; Q30011.
 XX Recombinant mammalian interleukin-8 receptor - used for screening
 PT interleukin-8 binding antagonists, used to treat inflammation
 XX
 XX Claim 2; Fig 1; 71pp; English.
 XX Rabbit high affinity IL-8 receptor gene was isolated from rabbit
 CC peritoneal neutrophils and used as a source of poly(A)+ RNA, to
 CC produce a rabbit neutrophil cDNA library. 250,000 recombinant
 CC plaques were screened for those which hybridized to an antisense
 CC oligonucleotide (Q30015). This probe was designed based on the
 CC sequence derived from the second transmembrane domain of G-protein-
 CC coupled receptors. After tertiary screening, six plaques were
 CC isolated. The insert of one of these plaques, termed F3R was of 2.5
 CC kb in size. This insert was sequenced. The protein deduced from
 CC the F3R clone demonstrates that it belongs to the family of
 CC G-protein-coupled receptors. The deduced protein sequence
 CC indicates seven putative transmembrane segments.
 XX
 XX Sequence 355 AA;
 SQ

Query Match 62.2%; Score 74; DB 13; Length 355;
 Best Local Similarity 66.7%; Pred. No. 0.00048;
 Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 1 VIIAVLVFLACQIPHNMLL 21
 II IIII:II I :I:IIII
 Db 248 vifavvlflclwlpynlavl 268

RESULT 10
 R33420
 ID R33420 standard; Protein; 355 AA.
 XX AC R33420;
 XX 26-JUL-1993 (first entry)
 XX Human IL-8 receptor from clone p2.
 DE
 XX Interleukin-8 receptor; probes; gene therapy; gro receptor;
 KW intracellular-calcium mobilising; ligand-binding; MIP-2 receptor.
 XX Homo sapiens.
 OS
 XX WO9306229-A.
 PN 01-APR-1993.
 PD 14-SEP-1992; 92WO-US07641.
 XX 13-SEP-1991; 91US-0759568.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICE.
 PA Murphy PM;
 XX
 XX WPI: 1993-117549/14.
 DR N-PSDB; Q38747.
 XX New interleukin-8 receptor aminoacid sequence - and corresp. cDNA
 PT expressed in Xenopus laevis oocytes or transfected host cells,
 PT for screening ligands of IL-8 receptor and gene therapy
 XX
 XX Claim 1; Fig 3; 39pp; English.
 XX cDNA libraries from 2 and 3.5 kb fractions of poly(A)+ RNA from HL60
 CC

CC neutrophils sepd. of a sucrose gradient were made in UnizAP. The
 CC libraries were screened with F3R oligonucleotide probe (from rabbit
 CC IL-8 receptor) and under low stringency with a p2 cDNA probe
 CC synthesised from random primers, to isolated the clone p2, encoding
 CC human IL-8 receptor protein. The presence or absence of the DNA
 CC encoding IL-8R or related MIP-2 receptor may be detected using
 CC portions of the p2 clone as probes. p2 may also be used to screen
 CC for ligands of IL-8R and may also be used in gene therapy to treat a
 CC patient deficient in IL-8R. The IL-8R is a gro receptor and has
 CC intracellular calcium-mobilising and ligand-binding properties.
 XX
 XX
 SQ Sequence 355 AA;

Query Match 62.2%; Score 74; DB 14; Length 355;
 Best Local Similarity 66.7%; Pred. No. 0.00048;
 Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIIAVLVFLACQIPHNVL 21
 II IIII:II I:IIII
 Db 247 vifavvllflcwlpynlvll 267

RESULT 11

R80950
 ID R80950 standard; Protein; 355 AA.

AC R80950;

DT 24-APR-1996 (first entry)

DE Recombinant high affinity interleukin-8 receptor subtype A.

XX IL-8A; IL-8B; receptor; monoclonal antibody; inflammatory disorder;
 KW anaphylaxis; systemic lupus erythematosus; rheumatoid arthritis;
 KW systemic necrotising vasculitis; psoriasis; asthma; allergy; ARDS;
 KW adult respiratory distress syndrome; neutrophil detection.

XX Oryctolagus cuniculus.

XX WO9525126-A1.

XX 21-SEP-1995.

XX 09-MAR-1995; 95WO-US03032.

XX 02-MAY-1994; 94US-0237937.

XX 15-MAR-1994; 94US-0210250.

XX (REPK) REPLIGEN CORP.

PA (UYBO-) UNIV BOSTON.

XX Greenfield EA, Larosa GJ, Navarro J, Thomas KM;

PI Witt DP;

XX WPI; 1995-336945/43.

DR N-PSDB; Q99949.

XX Monoclonal antibody against recombinant IL-8 receptor polypeptide -
 PT useful for treating inflammatory disorders, for detecting
 PT neutrophil(s) and for isolating IL-8 receptor from liq.mixt.

XX Claim 2; Fig 1A-B; 74pp; English.

XX Monoclonal antibodies were raised against recombinant interleukin-8
 CC (IL-8) receptor subtypes A and B from both human and rabbit sources
 CC (R80950-53 encoded by Q99949-52). The A subtype receptor (IL-8rA) is
 CC a high affinity receptor and the B subtype receptor (IL-8rB) is a
 CC low affinity receptor. The monoclonal antibody (mAb) pref. binds to
 CC the IL-8 binding domain thus blocking its activation. The mAbs are
 CC useful for treating inflammatory disorders (see key words) and for
 CC detecting the presence of neutrophils in a biological sample. The
 CC mAbs are also useful in the isolation of IL-8 receptors from a mixture.

XX
 SQ Sequence 355 AA;

Query Match 62.2%; Score 74; DB 16; Length 355;
 Best Local Similarity 66.7%; Pred. No. 0.00048;
 Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIIAVLVFLACQIPHNVL 21
 II IIII:II I:IIII
 Db 248 vifavvllflcwlpynlvll 268

RESULT 12

B09990

ID B09990 standard; Protein; 355 AA.

XX B09990;

DT 20-OCT-2000 (first entry)

DE Human IL-8 receptor protein hIL8RB.

XX IL-8 receptor protein; hIL8RA; hIL8RB; human; interleukin-8; drug;
 KW treatment; inflammatory disease; anti-tumor.

XX Homo sapiens.

XX JP08103276-A.

XX 23-APR-1996.

XX 06-OCT-1994; 94JP-0242534.

XX 06-OCT-1994; 94JP-0242534.

XX (TAKE) TAKEDA CHEM IND LTD.

XX WPI; 1996-253878/26.

DR N-PSDB; A40128.

XX Recombinant human interleukin 8 receptor protein, - its prepn. and
 PT application.

XX Example 2; Fig 4; 22pp; Japanese.

XX This invention describes a novel expression vector which carries a DNA
 CC encoding human interleukin 8 receptor protein and is expressed by
 CC pAKK01.11/hrIL8RA or pAKK01.11/hIL8RB. Also claimed are (I) CHO cell
 CC containing the above expression vector, (II) the preparation of a
 CC recombinant human interleukin 8 receptor protein in which the above CHO
 CC cell is cultured under a condition enabling the expression of a DNA
 CC coding human interleukin 8 receptor protein, (III) a CHO cell
 CC containing a recombinant human interleukin 8 receptor protein which can
 CC be prepared, by culturing the above CHO cell under a condition enabling
 CC the expression of a DNA coding human interleukin 8 receptor protein or
 CC its cell membrane fraction, (IV) a recombinant human interleukin 8
 CC receptor protein isolated from a CHO cell containing the above
 CC recombinant human interleukin 8 receptor protein, its partial peptide or
 CC their salt, (V) the screening of human interleukin 8 receptor agonist or
 CC antagonist in which the above CHO cell or its cell membrane fraction is
 CC used or the above recombinant human interleukin 8 receptor protein, its
 CC partial peptide or their salt is used (VI) a kit for screening the human
 CC interleukin 8 receptor agonist or antagonist containing the above CHO
 CC cell or its cell membrane fraction or the above recombinant human
 CC interleukin 8 receptor protein, its partial peptide or their salt, (VII)
 CC a human interleukin 8 receptor agonist or antagonist prepared by using
 CC the above screening method or the above screening kit or its salt, (VII)
 CC an activation promoter or a migration promoter of neutrophils containing
 CC the above agonist or its salt, and an activation inhibitor or a migration
 CC inhibitor containing the above antagonist or its salt. The agonist or the
 CC antagonist can be used in drug compositions for the prevention and
 CC treatment of inflammatory diseases and anti-tumor agents. The screening

CC method can select an agonist or an antagonist advantageously. This
 CC sequence represents the human IL-8 receptor protein hIL8RB which is
 CC described in the method of the invention.

XX Sequence 355 AA;

Query Match 62.2%; Score 74; DB 17; Length 355;
 Best Local Similarity 66.7%; Pred. No. 0.00048;
 Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIIAVLVFLACQIPHNMLL 21
 |||||:|:|:|:|:|:|
 Db 247 vifavvlflcwpynlavl 267

RESULT 13

R80952
 ID R80952 standard; Protein; 358 AA.

XX R80952;

DT 24-APR-1996 (first entry)

DE Recombinant high affinity interleukin-8 receptor subtype B.

KW IL-8A; IL-8B; receptor; monoclonal antibody; inflammatory disorder;
 KW anaphylaxis; systemic lupus erythematosus; rheumatoid arthritis;
 KW systemic necrotizing vasculitis; psoriasis; asthma; allergy; ARDS;
 KW adult respiratory distress syndrome; neutrophil detection.

XX Oryctolagus cuniculus.

XX WO9525126-A1.

XX 21-SEP-1995.

XX 09-MAR-1995; 95WO-US03032.

PR 02-MAY-1994; 94US-0237937.

PR 15-MAR-1994; 94US-0210250.

XX (REPK) REPLIGEN CORP.

PA (UYBO-) UNIV BOSTON.

XX Greenfield EA, Larosa GJ, Navarro J, Thomas KM;

PI Witt DT;

XX WPI; 1995-336945/43.

DR N-PSDB; Q99951.

XX Monoclonal antibody against recombinant IL-8 receptor polypeptide -
 PT useful for treating inflammatory disorders, for detecting
 PT neutrophil(s) and for isolating IL-8 receptor from liq.mixt.

XX Claim 6; Fig 3A-B; 74pp; English.

XX Monoclonal antibodies were raised against recombinant interleukin-8
 CC (IL-8) receptor subtypes A and B from both human and rabbit sources
 CC (R80950-53 encoded by Q99949-52). The A subtype receptor (IL-8rA) is
 CC a high affinity receptor and the B subtype receptor (IL-8rB) is a
 CC low affinity receptor. The monoclonal antibody (mAb) pref. binds to
 CC the IL-8 binding domain thus blocking its activation. The mAbs are
 CC useful for treating inflammatory disorders (see key words) and for
 CC detecting the presence of neutrophils in a biological sample. The
 CC mAbs are also useful in the isolation of IL-8 receptors from a mixture.

XX Sequence 358 AA;

Query Match 62.2%; Score 74; DB 16; Length 358;
 Best Local Similarity 66.7%; Pred. No. 0.00048;
 Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIIAVLVFLACQIPHNMLL 21
 |||||:|:|:|:|:|:|
 Db 250 vifavvlflcwpynlavl 270

RESULT 14

R28273
 ID R28273 standard; Protein; 360 AA.

XX R28273;

XX 04-APR-1993 (first entry)

DE Sequence in a low affinity recombinant human interleukin-8
 DE (IL-8) receptor polypeptide in 4AB.

KW IL-8 receptor polypeptide; G-protein-coupled receptor.

XX Homo sapiens.

XX WO9218641-A.

XX 29-OCT-1992.

XX 10-APR-1992; 92WO-US02977.

XX 10-APR-1991; 91US-0685101.

XX 09-JUL-1991; 91US-0726606.

XX 09-DEC-1991; 91US-0803842.

XX (REPK) REPLIGEN CORP.

XX (UYBO-) UNIV BOSTON.

XX Navarro J, Thomas KM, Witt DP;

XX WPI; 1992-382123/46.

XX N-PSDB; Q30012.

XX Recombinant mammalian interleukin-8 receptor - used for screening

PT interleukin-8 binding antagonists, used to treat inflammation

XX Disclosure; Fig 2; 71pp; English.

XX Rabbit high affinity IL-8 receptor gene was isolated from rabbit
 CC peritoneal neutrophils and used as a source of poly(A)⁺ RNA, to
 CC produce a rabbit neutrophil cDNA library. 250,000 recombinant
 CC plaques were screened for those which hybridized to an antisense
 CC oligonucleotide (Q30015). This probe was designed based on the
 CC sequence derived from the second transmembrane domain of G-protein-
 CC coupled receptors. After tertiary screening, six plaques were
 CC isolated. The insert of one of these plaques, termed F3R was of 2.5
 CC kb in size. This insert was sequenced. The protein deduced from
 CC the F3R clone demonstrates that it belongs to the family of
 CC G-protein-coupled receptors. The deduced protein sequence
 CC indicates seven putative transmembrane segments. A human
 CC peripheral blood leukocyte lambda gt11 cDNA library (5' stretch) was
 CC screened with a 652 bp EcoRI/BamHI fragment (including nucleotides
 CC -27 to 625) of the rabbit F3R clone. After tertiary screening
 CC several human clones which hybridized to the rabbit IL-8 probe
 CC were isolated. The insert of one such clone, termed 4AB was
 CC sequenced (Q30012).

XX Sequence 360 AA;

Query Match 62.2%; Score 74; DB 13; Length 360;
 Best Local Similarity 66.7%; Pred. No. 0.00048;
 Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIIAVLVFLACQIPHNMLL 21
 |||||:|:~|:|:|:|:|
 Db 252 vifavvlflcwpynlavl 272

RESULT 15

R80758
ID R80758 standard; Protein; 360 AA.

XX AC R80758;

XX XX 26-MAR-1996 (first entry)

XX DE Interleukin 8 receptor B.

XX KW Interleukin; IL-8; inflammation; psoriasis; dermatitis;
KW rheumatoid arthritis; inflammatory bowel disease;
KW chronic lung inflammation; treatment; antibody;
KW affinity purification; detection.

XX OS Homo sapiens.

XX PN US5440021-A.

XX PD 08-AUG-1995.

XX PF 29-MAR-1991; 91US-0677211.

XX PR 25-FEB-1994; 94US-0202056.

XX PR 29-MAR-1991; 91US-0677211.

XX PA (CHUN/) CHUNTHARAPAI A.

XX PA (HEBE/) HEBERT C.

XX PA (KIMK/) KIM K J.

XX PA (LEEJ/) LEE J.

XX PI Chuntharapai A, Hebert C, Kim KJ, Lee J;

XX DR WPI; 1995-283151/37.

XX DR N-PSDB; Q99008.

XX PT New antibodies against interleukin 8 type B receptor - used to treat
PT or prevent inflammation, also for detecting receptor expression and
PT purification.

XX PS Disclosure; Columns 53-56; 62pp; English.

XX CC Antibodies directed against the interleukin-8 receptor B can be used
CC to treat or prevent inflammation e.g. psoriasis, dermatitis,
CC rheumatoid arthritis and particularly inflammatory bowel disease and
CC chronic lung inflammation. When immobilised, these antibodies may
CC be used to detect interleukin-8 receptor B expression in cells and
CC tissues and for affinity purification of interleukin-8 receptor B
CC from cells.

XX SQ Sequence 360 AA;

Query Match 62.2%; Score 74; DB 16; Length 360;

Best Local Similarity 66.7%; Pred. No. 0.00048;

Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

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II III:II I:II:II

Db 252 vifavvlflcwlplnvl 272

Search completed: May 23, 2001, 15:28:32
Job time: 409 sec

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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:30:08 ; Search time 95.91 Seconds
(without alignments)
5.008 Million cell updates/sec

Title: US-08-887-977-10_COPY_246_270
Perfect score: 119
Sequence: 1 VIIIAVLVFLACQIPHNVLIVTAA 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
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5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	62.2	350	1	US-08-202-056-1
2	74	62.2	350	1	US-08-076-093A-2
3	74	62.2	350	1	US-08-450-393A-7
4	74	62.2	350	1	US-08-410-453A-1
5	74	62.2	350	1	US-08-701-265-2
6	74	62.2	350	1	US-08-410-454A-1
7	74	62.2	350	2	US-08-284-586-2
8	74	62.2	350	2	US-08-410-456A-1
9	74	62.2	350	2	US-08-805-478-2
10	74	62.2	350	2	US-08-802-627A-2
11	74	62.2	350	2	US-08-801-238-2
12	74	62.2	350	2	US-08-801-228-2
13	74	62.2	350	3	US-09-104-296-2
14	74	62.2	350	4	US-08-446-669-7
15	74	62.2	350	5	PCT-US95-00476-7
16	74	62.2	354	1	US-07-759-568-2
17	74	62.2	355	1	US-07-759-568-1
18	74	62.2	355	1	US-08-450-393A-8
19	74	62.2	355	2	US-08-390-000A-5
20	74	62.2	355	4	US-08-446-669-8
21	74	62.2	355	5	PCT-US95-00476-8
22	74	62.2	360	1	US-08-202-056-7
23	72	60.5	312	1	US-08-118-270-38
24	72	60.5	312	5	PCT-US93-08528-38
25	70	58.8	380	4	US-08-969-815-4
26	67	56.3	382	4	US-08-969-815-2
27	63	52.9	358	1	US-08-153-848-19

28	63	52.9	358	3	US-09-299-843A-19	Sequence 19, Appl
29	63	52.9	358	5	PCT-US93-11153-19	Sequence 19, Appl
30	63	52.9	359	1	US-08-153-848-24	Sequence 24, Appl
31	63	52.9	359	3	US-09-299-843A-24	Sequence 24, Appl
32	63	52.9	359	5	PCT-US93-11153-24	Sequence 24, Appl
33	63	52.9	361	2	US-08-902-294-2	Sequence 2, Appl
34	63	52.9	361	3	US-09-178-637-2	Sequence 2, Appl
35	63	52.9	378	1	US-08-383-750-2	Sequence 2, Appl
36	63	52.9	378	1	US-08-383-751A-2	Sequence 2, Appl
37	63	52.9	378	1	US-08-153-848-15	Sequence 15, Appl
38	63	52.9	378	3	US-08-352-678-2	Sequence 2, Appl
39	63	52.9	378	3	US-09-299-843A-15	Sequence 15, Appl
40	63	52.9	378	3	US-09-299-843A-66	Sequence 66, Appl
41	63	52.9	378	4	US-09-251-545-1	Sequence 1, Appl
42	63	52.9	378	5	PCT-US93-09636-2	Sequence 2, Appl
43	63	52.9	378	5	PCT-US93-11153-15	Sequence 15, Appl
44	63	52.9	410	1	US-08-153-848-7	Sequence 7, Appl
45	63	52.9	410	3	US-09-299-843A-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-08-202-056-1
: Sequence 1, Application US/08202056
: Patent No. 5440021
: GENERAL INFORMATION:
: APPLICANT: Chuntharapal, Anan
: APPLICANT: Hebert, Caroline
: APPLICANT: Kim, Kyung Jin
: APPLICANT: Lee, James
: TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: patin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/202,056
: FILING DATE: 25-FEB-1994
: CLASSIFICATION: 436
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/677211
: FILING DATE: 29-MAR-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Love, Richard B.
: REGISTRATION NUMBER: 34,659
: REFERENCE/DOCKET NUMBER: 706P3
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-5530
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 350 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: US-08-202-056-1

Query Match 62.2%; Score 74; DB 1; Length 350;
Best Local Similarity 66.7%; Pred. No. 0.00089;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Caps 0;

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QY 1 VIIAVVLVFLACQIPHNVLL 21
  || |||||:| | :|:|:|
Db 243 VIFAVVLFLCWLCPYNLVL 263

RESULT 2
US-08-076-093A-2
; Sequence 2, Application US/08076093A
; Patent No. 5543503
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: Jin Kim, K.
; TITLE OF INVENTION: Antibodies to Human PF4A Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/076,093A
; FILING DATE: 11-Jun-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/677211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 706P2
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-076-093A-2

Query Match 62.2%; Score 74; DB 1; Length 350;
Best Local Similarity 66.7%; Pred. No. 0.00089;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIIAVVLVFLACQIPHNVLL 21
  || |||||:| | :|:|:|
Db 243 VIFAVVLFLCWLCPYNLVL 263

RESULT 3
US-08-450-393A-7
; Sequence 7, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14

```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cseri, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/0205
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816Cooileypa
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-450-393A-7

Query Match 62.2%; Score 74; DB 1; Length 350;
Best Local Similarity 66.7%; Pred. No. 0.00089;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIIAVVLVFLACQIPHNVLL 21
  || |||||:| | :|:|:|
Db 243 VIFAVVLFLCWLCPYNLVL 263

RESULT 4
US-08-410-453A-1
; Sequence 1, Application US/08410453A
; Patent No. 5767063
; GENERAL INFORMATION:
; APPLICANT: Lee, James,
; APPLICANT: Holmes, William E.,
; APPLICANT: Woods, William I.,
; TITLE OF INVENTION: Human PF4A Receptors and Their Use
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,453A
; FILING DATE: 24-Mar-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/234494
; FILING DATE: 28-APR-1994

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/677211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-410-453A-1

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Query Match 62.2%; Score 74; DB 1; Length 350;
Best Local Similarity 66.7%; Pred. No. 0.00089;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

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QY 1 VIIAVLVFLACQIPHNMVLL 21
   |||||:| | :|:|:|
Db 243 VIFAVLFLCWLPLYNLVLL 263

```

RESULT 5

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; Sequence 2, Application US/08701265
; Patent No. 5776457
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: Jin Kim, K.
; TITLE OF INVENTION: Antibodies to Human PF4A Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/701,265
; FILING DATE: 22-AUG-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-Jun-1993
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/677211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 706P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids

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; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-701-265-2

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Query Match 62.2%; Score 74; DB 1; Length 350;
Best Local Similarity 66.7%; Pred. No. 0.00089;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

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QY 1 VIIAVLVFLACQIPHNMVLL 21
   |||||:| | :|:|:|
Db 243 VIFAVLFLCWLPLYNLVLL 263

```

RESULT 6

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; Sequence 1, Application US/08410454A
; Patent No. 5783415
; GENERAL INFORMATION:
; APPLICANT: Lee, James,
; APPLICANT: Holmes, William E.,
; APPLICANT: Woods, William I.,
; TITLE OF INVENTION: Human PF4A Receptors and Their Use
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,454A
; FILING DATE: 24-Mar-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/234494
; FILING DATE: 28-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/677211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706C1D3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-410-454A-1

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```

Query Match 62.2%; Score 74; DB 1; Length 350;
Best Local Similarity 66.7%; Pred. No. 0.00089;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

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```

QY 1 VIIAVLVFLACQIPHNMVLL 21
   |||||:| | :|:|:|
Db 243 VIFAVLFLCWLPLYNLVLL 263

```

RESULT 7

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US-08-284-586-2

```

; Sequence 2, Application US/08284586
; Patent No. 5840856
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: Jin Kim, K.
; TITLE OF INVENTION: Antibodies to Human PF4A Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/284,586
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/076,093A
; FILING DATE: 11-Jun-1993
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/677211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 706P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-284-586-2

Query Match 62.2%; Score 74; DB 2; Length 350;
Best Local Similarity 66.7%; Pred. No. 0.00089;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Caps 0;

QY 1 VIIAVVLVFLACQIPHNVL 21
|| ||||| || | : | : |||
Db 243 VIFAVVLFLCWLPLNVL 263

RESULT 8
US-08-410-456A-1
; Sequence 1, Application US/08410456A
; Patent No. 5856457
; GENERAL INFORMATION:
; APPLICANT: Lee, James,
; APPLICANT: Holmes, William E.,
; APPLICANT: Woods, William I.
; TITLE OF INVENTION: Human PF4A Receptors and Their Use
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California

; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,456A
; FILING DATE: 24-Mar-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/234494
; FILING DATE: 28-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/677211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706C1D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-410-456A-1

Query Match 62.2%; Score 74; DB 2; Length 350;
Best Local Similarity 66.7%; Pred. No. 0.00089;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Caps 0;

QY 1 VIIAVVLVFLACQIPHNVL 21
|| ||||| || | : | : |||
Db 243 VIFAVVLFLCWLPLNVL 263

RESULT 9
US-08-805-478-2
; Sequence 2, Application US/08805478
; Patent No. 5874543
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: Jin Kim, K.
; TITLE OF INVENTION: ANTIBODIES TO PF4A RECEPTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/805,478
; FILING DATE: 25-Feb-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/284586
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093

```
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2P1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-805-478-2

Query Match 62.2%; Score 74; DB 2; Length 350;
Best Local Similarity 66.7%; Pred. No. 0.00089;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VIIAVLVFLACQIPHNVL 21
Db 243 VIFAVLFLCWLPLNVL 263

RESULT 10
US-08-802-627A-2
; Sequence 2, Application US/08802627A
; Patent No. 5892017
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING PF4A RECEPTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,627A
; FILING DATE: 19-Feb-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/284586
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 11-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2PID2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-805-478-2

Query Match 62.2%; Score 74; DB 2; Length 350;
Best Local Similarity 66.7%; Pred. No. 0.00089;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VIIAVLVFLACQIPHNVL 21
Db 243 VIFAVLFLCWLPLNVL 263

RESULT 11
US-08-801-238-2
; Sequence 2, Application US/08801238
; Patent No. 5919896
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: PF4A RECEPTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,238
; FILING DATE: 19-Feb-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/284586
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2PID1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-801-238-2

Query Match 62.2%; Score 74; DB 2; Length 350;
Best Local Similarity 66.7%; Pred. No. 0.00089;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VIIAVLVFLACQIPHNVL 21
Db 243 VIFAVLFLCWLPLNVL 263

SEQUENCE CHARACTERISTICS:
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; LENGTH: 350 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-802-627A-2

Query Match 62.2%; Score 74; DB 2; Length 350;
Best Local Similarity 66.7%; Pred. No. 0.00089;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VIIAVLVFLACQIPHNVL 21
Db 243 VIFAVLFLCWLPLNVL 263

RESULT 11
US-08-801-238-2
; Sequence 2, Application US/08801238
; Patent No. 5919896
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: PF4A RECEPTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,238
; FILING DATE: 19-Feb-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/284586
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2PID1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-801-238-2

Query Match 62.2%; Score 74; DB 2; Length 350;
Best Local Similarity 66.7%; Pred. No. 0.00089;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VIIAVLVFLACQIPHNVL 21
Db 243 VIFAVLFLCWLPLNVL 263

SEQUENCE CHARACTERISTICS:
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; LENGTH: 350 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-801-238-2

Query Match 62.2%; Score 74; DB 2; Length 350;
Best Local Similarity 66.7%; Pred. No. 0.00089;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VIIAVLVFLACQIPHNVL 21
Db 243 VIFAVLFLCWLPLNVL 263

SEQUENCE CHARACTERISTICS:
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RESULT 12

US-08-801-228-2
; Sequence 2, Application US/08801228
; Patent No. 5922541
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: METHODS FOR DETECTION AND AMPLIFICATION OF
; TITLE OF INVENTION: PF4A RECEPTOR NUCLEIC ACID
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,228
; FILING DATE: 19-Feb-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/284586
; FILING DATE: 10-AUG-1994

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991

ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2P1D3
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear

US-08-801-228-2

Query Match 62.2%; Score 74; DB 2; Length 350;
Best Local Similarity 66.7%; Pred. No. 0.00089;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VIIAVVLVFLACQIPHNMVLL 21
|| ||||| || | : | : |||||
Db 243 VIFAVVLIFLLCWLPLNVL 263

RESULT 13

US-09-104-296-2
; Sequence 2, Application US/09104296
; Patent No. 6087475
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: PF4A Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way

CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/104,296
; FILING DATE: 24-June-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/701265
; FILING DATE: 22-AUG-1996

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/664228
; FILING DATE: 06-JUN-1996
; APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2C2

TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear

US-09-104-296-2

Query Match 62.2%; Score 74; DB 3; Length 350;
Best Local Similarity 66.7%; Pred. No. 0.00089;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VIIAVVLVFLACQIPHNMVLL 21
|| ||||| || | : | : |||||
Db 243 VIFAVVLIFLLCWLPLNVL 263

RESULT 14

US-08-446-669-7
; Sequence 7, Application US/08446669
; Patent No. 6132987
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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: APPLICATION NUMBER: US/08/446,669
: FILING DATE: May 25, 1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Neeley, Richard
: REGISTRATION NUMBER: 30,092
: REFERENCE/DOCKET NUMBER: UCAL-237/01US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-843-5000
: TELEFAX: 415-857-0663
: TELEX: 380816CcooleyPA
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 350 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: US-08-446-669-7

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Query Match 62.2%; Score 74; DB 4; Length 350;
Best Local Similarity 66.7%; Pred. No. 0.00089;
Matches 14; Conservative 4; Mismatches 3; Indels

QY 1 V I I A V V L V F L A C Q I P H N M V L L 21
|| ||||:| | :|:|:| |
Db 243 V I F A V V L I F L L C W L P Y N L V L L 263

RESULT 15

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PCT-US95-00476-7
; Sequence 7, Application PC/TUS9500476
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Robbins, Berliner & Carson
; STREET: 201 N. Figueroa Street, 5th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012-2628
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00476
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berliner, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-977-1001
; TELEFAX: 310-977-1003
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PCT-US95-00476-7

```


GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:32:02 ; Search time 110.15 Seconds
(without alignments)
15.598 Million cell updates/sec

Title: US-08-887-977-10_COPY_246_270

Perfect score: 119

Sequence: 1 VIIAVLVFLACQIPHNMLLVTA 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_67:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	119	100.0	369	2 JC5068	G protein-coupled
2	74	62.2	350	2 A39445	interleukin-8 rece
3	74	62.2	354	2 A23669	interleukin-8 rece
4	74	62.2	355	2 QJ1231	interleukin-8 rece
5	74	62.2	358	2 A53752	interleukin-8 rece
6	74	62.2	359	2 A53611	interleukin-8 rece
7	71	59.7	359	2 A48921	interleukin-8 rece
8	70	58.8	356	2 S42096	interleukin-8 rece
9	63	52.9	378	2 A45680	G protein-coupled
10	63	52.9	378	2 B55735	lymphocyte-specifi
11	63	52.9	378	2 A55735	G protein-coupled
12	61	51.3	361	2 JC5653	G protein-coupled
13	61	51.3	365	2 S68208	G protein-coupled
14	59	49.6	358	2 G02670	IL8-related recept
15	59	49.6	375	2 JC5069	G protein-coupled
16	56	47.1	362	2 A30341	G protein-coupled
17	56	47.1	375	2 JC5509	G protein-coupled
18	55	46.2	323	1 Q0BED3	HHRE3 protein - hu
19	55	46.2	354	2 T09353	G protein-coupled
20	55	46.2	354	2 B57333	G protein-coupled
21	54.5	45.8	473	2 JC5835	anaphylatoxin C3a
22	54	45.4	349	1 JC5490	opsin, pineal glan
23	54	45.4	350	2 JN0621	G protein-coupled
24	53	44.5	342	2 S13638	platelet-activatin
25	53	44.5	363	2 I57940	somatostatin recep
26	52	43.7	351	1 A55962	opsin, pineal glan
27	52	43.7	362	2 A39714	G protein-coupled
28	50	42.0	341	2 S63666	platelet activatin
29	50	42.0	342	2 A40191	platelet-activatin

30	50	42.0	362	2 JN0694	angiotensin II rec
31	50	42.0	367	2 JE0349	interferon-inducib
32	50	42.0	394	2 JC7209	galanin receptor -
33	50	42.0	465	1 J01517	neurokinin 3 recep
34	50	42.0	519	2 S17783	tachykinin recepto
35	49	41.2	341	2 S43252	platelet-activatin
36	49	41.2	359	2 I49341	MIP-1 alpha recept
37	49	41.2	360	2 A57160	chemokine (C-C) re
38	49	41.2	385	2 S55524	neurokinin 3 recep
39	49	41.2	440	2 A44081	kappa-type opioid
40	49	41.2	449	2 A41738	neuropeptide Y rec
41	49	41.2	452	2 A34916	neurokinin 3 recep
42	48	40.3	363	2 I57955	somatostatin recep
43	48	40.3	364	2 JN0763	somatostatin recep
44	48	40.3	380	2 JC2434	kappa opioid recep
45	48	40.3	380	2 A48227	kappa opioid recep

ALIGNMENTS

RESULT 1

JC5068

G protein-coupled receptor CKR-L3 - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000

C:Accession: JC5068

R:Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.

Biochem. Biophys. Res. Commun. 227, 846-853, 1996

A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-lik

A:Reference number: JC5067; MUID:97040707

A:Accession: JC5068

A:Molecule type: DNA

A:Residues: 1-369 <ZAB>

A:Cross-references: EMBL:Z79784; NID:g1668737; PIDN:CA02144.1; PID:g1668738

C:Comment: This protein belongs to the family of alpha chemokine receptors.

C:Genetics:

A:Gene: GDB:CMKBR6; STR122; GPR29; CCR6; CKR-L3; GPR-CY4

A:Cross-references: GDB:5370639; OMIM:601835

A:Map position: 6q27-q27

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

F:42-68/Domain: transmembrane #status predicted <TM1>

F:79-99/Domain: transmembrane #status predicted <TM2>

F:115-136/Domain: transmembrane #status predicted <TM3>

F:160-180/Domain: transmembrane #status predicted <TM4>

F:212-233/Domain: transmembrane #status predicted <TM5>

F:250-271/Domain: transmembrane #status predicted <TM6>

F:292-315/Domain: transmembrane #status predicted <TM7>

Query Match 100.0%; Score 119; DB 2; Length 369;

Best Local Similarity 100.0%; Pred. No. 6.5e-10;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIIAVLVFLACQIPHNMLLVTA 25

DB 250 VIIAVLVFLACQIPHNMLLVTA 274

RESULT 2

A39445

interleukin-8 receptor type A - human

N:Alternate names: interleukin-8 receptor, high-affinity

C:Species: Homo sapiens (man)

C:Date: 22-Jan-1993 #sequence_revision 12-Apr-1996 #text_change 05-Nov-1999

C:Accession: I37449; I38710; I38711; A39445

R:Mollereau, C.; Muscatelli, F.; Mattei, M.G.; Vassart, G.; Parmentier, M.

Genomics 16, 248-251, 1993

A:Title: The high-affinity interleukin 8 receptor gene (IL8RA) maps to the 2q33-q36 r

A:Reference number: I37449; MUID:93252387

A:Accession: I37449

A:Molecule type: DNA

A:Residues: 1-350 <RES>
A:Cross-references: EMBL:X65858; NID:g312046; PIDN:CAA46688.1; PID:g312047
R:Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
J. Biol. Chem. 269, 26381-26389, 1994
A:Title: Comparison of the genomic organization and promoter function for human interleukin-8 receptor.
A:Reference number: 137898; MUID:95014476
A:Accession: J38710
A:Molecule type: DNA
A:Residues: 1-350 <RE2>
A:Cross-references: EMBL:U11870; NID:g511804; PIDN:AAA64378.1; PID:g511805
A:Accession: J38711
A:Molecule type: mRNA
A:Residues: 1-16 <RE3>
A:Cross-references: EMBL:U11871; NID:g511806; PIDN:AAA64379.1; PID:g733002
R:Holmes, W.E.; Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.
Science 253, 1278-1280, 1991
A:Title: Structure and functional expression of a human interleukin-8 receptor.
A:Reference number: A39445; MUID:91368199
A:Accession: A39445
A:Molecule type: mRNA
A:Residues: 1-275, 'T', 277-350 <HOL>
A:Cross-references: GB:M68932; NID:g186369; PIDN:AAA59159.1; PID:g186370
C:Genetics:
A:Gene: GDB:IL8RA
A:Cross-references: GDB:135039; OMIM:146929
A:Map position: 2q35-2q35
A:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein

Query Match 62.2%; Score 74; DB 2; Length 350;
Best Local Similarity 66.7%; Pred. No. 0.002;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 VTIATVVLFLACQIPHNWLL 21
|| ||||| || | : : : |||
DB 243 VIFAVVLIFLLCWLPLNVL 263

RESULT 3
A23669
Interleukin-8 receptor, high affinity - rabbit
N:Alternate names: fMLP receptor
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 05-Nov-1999
C:Accession: A23669
R:Thomas, K.M.; Pyun, H.Y.; Navarro, J.
J. Biol. Chem. 265, 20061-20064, 1990
A:Title: Molecular cloning of the fMet-Leu-Phe receptor from neutrophils.
A:Reference number: A23669; MUID:91056034
A:Accession: A23669
A:Molecule type: mRNA
A:Residues: 1-354 <THO>
A:Cross-references: GB:M58021; GB:J05705; NID:g165442; PIDN:AAA31377.1; PID:g165443
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein; neutrophil

Query Match 62.2%; Score 74; DB 2; Length 354;
Best Local Similarity 66.7%; Pred. No. 0.002;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 VTIATVVLFLACQIPHNWLL 21
|| ||||| || | : : : |||
DB 247 VIFAVVLIFLLCWLPLNVL 267

RESULT 4
J01231
Interleukin-8 receptor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Nov-1999
C:Accession: J01231; A46483

R:Beckmann, M.P.; Munger, W.E.; Kozlosky, C.; VandenBos, T.; Price, V.; Lyman, S.; Ge
Biochem. Biophys. Res. Commun. 179, 784-789, 1991
A:Title: Molecular characterization of the interleukin-8 receptor.
A:Reference number: J01231; MUID:91378994
A:Accession: J01231
A:Molecule type: DNA
A:Residues: 1-355 <BEC>
A:Cross-references: GB:M74240; NID:g165438; PIDN:AAA31375.1; PID:g165439
R:Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.
J. Immunol. 148, 1261-1264, 1992
A:Title: Characterization of complementary DNA clones encoding the rabbit IL-8 receptor
A:Reference number: A46483; MUID:92148149
A:Accession: A46483
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-355 <LEE>
A:Cross-references: GB:M82873; NID:g165440; PIDN:AAA31376.1; PID:g165441
A:Experimental source: neutrophils
A:Note: sequence extracted from NCBI backbone (NCBIN:81526, NCBIP:81530)
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 62.2%; Score 74; DB 2; Length 355;
Best Local Similarity 66.7%; Pred. No. 0.002;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 VTIATVVLFLACQIPHNWLL 21
|| ||||| || | : : : |||
DB 248 VIFAVVLIFLLCWLPLNVL 268

RESULT 5
A53752
Interleukin-8 receptor (clone 5Bla) - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: A53752
R:Prado, G.N.; Thomas, K.M.; Suzuki, H.; LaRosa, G.J.; Wilkinson, N.; Folco, E.; Nava
J. Biol. Chem. 269, 12391-12394, 1994
A:Title: Molecular characterization of a novel rabbit interleukin-8 receptor isotype.
A:Reference number: A53752; MUID:94230294
A:Accession: A53752
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-358 <PRA>
A:Cross-references: GB:L24445; NID:g437661; PIDN:AAA31378.1; PID:g437662
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 62.2%; Score 74; DB 2; Length 358;
Best Local Similarity 66.7%; Pred. No. 0.002;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 VTIATVVLFLACQIPHNWLL 21
|| ||||| || | : : : |||
DB 250 VIFAVVLIFLLCWLPLNVL 270

RESULT 6
A53611
Interleukin-8 receptor type B - human
C:Species: Homo sapiens (man)
C:Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 05-Nov-1999
C:Accession: J37898; J38712; A53611; A39446
R:Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
J. Biol. Chem. 269, 26381-26389, 1994
A:Title: Comparison of the genomic organization and promoter function for human inter
A:Reference number: J37898; MUID:95014476
A:Accession: J37898
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-360 <RES>
A:Cross-references: EMBL:U11869; NID:9511801; PIDN:AAB60656.1; PID:9511803
A:Accession: I38712
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-15 <RE2>
A:Cross-references: EMBL:U11872; NID:9511808; PIDN:AAA64380.1; PID:9511809; EMBL:U11873;
L11876; NID:9511816; PID:9511817; EMBL:U11877; NID:9511818; PID:9511819; EMBL:U11878; NID:
J. Biol. Chem. 269, 11065-11072, 1994
A:Title: Structure, genomic organization, and expression of the human interleukin-8 rece
A:Reference number: A53611; MUID:94209273
A:Accession: A53611
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 6-360 <SPR>
A:Cross-references: GB:M99412; GB:L119593
R:Murphy, P.M.; Tiffany, H.L.
Science 253, 1280-1283, 1991
A:Title: Cloning of complementary DNA encoding a functional human interleukin-8 receptor
A:Reference number: A39446; MUID:91368200
A:Accession: A39446
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 6-360 <MUR>
A:Cross-references: GB:M73969
C:Comment: This receptor, unlike IL8RA, binds several peptides besides interleukin-8, in
C:Genetics:
A:Gene: GDB:IL8RB; IL8RA
A:Cross-references: GDB:I27868; OMIM:146928
A:Map position: 2q35-2q35
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

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Query Match          62.2%; Score 74; DB 2; Length 360;
Best Local Similarity 66.7%; Pred. No. 0.002;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      1 VIIAVVLFLACQIPHNMYLL 21
      || |||||:| | :|:|:| |
Db      252 VIFAVLFLCWLPNYVLL 272

RESULT      7
A#8921
N:Interleukin-8 receptor type B - mouse
N:Alternate names: G-protein coupled receptor Gpcrl6
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999
C:Accession: A48921; A53677; I49348; I54421; H48909; I53774
R:Cerretti, D.P.; Nelson, N.; Kozlosky, C.J.; Morrissey, P.J.; Copeland, N.G.; Gilbert,
  Genomics 18, 410-413, 1993
A:Title: The murine homologue of the human interleukin-8 receptor type B maps near the
A:Reference number: A48921; MUID:94117014
A:Accession: A48921
A:Molecule type: DNA
A:Residues: 1-359 <CER>
A:Cross-references: GB:L23637; NID:g435093; PIDN:AAA39305.1; PID:g435094
R:Suzuki, H.; Prado, G.N.; Wilkinson, N.; Navarro, J.
  J. Biol. Chem. 269, 18263-18266, 1994
A:Title: The N terminus of interleukin-8 (IL-8) receptor confers high affinity binding
A:Reference number: A53677; MUID:94308043
A:Accession: A53677
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-359 <SUZ>
A:Cross-references: GB:L26549
A:Note: sequence extracted from NCBI backbone (NCBIP:149812)
R:Lee, J.; Cacalano, G.; Camerato, T.; Toy, K.; Moore, M.W.; Wood, W.I.
  J. Immunol. 155, 2158-2164, 1995
A:Title: Chemokine binding and activities mediated by the mouse IL-8 receptor.
A:Reference number: I49348; MUID:95363183

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A:Accession: I49348
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-359 <RES>
A:Cross-references: EMBL:U31207; NID:g950174; PIDN:AA052239.1; PID:g950175
R:Bozic, C.R.; Gerard, N.P.; von Uexkull-Guldenband, C.; Kolakowski, L.F.
J. Biol. Chem. 269, 29355-29358, 1994
A:Title: The murine interleukin 8 type B receptor homologue and its ligands. Expressi
A:Reference number: I55421; MUID:95050766
A:Accession: I55421
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-359 <R22>
A:Cross-references: GB:I13239; NID:g293665; PIDN:AAA62109.1; PID:g293666
R:Wilke, T.M.; Chen, Y.; Gilbert, D.J.; Moore, K.J.; Yu, L.; Simon, M.I.; Copeland,
Genomics 18, 175-184, 1993
A:Title: Identification, chromosomal location, and genome organization of mammalian G
A:Reference number: A48909; MUID:94116980
A:Accession: H48909
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 145-258 <WIL>
A:Cross-references: GB:I20337; NID:g438800; PIDN:AAA15853.1; PID:g438801
R:Harada, A.; Kuno, K.; Nomura, H.; Mukaida, N.; Murakami, S.; Matsushima, K.
Gene 142, 297-300, 1994
A:Title: Cloning of a cDNA encoding a mouse homolog of the Interleukin-8 receptor.
A:Reference number: I53774; MUID:94252584
A:Accession: I53774
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-359 <R2>
A:Cross-references: GB:D17630; NID:g493671; PIDN:BA04536.1; PID:g493672
C:Genetics:
A:Gene: IL8rb
C:Supersfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
F:49-74/Domain: transmembrane #status predicted <TM1>
F:84-106/Domain: transmembrane #status predicted <TM2>
F:120-141/Domain: transmembrane #status predicted <TM3>
F:163-182/Domain: transmembrane #status predicted <TM4>
F:213-234/Domain: transmembrane #status predicted <TM5>
F:251-271/Domain: transmembrane #status predicted <TM6>
F:308-328/Domain: transmembrane #status predicted <TM7>

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Query Match          59.7%; Score 71; DB 2; Length 359;
Best Local Similarity 70.0%; Pred. No. 0.0054;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      1 VIIAVLVFLACQIPHNNVL 20
      || ||||| | :|:|
Db       251 VIFAVLVFLCWLFPYNLV 270

RESULT      8
S42096
interleukin-8 receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-Aug-1999
C:Accession: S42096
R:Gobl, A.E.; Wang, S.; Zhou, Y.; Oeberg, K.
submitted to the EMBL Data Library, February 1994
A:Description: Molecular cloning of the rat IL8 receptor.
A:Reference number: S42096
A:Accession: S42096
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-356 <GOB>
A:Cross-references: EMBL:X77797
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

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Query Match 58.8%; Score 70; DB 2; Length 356;
Best Local Similarity 70.0%; Pred. No. 0.0075;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIIAVVLVFLACQIPHNWVL 20
|||||:|:|:|:|:|:|
DB 251 VIIAVVLVFLCPLPNIVL 270

RESULT 9

G protein-coupled peptide receptor EBI 1 - human
C:Species: Homo sapiens (man)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C:Accession: A45680
R:Birkenbach, M.; Josefsen, K.; Yalamanchili, R.; Lenoir, G.; Kieff, E.
J. Virol. 67, 2209-2220, 1993
A:Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-coupled R
A:Reference number: A45680; MUID:93188173
A:Accession: A45680
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-378 <BIR>
A:Cross-references: GB:L08176; NID:g183484; PID:g183485
A:Experimental source: B-lymphocytes
A:Note: sequence extracted from NCBI backbone (NCBIN:127094, NCBIIP:127095)
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 52.9%; Score 63; DB 2; Length 378;
Best Local Similarity 61.9%; Pred. No. 0.081;
Matches 13; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIIAVVLVFLACQIPHNWVL 21
|||||:|:|:|:|:|:|
DB 264 VIIAVVVVIFVLPYNGVVL 284

RESULT 10

B55735
Lymphocyte-specific G protein-coupled receptor EBI1 - human
N:Alternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1
C:Species: Homo sapiens (man)
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 19-May-2000
C:Accession: B55735; S52443
R:Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.
Genomics 23, 643-650, 1994
A:Title: Cloning of human and mouse EBI1, a lymphoid-specific G-protein-coupled receptor
A:Reference number: A55735; MUID:95154835
A:Accession: B55735
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-378 <SCH>
A:Cross-references: GB:L31581; NID:g468319; PIDN:AAA74231.1; PID:g468320
R:Burgstahler, R.; Kempkes, B.; Staube, K.; Lipp, M.
submitted to the EMBL Data Library, February 1995
A:Description: The expression of the chemokine receptor BLR2/EBI1 is specifically trans
A:Reference number: S52443
A:Accession: S52443
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 21-378 <BUR>
A:Cross-references: EMBL:X84702
C:Genetics:
A:Gene: GDB:CMKBR7; EBI1; BLR2; CCR7
A:Cross-references: GDB:342065; OMIM:600242
A:Map position: 17q12-17q21.2
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

Query Match 52.9%; Score 63; DB 2; Length 378;
Best Local Similarity 61.9%; Pred. No. 0.081;
Matches 13; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIIAVVLVFLACQIPHNWVL 21
|||||:|:|:|:|:|:|
DB 264 VIIAVVVVIFVLPYNGVVL 284

RESULT 11

A55735
G protein-coupled receptor EBI1 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 24-Nov-1999
C:Accession: A55735
R:Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.
Genomics 23, 643-650, 1994
A:Title: Cloning of human and mouse EBI1, a lymphoid-specific G-protein-coupled recep
A:Reference number: A55735; MUID:95154835
A:Accession: A55735
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-378 <SCH>
A:Cross-references: GB:L31580; NID:g468340; PIDN:AAA74232.1; PID:g468341
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

Query Match 52.9%; Score 63; DB 2; Length 378;
Best Local Similarity 61.9%; Pred. No. 0.081;
Matches 13; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIIAVVLVFLACQIPHNWVL 21
|||||:|:~|:|:|:|:|:|
DB 264 VIIAVVVVIFVLPYNGVVL 284

RESULT 12

JC5653
G protein-coupled receptor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 17-Nov-1997 #sequence_revision 17-Nov-1997 #text_change 21-Jul-2000
C:Accession: JC5653
R:Freder-Martinez, A.; Felipe, A.; Mata, J.F.; Casado, F.J.; Pastor-Anglada, M.
Biochem. Biophys. Res. Commun. 238, 107-112, 1997
A:Title: Molecular cloning of a bovine renal G-protein coupled receptor gene (bRGR):
A:Reference number: JC5653; MUID:97445134
A:Accession: JC5653
A:Molecule type: mRNA
A:Residues: 1-361 <FER>
A:Cross-references: GB:U88366; NID:g2827875; PIDN:AAC05611.1; PID:g2827876
A:Experimental source: renal epithelial cell
C:Superfamily: G protein-coupled receptor 4
C:Keywords: glycoprotein; phosphoprotein
F:24-46/Domain: transmembrane #status predicted <TM1>
F:58-79/Domain: transmembrane #status predicted <TM2>
F:96-117/Domain: transmembrane #status predicted <TM3>
F:137-159/Domain: transmembrane #status predicted <TM4>
F:189-207/Domain: transmembrane #status predicted <TM5>
F:229-253/Domain: transmembrane #status predicted <TM6>
F:265-289/Domain: transmembrane #status predicted <TM7>
F:3-8,62/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:134,218,293,313/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #sta
F:204,221,328/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status

Query Match 51.3%; Score 61; DB 2; Length 361;
Best Local Similarity 40.9%; Pred. No. 0.15;
Matches 9; Conservative 11; Mismatches 2; Indels 0; Gaps 0;

QY 1 VIIAVVLVFLACQIPHNWVL 22
||||:|:|:|:|:|:|
DB 229 LVLTWTWIFLACFLPYHVLV 250

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:36:20 ; Search time 62.39 seconds
(without alignments)
13.726 Million cell updates/sec

Title: US-08-887-977-10_COPY_246_270
Perfect score: 119
Sequence: 1 VITAVLVFLACQIPHNVLVTAA 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	ID	Description
1	119	100.0	374	1	CKR6_HUMAN	P51684 homo sapien
2	114	95.8	367	1	CKR6_MOUSE	O54689 mus musculus
3	74	62.2	349	1	IL8A_RAT	P70612 rattus norv
4	74	62.2	350	1	IL8A_GORGO	P55919 gorilla gor
5	74	62.2	350	1	IL8A_HUMAN	P25024 homo sapien
6	74	62.2	350	1	IL8A_PANTR	P55920 pan troglod
7	74	62.2	353	1	IL8B_GORGO	Q28422 gorilla gor
8	74	62.2	353	1	IL8B_PANTR	Q28807 pan troglod
9	74	62.2	355	1	IL8A_RABIT	P21109 oryctolagus
10	74	62.2	358	1	IL8B_RABIT	P35344 oryctolagus
11	74	62.2	360	1	IL8B_HUMAN	P25025 homo sapien
12	73	61.3	360	1	IL8B_BOVIN	Q28003 bos taurus
13	71	59.7	359	1	IL8B_MOUSE	P35343 mus musculus
14	70	58.8	359	1	IL8B_RAT	P35407 rattus norv
15	69	58.0	353	1	IL8B_MACMU	Q28519 macaca mula
16	67	56.3	356	1	IL8B_CANFA	O97571 canis famil
17	63	52.9	378	1	CKR7_HUMAN	P32248 homo sapien
18	63	52.9	378	1	CKR7_MOUSE	P47774 mus musculus
19	61	51.3	365	1	GP68_HUMAN	P17543 homo sapien
20	59	49.6	375	1	CM12_HUMAN	O99527 homo sapien
21	57	47.9	362	1	CKRA_MOUSE	O99121 mus musculus
22	56	47.1	362	1	RDC1_CANFA	P11613 canis famil
23	56	47.1	363	1	AG2S_XENLA	P35373 xenopus lae
24	56	47.1	375	1	CM12_RAT	O08878 rattus norv
25	55	46.2	354	1	US28_HCMVA	P09704 human cytom
26	55	46.2	362	1	CKRA_HUMAN	P46092 homo sapien
27	55	46.2	362	1	RDC1_MOUSE	P56485 mus musculus
28	55	46.2	362	1	RDC1_RAT	O89039 rattus norv
29	55	46.2	369	1	CKR9_MOUSE	O99077 mus musculus
30	54	45.8	473	1	C3AR_RAT	O55197 rattus norv
31	54	45.4	349	1	OPSP_COLLI	P51476 columba liv
32	54	45.4	350	1	GUSB_BOVIN	P35350 bos taurus
33	54	45.4	357	1	CKR9_HUMAN	P51686 homo sapien

RESULT 1

ID	CKR6_HUMAN	STANDARD;	PRT;	374 AA.
AC	P51684: Q92846; P78553;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CCR-6) (LARC			
DE	RECEPTOR) (GPR-CY4) (GPCY4) (CHEMOKINE RECEPTOR-LIKE 3) (CKR-L3)			
DE	(DRY6).			
GN	CCR6 OR CMKBR6 OR STRL22 OR GPR29 OR CKRL3.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RX	SEQUENCE FROM N.A., AND FUNCTION.			
RX	MEDLINE=97313465; PubMed=9169459;			
RA	Baba M., Imai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K.,			
RA	Nomiya H., Yoshie O.;			
RT	"Identification of CCR6, the specific receptor for a novel			
RT	lymphocyte-directed CC chemokine LARC.";			
RL	J. Biol. Chem. 272:14893-14898(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RP	Lautens L.L., Modi W., Bonner T.I.;			
RL	Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97040707; PubMed=8886020;			
RA	Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G.;			
RT	"Molecular cloning and RNA expression of two new human chemokine			
RT	receptor-like genes.";			
RL	Biochem. Biophys. Res. Commun. 227:846-853(1996).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RP	McCoy R., Perlmutter D.H.;			
RL	Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RX	SEQUENCE FROM N.A.			
RX	MEDLINE=97224503; PubMed=9070937;			
RA	Liao F., Lee H.-H., Farber J.M.;			
RT	"Cloning of STRL22, a new human gene encoding a G-protein-coupled			
RT	receptor related to chemokine receptors and located on chromosome			
RT	6q27.";			
RL	Genomics 40:175-180(1997).			
CC	-!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-			
CC	ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE			
CC	INTRACELLULAR CALCIUM IONS LEVEL.			
CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	-!- TISSUE SPECIFICITY: SPLEEN, LYMPH NODES, APPENDIX, AND FETAL			
CC	LIVER. EXPRESSED IN LYMPHOCYTES, T CELLS AND B CELLS BUT NOT IN			
CC	NATURAL KILLER CELLS, MONOCYTES, OR GRANULOCYTES.			
CC	-!- INDUCTION: INTERLEUKIN-2.			
CC	-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-6 IS THE INITIATOR.			

P21556 cavia porce
O08858 mus musculus
P30938 rattus norv
O09047 mus musculus
P51475 gallus gall
P25106 homo sapien
O54814 rattus norv
P49682 homo sapien
Q62035 mus musculus
P25105 homo sapien
P51682 mus musculus
O08556 rattus norv

34 53 44.5 342 1 PAFR_CAVPO
35 53 44.5 362 1 SSR5_MOUSE
36 53 44.5 363 1 SSR5_RAT
37 52.5 44.1 477 1 C3AR_MOUSE
38 52 43.7 351 1 OPSP_CHICK
39 52 43.7 362 1 RDC1_HUMAN
40 51 42.9 359 1 CCR3_HUMAN
41 51 42.9 368 1 CCR3_HUMAN
42 50 42.0 341 1 PAFR_MOUSE
43 50 42.0 342 1 PAFR_HUMAN
44 50 42.0 354 1 CKR5_MOUSE
45 50 42.0 354 1 CKR5_RAT

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 CC -----
 DR EMBL; U45984; AAB62714.1; -
 DR EMBL; 279784; CAB02144.1; ALT_INIT.
 DR EMBL; U60000; AAB06949.1; -
 DR EMBL; U68030; AAC51124.1; -
 DR EMBL; U68032; AAC51125.1; -
 DR HSSP; P34996; IDDD.
 DR GCRDB; GCR_1037; -
 DR GCRDB; GCR_1075; -
 DR GCRDB; GCR_1906; -
 DR GCRDB; GCR_1919; -
 DR GCRDB; GCR_1941; -
 DR GCRDB; GCR_2110; -
 DR MIM; 601835; -
 DR InterPro; IPR000276; -
 DR Pfam; PF00001; 7tm1.1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 47 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 48 74
 FT DOMAIN 75 83 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 84 104
 FT DOMAIN 105 119 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 120 141
 FT DOMAIN 142 159 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 160 180
 FT DOMAIN 181 211 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 212 238
 FT DOMAIN 239 254 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 255 279
 FT DOMAIN 280 303 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 304 321
 FT DOMAIN 322 374 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 118 197 BY SIMILARITY.
 FT CARBOHYD 7 7 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 23 23 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CONFLICT 60 60 G -> A (IN REF. 4).
 FT CONFLICT 74 74 Y -> N (IN REF. 4).
 FT CONFLICT 86 86 L -> V (IN REF. 4).
 FT CONFLICT 164 164 S -> T (IN REF. 5).
 FT CONFLICT 182 182 T -> S (IN REF. 4).
 FT CONFLICT 192 192 Q -> L (IN REF. 4).
 FT CONFLICT 206 206 E -> V (IN REF. 4).
 FT CONFLICT 225 225 I -> F (IN REF. 4).
 FT CONFLICT 370 374 SEFTM -> VLVHVIIES (IN REF. 4).
 FT CONFLICT 374 AA; 42494 MR; D7F963534E990BC4 CRC64;
 SQ SEQUENCE 374 AA; 42494 MR; D7F963534E990BC4 CRC64;

Query Match 100.0%; Score 119; DB 1; Length 374;
 Best Local Similarity 100.0%; Pred. No. 9, 1e-10;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIIAVLVFLACQIPHNNVLLVTA 25
 DB 255 VIIAVLVFLACQIPHNNVLLVTA 279

RESULT 2
 CKR6_MOUSE STANDARD; PRT; 367 AA.
 AC 054689;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CCR-6) (KY411).
 GN CCR6 OR CCKBR6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yanagihara S., Komura E., Yamaguchi Y.;
 RT "Mouse G protein-coupled receptor Ky411.";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99077268; PubMed=9862452;
 RA Varona R., Zaballós A., Gutierrez J., Martin P., Roncal F.,
 RA Albar J.P., Ardavin C., Marquez G.;
 RT "Molecular cloning, functional characterization and mRNA expression
 RT analysis of the murine chemokine receptor CCR6 and its specific ligand
 RT MIP-3alpha.";
 RL FEBS Lett. 440:188-194(1998).
 CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-
 CC ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE
 CC INTRACELLULAR CALCIUM IONS LEVEL.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 DR EMBL; AB009369; BAA23776.1; -
 DR EMBL; AJ227114; CAA10956.1; -
 DR MGD; MGI:133379; Cmkbr6.
 DR InterPro; IPR000276; -
 DR Pfam; PF00001; 7tm1.1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 40 66
 FT DOMAIN 67 75 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 76 96
 FT DOMAIN 97 111 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 112 133
 FT DOMAIN 134 151 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 152 172
 FT DOMAIN 173 203 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 204 230
 FT DOMAIN 231 246 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 247 271
 FT DOMAIN 272 295 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 296 313
 FT DOMAIN 314 367 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 110 189 BY SIMILARITY.
 FT CARBOHYD 2 2 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 35 35 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 367 AA; 42102 MW; 6A309AF833B1117E CRC64;

Query Match 95.8%; Score 114; DB 1; Length 367;
 Best Local Similarity 95.8%; Pred. No. 4, 5e-09;
 Matches 23; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIIAVLVFLACQIPHNNVLLVTA 24
 DB 247 VIIAVLVFLACQIPHNNVLLVTA 270

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RESULT 3
IL8A_RAT
ID IL8A_RAT STANDARD; PRT; 349 AA.
AC P70612;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR A (IL-8R A) (CXCR-1).
GN IL8A OR CXCR1
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN-WISTAR; TISSUE=Lung;
RX MEDLINE=97115810; PubMed=8955112;
RA Dunstan C.-A.N., Salafra M.N., Adhikari S., Xia Y., Feng L.,
RA Harrison J.K.;
RT "Identification of two rat genes-orthologous to the human
interleukin-8 receptors";
RL J. Biol. Chem. 271:32770-32776(1996).
CC -1- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC MESSENGER SYSTEM (BY SIMILARITY)
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC EMBL; U71089; AAC52962.1; -
CC HSPSP; P34996; IDDD.
CC GCRdb; GCR_1404; -
CC InterPro; IPR000276; -
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Chemotaxis.
CC
CC DOMAIN 1 44 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 45 71 1 (POTENTIAL).
CC DOMAIN 72 80 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 81 101 2 (POTENTIAL).
CC DOMAIN 102 116 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 117 138 3 (POTENTIAL).
CC DOMAIN 139 159 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 160 179 4 (POTENTIAL).
CC DOMAIN 180 204 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 205 225 5 (POTENTIAL).
CC DOMAIN 226 247 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 248 269 6 (POTENTIAL).
CC DOMAIN 270 290 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 291 313 7 (POTENTIAL).
CC DOMAIN 314 349 CYTOPLASMIC (POTENTIAL).
CC CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC DISULFID 115 192 BY SIMILARITY.
CC SEQUENCE 349 AA; 39944 MW; 9B1CDCE61568EABA CRC64;

Query Match 62.2%; Score 74; DB 1; Length 349;
Best Local Similarity 71.4%; Pred. No. 0.0017;
Matches 15; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIIAVLVFLACQIPHNVL 21
Db 248 VIFAVLVFLCCLPYNLVLL 268

RESULT 4
IL8A_GORGO
ID IL8A_GORGO STANDARD; PRT; 350 AA.
AC P55919;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR A (IL-8R A) (IL-8 RECEPTOR TYPE
GN 1) (CXCR-1) (CDW128).
DE IL8A OR CXCR1.
OS Gorilla gorilla gorilla (Lowland gorilla), and
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
ON NCBI_TaxID=9595, 9600;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96175151; PubMed=9110929;
RA Alvarez V., Coto E., Setien F., Gonzalez S., Gonzalez-Roces S.,
RA Lopez-Larrea C.;
RT "Characterization of interleukin-8 receptors in non-human primates.";
RL Immunogenetics 43:261-267(1996).
CC -1- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
CC AND TO MGSA (GRO) WITH A LOW AFFINITY.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC
CC EMBL; X91110; CAB37671.1; -
CC HSPSP; P34996; IDDD.
CC InterPro; IPR000174; -
CC InterPro; IPR000276; -
CC InterPro; IPR001355; -
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PRINTS; PR00427; INTRLEUKIN8R.
CC PRINTS; PR00572; INTRLEUKIN8R.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Chemotaxis.
CC
CC DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 40 66 1 (POTENTIAL).
CC DOMAIN 67 75 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 76 96 2 (POTENTIAL).
CC DOMAIN 97 111 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 112 133 3 (POTENTIAL).
CC DOMAIN 134 154 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 155 174 4 (POTENTIAL).
CC DOMAIN 175 199 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 200 220 5 (POTENTIAL).
CC DOMAIN 221 242 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 243 264 6 (POTENTIAL).
CC DOMAIN 265 285 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 286 308 7 (POTENTIAL).
CC DOMAIN 309 350 CYTOPLASMIC (POTENTIAL).
CC CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 16 16 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 110 187 BY SIMILARITY.
SQ SEQUENCE 350 AA; 39790 MW; DB99591CD6C10757 CRC64;

Query Match 62.2%; Score 74; DB 1; Length 350;
Best Local Similarity 66.7%; Pred. No. 0.0017;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 VVIADVFLVFLACQIPHNVL 21
DB 243 VIFAVLFLVFLVFLVFLVFL 263

RESULT 5
IL8A_HUMAN STANDARD; PRT; 350 AA.
AC P25024;
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR A (IL-8R A) (IL-8 RECEPTOR TYPE
1) (CXCR-1) (CDW128A).
DE IL8RA OR CXCR1.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91368199; PubMed=1840701;
RA Holmes W.E., Lee J., Kuang W.-J., Rice G.C., Wood W.I.;
RT "Structure and functional expression of a human interleukin-8
RT receptor.";
RL Science 253:1278-1280(1991).
RN [2]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX MEDLINE=93205012; PubMed=8384312;
RA Cerretti D.P., Kozlosky C.J., Vanden Bos T., Nelson N., Gearing D.P.,
RA Beckmann M.P.;
RT "Molecular characterization of receptors for human interleukin-8,
RT GRO/melanoma growth-stimulatory activity and neutrophil activating
RT peptide-2.";
RL Mol. Immunol. 30:359-367(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93252387; PubMed=8486366;
RA MollerEAU C., Passage E., Mattei M.-G., Vassart G., Parmentier M.;
RT "The high-affinity interleukin 8 receptor gene (IL8RA) maps to the
RT 2q33-q36 region of the human genome: cloning of a pseudogene
RT (IL8RB) for the low-affinity receptor.";
RL Genomics 16:248-251(1993).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=95014476; PubMed=7929358;
RA Ahuja S.K., Shetty A., Tiffany H.L., Murphy P.M.;
RT "Comparison of the genomic organization and promoter function for
RT human interleukin-8 receptors A and B.";
RL J. Biol. Chem. 269:26381-26389(1994).
RN [5]
RP CHARACTERIZATION.
RX MEDLINE=92355587; PubMed=1379593;
RA Lee J., Horuk R., Rice G.C., Bennett G.L., Camerato T., Wood W.I.;
RT "Characterization of two high affinity human interleukin-8
RT receptors.";
RL J. Biol. Chem. 267:16283-16287(1992).
RN [6]
RP STRUCTURE BY NMR OF 9-29 IN COMPLEX WITH IL-8.
RX MEDLINE=99148123; PubMed=10368283;
RA Skelton N.J., Qian C., Reilly D., Lowman H.;
RT "Structure of a CXCR chemokine-receptor fragment in complex with
RT interleukin-8.";

RL Structure 7:157-168(1999).
CC -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
CC AND TO MSGA (GRO) WITH A LOW AFFINITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CDw128a entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw128a.htm".
CC -----
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CC -----
DR EMBL; L19591; AAB59436.1; -;
DR EMBL; L19592; AAA59160.1; -;
DR EMBL; M68932; AAA59159.1; -;
DR EMBL; X65858; CAA46688.1; -;
DR EMBL; U11870; AAA64378.1; -;
DR PIR; A39445; A39445
DR PDB; ILP; 23-DEC-98.
DR PDB; ILQ; 23-DEC-98.
DR GCRDB; GCR_0175; -;
DR GCRDB; GCR_0696; -;
DR GCRDB; GCR_1832; -;
DR GCRDB; GCR_1833; -;
DR GCRDB; GCR_2052; -;
DR MIM; 146929; -;
DR InterPro; IPR000174; -;
DR InterPro; IPR000276; -;
DR InterPro; IPR001355; -;
DR Pfam; PF00001; 7tm.1; 1
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR00427; INTRLEUKIN8R.
DR PRINTS; PR00572; INTRLEUKIN8R.
DR PROSITE; PS00237; G-PROTEIN RECF_F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN RECF_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Chemotaxis; Polymorphism; 3D-structure.
FT DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 40 66 1 (POTENTIAL).
FT DOMAIN 67 75 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 76 96 2 (POTENTIAL).
FT DOMAIN 97 111 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 112 133 3 (POTENTIAL).
FT DOMAIN 134 154 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 155 174 4 (POTENTIAL).
FT DOMAIN 175 199 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 200 220 5 (POTENTIAL).
FT DOMAIN 221 242 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 243 264 6 (POTENTIAL).
FT DOMAIN 265 285 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 286 308 7 (POTENTIAL).
FT DOMAIN 309 350 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 16 16 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 110 187 BY SIMILARITY.
FT VARIANT 276 276 T -> S.
SQ SEQUENCE 350 AA; 39805 MW; 2463EBB51BEDD039 CRC64;
/FTID=VAR_003479.

Query Match 62.2%; Score 74; DB 1; Length 350;
Best Local Similarity 66.7%; Pred. No. 0.0017;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 VVIADVFLVFLACQIPHNVL 21

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Db 243 VIFAVLVFLCWLPLYNLVLL 263

RESULT 6
IL8A_PANTR
ID IL8A_PANTR STANDARD; PRT; 350 AA.
AC P55920;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR A (IL-8R A) (IL-8 RECEPTOR TYPE
DE 1) (CXCR-1) (CDW128).
GN IL8A OR CXCR1.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96175151; PubMed=9110929;
RA Alvarez V., Coto E., Setien F., Gonzalez S., Gonzalez-Roces S.,
RA Lopez-Larrea C.;
RT "Characterization of interleukin-8 receptors in non-human primates.";
RL Immunogenetics 43:261-267(1996).
CC -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
CC AND TO MGSA (GRO) WITH A LOW AFFINITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL; X91109; ; NOT_ANNOTATED_CDS.
CC HSSP; P34996; 1DDO.
CC InterPro; IPR000174; ;
CC InterPro; IPR000276; ;
CC InterPro; IPR001355; ;
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PRINTS; PR00427; INTRLEUKIN8R.
CC PRINTS; PR00572; INTRLEUKIN8R.
CC PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
CC PROSITE; PS00262; G_PROTEIN_RECEPTOR_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Chemotaxis.
KW DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 40 66 1 (POTENTIAL).
FT DOMAIN 67 75 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 76 96 2 (POTENTIAL).
FT DOMAIN 97 111 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 112 133 3 (POTENTIAL).
FT DOMAIN 134 154 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 155 174 4 (POTENTIAL).
FT DOMAIN 175 199 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 200 220 5 (POTENTIAL).
FT DOMAIN 221 242 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 243 264 6 (POTENTIAL).
FT DOMAIN 265 285 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 286 308 7 (POTENTIAL).
FT DOMAIN 309 350 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 3 3 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 16 16 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 110 187 BY SIMILARITY.

SQ SEQUENCE 350 AA; 39818 MW; A56FD0246E1D440 CRC64;

Query Match 62.2%; Score 74; DB 1; Length 350;
Best Local Similarity 66.7%; Pred. No. 0.0017;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 VITAVLVFLACQIPHNVL 21
II IIII:II I :I:IIII
Db 243 VIFAVLVFLCWLPLYNLVLL 263

RESULT 7
IL8B_GORGO
ID IL8B_GORGO STANDARD; PRT; 353 AA.
AC O28472;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (FRAGMENT).
GN IL8RB OR CXCR2.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96175151; PubMed=9110929;
RA Alvarez V., Coto E., Setien F., Gonzalez S., Gonzalez-Roces S.,
RA Lopez-Larrea C.;
RT "Characterization of interleukin-8 receptors in non-human primates.";
RL Immunogenetics 43:261-267(1996).
CC -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
CC AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X91114; CAA62564.1; ;
CC HSSP; P34996; 1DDO.
CC InterPro; IPR000276; ;
CC Pfam; PF00001; 7tm_1; 1.
CC PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
CC PROSITE; PS00262; G_PROTEIN_RECEPTOR_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Chemotaxis.
KW DOMAIN 1 1 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM <1 45 1 (POTENTIAL).
FT DOMAIN 46 72 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 73 81 2 (POTENTIAL).
FT TRANSMEM 82 102 2 (POTENTIAL).
FT DOMAIN 103 117 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 118 139 3 (POTENTIAL).
FT DOMAIN 140 160 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 161 180 4 (POTENTIAL).
FT DOMAIN 181 205 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 206 228 5 (POTENTIAL).
FT DOMAIN 229 248 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 249 270 6 (POTENTIAL).
FT DOMAIN 271 291 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 292 312 7 (POTENTIAL).
FT DOMAIN 313 >353 CYTOPLASMIC (POTENTIAL).
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FT DISULFID 116 193 BY SIMILARITY.
 FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT NON_TER 353 353
 SQ SEQUENCE 353 AA; 39919 MW; 1FF04E31A7E825E4 CRC64;
 Query Match 62.2%; Score 74; DB 1; Length 353;
 Best Local Similarity 66.7%; Pred. No. 0.0017;
 Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 1 VIIAVVLVFLACQIPHNVL 21
 Db 249 VIFAVVLFLCWLPLYNVL 269
 RESULT 8
 IL8B_PANTR STANDARD; PRT; 353 AA.
 AC Q28807;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (FRAGMENT).
 GN IL8RB OR CXCR2.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96175151; PubMed=9110929;
 RA Alvarez V., Coto E., Setien F., Gonzalez S., Gonzalez-Roces S.,
 RA Lopez-Larrea C.;
 RT "Characterization of interleukin-8 receptors in non-human primates."
 RL Immunogenetics 43:261-267(1996).
 CC -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
 CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
 CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
 CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
 CC AND TO GPRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 CC EMBL; X91113; CAA62563.1; -
 DR HSSP; P34996; 1DDD.
 DR InterPro; IPR000276; -
 DR Pfam; PF00001; 7tm.1; 1.
 DR PROSITE; PS00237; G-PROTEIN RECP_FL_1; 1.
 DR PROSITE; PS0262; G-PROTEIN RECP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 FT NON_TER 1 1
 FT DOMAIN <1 45 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 46 72 1 (POTENTIAL).
 FT DOMAIN 73 81 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 82 102 2 (POTENTIAL).
 FT DOMAIN 103 117 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 118 139 3 (POTENTIAL).
 FT DOMAIN 140 160 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 161 180 4 (POTENTIAL).
 FT DOMAIN 181 205 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 206 228 5 (POTENTIAL).
 FT DOMAIN 229 248 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 249 270 6 (POTENTIAL).

FT DOMAIN 271 291 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 292 312 7 (POTENTIAL).
 FT DOMAIN 313 >353 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 116 193 BY SIMILARITY.
 FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT NON_TER 353 353
 SQ SEQUENCE 353 AA; 39998 MW; E745ACD9EC10C1E2 CRC64;
 Query Match 62.2%; Score 74; DB 1; Length 353;
 Best Local Similarity 66.7%; Pred. No. 0.0017;
 Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 1 VIIAVVLVFLACQIPHNVL 21
 Db 249 VIFAVVLFLCWLPLYNVL 269
 RESULT 9
 IL8A_RABIT STANDARD; PRT; 355 AA.
 AC P21109;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR A (IL-8R A) (CXCR-1).
 GN IL8RA OR CXCR1.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91378994; PubMed=1898400;
 RA Beckmann M.P., Mungler W.E., Kozlosky C., Vandenbos T., Price V.,
 RA Lyman S., Gerard N.P., Gerard C., Cerretti D.P.;
 RT "Molecular characterization of the interleukin-8 receptor."
 RL Biochem. Biophys. Res. Commun. 179:784-789(1991).
 CC [2]
 CC SEQUENCE FROM N.A.
 CC STRAIN=ALBINO; TISSUE=Neutrophils;
 CC MEDLINE=91056034; PubMed=1700779;
 CC Thomas K.M., Pyun H.Y., Navarro J.;
 CC "Molecular cloning of the fmet-Leu-Phe receptor from neutrophils."
 CC J. Biol. Chem. 265:20061-20064(1990).
 CC [3]
 CC SEQUENCE FROM N.A.
 CC TISSUE=Neutrophils;
 CC MEDLINE=92148149; PubMed=1737938;
 CC Lee J., Kuang W.-J., Rice G.C., Wood W.I.;
 CC "Characterization of complementary DNA clones encoding the rabbit
 CC IL-8 receptor."
 CC J. Immunol. 148:1261-1264(1992).
 CC -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
 CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
 CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
 CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER SYSTEM.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: NEUTROPHILS.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -!- CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE THE RECEPTOR FOR
 CC FMET-LEU-PHE (N-FORMYL PEPTIDE RECEPTOR).
 CC -----
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 CC -----
 CC EMBL; M74240; AAA31375.1; -

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DR EMBL; M58021; AAA31377.1; -
DR EMBL; M82873; AAA31376.1; -
DR PIR; A23669; A23669.
DR PIR; A46483; A46483.
DR PIR; J01231; J01231.
DR GCRDB; GCR_0107; -
DR GCRDB; GCR_0108; -
DR GCRDB; GCR_0298; -
DR InterPro; IPR000174; -
DR InterPro; IPR000276; -
DR InterPro; IPR001355; -
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00427; INTRLEUKIN8R.
DR PRINTS; PR00572; INTRLEUKIN8R.
DR PROSITE; PS00237; G_PROTEIN_RECP_FL_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Chemotaxis.
FT DOMAIN 1 40 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 41 67 1 (POTENTIAL).
FT DOMAIN 68 73 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 74 92 2 (POTENTIAL).
FT DOMAIN 93 114 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 115 138 3 (POTENTIAL).
FT DOMAIN 139 159 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 160 184 4 (POTENTIAL).
FT DOMAIN 185 204 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 205 232 5 (POTENTIAL).
FT DOMAIN 233 247 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 248 270 6 (POTENTIAL).
FT DOMAIN 271 290 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 291 313 7 (POTENTIAL).
FT DOMAIN 314 355 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 7 7 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 21 21 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 115 192 BY SIMILARITY.
FT CONFLICT 90 111 DLLFALTPMIVAWSKSGWIFG ->
PACPDHVLGRLOKRLDER (IN REF. 2).
FT CONFLICT 146 147 HA -> QS (IN REF. 2).
FT CONFLICT 204 204 R -> C (IN REF. 2).
FT CONFLICT 287 288 DI -> EL (IN REF. 2).
SQ SEQUENCE 355 AA; 40622 MW; EFE49ACB9D1E0F21 CRC64;

Query Match 62.2%; Score 74; DB 1; Length 355;
Best Local Similarity 66.7%; Pred. No. 0.0018;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIIAVLVFLACQIPHNMVLL 21
||| ||||| ||| | :| :| :| :|
Db 248 VIFAVLFLCWLPLNVL 268

RESULT 10
IL8B_RABIT
ID IL8B_RABIT STANDARD; PRT; 358 AA.
AC P35344;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GRO/MGSA
DE RECEPTOR).
DE IL8RB OR CXCR2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ALBINO; TISSUE=Blood;
RX MEDLINE=94230294; PubMed=8175642;
RA Prado G.N., Thomas K.M., Suzuki H., Larosa G.J., Wilkinson N.C.,

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RA Polco E., Navarro J.;
RT "Molecular characterization of a novel rabbit interleukin-8 receptor
RT isotype.";
RL J. Biol. Chem. 269:12391-12394(1994).
CC -I- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC MESSENGER SYSTEM. THE AFFINITY OF THIS RECEPTOR IS IL-8 >> NAP-2 >
CC MGSA (GRO).
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -I- TISSUE SPECIFICITY: EXPRESSED PREFERENTIALLY IN NEUTROPHILS.
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
EMBL; L24445; AAA31378.1; -
DR GCRDB; GCR_0861; -
DR PIR; A53752; A53752.
DR InterPro; IPR000057; -
DR InterPro; IPR000174; -
DR InterPro; IPR000276; -
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00427; INTRLEUKIN8R.
DR PRINTS; PR00573; INTRLEUKIN8R.
DR PROSITE; PS00237; G_PROTEIN_RECP_FL_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Chemotaxis.
FT DOMAIN 1 46 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 47 73 1 (POTENTIAL).
FT DOMAIN 74 82 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 83 103 2 (POTENTIAL).
FT DOMAIN 104 118 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 119 140 3 (POTENTIAL).
FT DOMAIN 141 161 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 162 181 4 (POTENTIAL).
FT DOMAIN 182 206 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 207 229 5 (POTENTIAL).
FT DOMAIN 230 249 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 250 271 6 (POTENTIAL).
FT DOMAIN 272 292 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 293 313 7 (POTENTIAL).
FT DOMAIN 314 358 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 117 194 BY SIMILARITY.
SQ SEQUENCE 358 AA; 40632 MW; 6899716944D6126A CRC64;

Query Match 62.2%; Score 74; DB 1; Length 358;
Best Local Similarity 66.7%; Pred. No. 0.0018;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIIAVLVFLACQIPHNMVLL 21
||| ||||| ||| | :| :| :| :|
Db 250 VIFAVLFLCWLPLNVL 270

RESULT 11
IL8B_HUMAN
ID IL8B_HUMAN STANDARD; PRT; 360 AA.
AC P25025;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)

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CC -----
 DR EMBL; U19947; AAA84996.1; -;
 DR GCRDB; GCR_1224; -;
 DR InterPro; IPR000174; -;
 DR InterPro; IPR000276; -;
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PRINTS; PR00427; INTRLEUKIN8R.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL_1; 1.
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL_2; 1.
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Chemotaxis.
 FT DOMAIN 1 48 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 49 75 1 (POTENTIAL).
 FT DOMAIN 76 84 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 85 105 2 (POTENTIAL).
 FT DOMAIN 106 120 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 121 142 3 (POTENTIAL).
 FT DOMAIN 143 163 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 164 183 4 (POTENTIAL).
 FT DOMAIN 184 208 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 209 231 5 (POTENTIAL).
 FT DOMAIN 232 251 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 252 273 6 (POTENTIAL).
 FT DOMAIN 274 294 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 295 315 7 (POTENTIAL).
 FT DOMAIN 316 360 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 119 196 BY SIMILARITY.
 FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 24 24 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 360 AA; 40625 MW; 9A7F70C982A632D1 CRC64;

Query Match 61.3%; Score 73; DB 1; Length 360;
 Best Local Similarity 66.7%; Pred. No. 0.0025;
 Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 VIIAVLVFLACQIPHNVL 21
 DB 252 VIFAVLVFLCWLPLNVL 272
 RESULT 13
 IL8B_MOUSE
 ID IL8B_MOUSE STANDARD; PRT; 359 AA.
 AC P35343;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GRO/MGSA
 DE RECEPTOR).
 GN IL8RB OR CXCR2 OR CMKAR2 OR GPCR16.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=94117014; PubMed=8288247;
 RX Cerretti D.P., Nelson N., Kozlosky C.J., Morrissey P.J.,
 RA Copeland N.G., Gilbert D.J., Jenkins N.A., Dosik J.K., Mock B.A.;
 RT "The murine homologue of the human interleukin-8 receptor type B maps
 RT near the Ity-Ish-Bcg disease resistance locus.";
 RL Genomics 18:410-413(1993).
 RN [2]
 RP SEQUENCE FROM N.A.

RC STRAIN=BALB/C;
 RX MEDLINE=95050766; PubMed=7961909;
 RA Bozic C.R., Gerard N.P., von Uexkull-Guldenband C.,
 RA Kolakowski L.F. Jr., Conklyn M.J., Breslow R., Showell H.J.,
 RA Gerard C.;
 RT "The murine interleukin 8 type B receptor homologue and its ligands.
 RT Expression and biological characterization.";
 RL J. Biol. Chem. 269:29355-29358(1994).
 RN [3]
 RN SEQUENCE FROM N.A.
 RP STRAIN=129/SV;
 RC MEDLINE=95363183; PubMed=7636264;
 RX Lee J., Cacalano G., Camerato T., Toy K., Moore M.W., Wood W.I.;
 RA "Chemokine binding and activities mediated by the mouse IL-8
 RT receptor.";
 RL J. Immunol. 155:2158-2164(1995).
 RN [4]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=94252584; PubMed=8194768;
 RX Harada A., Kuno K., Nomura H., Mukaida N., Murakami S., Matsushima K.;
 RA "Cloning of a cDNA encoding a mouse homolog of the interleukin-8
 RT receptor.";
 RL Gene 142:297-300(1994).
 RN [5]
 RN SEQUENCE OF 145-258 FROM N.A.
 RP TISSUE=Testis;
 RC MEDLINE=94116980; PubMed=8288218;
 RX Wilkie T.M., Chen Y., Gilbert D.J., Moore K.J., Yu L., Simon M.I.,
 RA Copeland N.G., Jenkins N.A.;
 RT "Identification, chromosomal location, and genome organization of
 RT mammalian G-protein-coupled receptors.";
 RL Genomics 18:175-184(1993).
 CC -1- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
 CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
 CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
 CC G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
 CC AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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DR EMBL; L23637; AAA39305.1; -;
 DR EMBL; L13239; AAA62109.1; -;
 DR EMBL; U31207; AAC52239.1; -;
 DR EMBL; D17630; BAA04536.1; -;
 DR EMBL; L20337; AAA16853.1; -;
 DR PIR; A53677; A53677.
 DR GCRDB; GCR_0550; -;
 DR GCRDB; GCR_0812; -;
 DR GCRDB; GCR_0838; -;
 DR GCRDB; GCR_1027; -;
 DR GCRDB; GCR_1670; -;
 DR MGD; MGI:105303; Cmkar2.
 DR InterPro; IPR000057; -;
 DR InterPro; IPR000174; -;
 DR InterPro; IPR000276; -;
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PRINTS; PR00427; INTRLEUKIN8R.
 DR PRINTS; PR00573; INTRLEUKIN8R.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL_1; 1.
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Chemotaxis.
 FT DOMAIN 1 47 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 48 74 1 (POTENTIAL).
 FT DOMAIN 75 83 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 84 104 2 (POTENTIAL).
 FT DOMAIN 105 119 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 120 141 3 (POTENTIAL).
 FT DOMAIN 142 162 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 163 182 4 (POTENTIAL).
 FT DOMAIN 183 207 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 208 230 5 (POTENTIAL).
 FT DOMAIN 231 250 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 251 272 6 (POTENTIAL).
 FT DOMAIN 273 293 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 294 314 7 (POTENTIAL).
 FT DOMAIN 315 359 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 23 23 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 118 195 BY SIMILARITY.
 SQ SEQUENCE 359 AA; 40425 MW; 74BD166E9B679F88 CRC64;

Query Match 59.7%; Score 71; DB 1; Length 359;
 Best Local Similarity 70.0%; Pred. No. 0.0047;
 Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIIAVVLVFLACOIPHNVL 20
 II ||||| | : : : : :
 Db 251 VIFAVVLVFLCWPYNVL 270

RESULT 14
 IL8B_RAT STANDARD; PRT; 359 AA.
 AC P35407;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GRO/MGSA RECEPTOR).
 GN IL8RB OR CXCR2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 [1]
 SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Lung;
 RX MEDLINE=97361587; PubMed=9218548;
 RA Gobl A.E., Huang M.K., Wang S., Zhou Y., Oeberg K.;
 RT "Molecular cloning and characterization of a cDNA encoding the rat interleukin-8 receptor.";
 RL Biochim. Biophys. Acta 1326:171-177(1997).
 [2]
 SEQUENCE FROM N.A.
 RC STRAIN=WISTAR; TISSUE=Liver;
 RA Konishi K., Shibata F., Watanabe K., Tsurufuji S., Nakagawa H.,
 RA Fujioka M.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 [3]
 SEQUENCE FROM N.A.
 RC STRAIN=WISTAR; TISSUE=Spleen, and Lung;
 RX MEDLINE=97115810; PubMed=8955112;
 RA Dunstan C.A.N., Salafraanca M.N., Adhikari S., Xia Y., Feng L.,
 RA Harrison J.K.;
 RT "Identification of two rat genes orthologous to the human interleukin-8 receptors.";
 RL J. Biol. Chem. 271:32770-32776(1996).
 CC -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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 CC -----

DR EMBL; X77797; CAA54824.1; -
 DR EMBL; D63584; BAA09797.1; -
 DR EMBL; U70988; AAC52961.1; -
 DR PIR; S42096; S42096.
 DR GCRDB; GCR.0913; -
 DR GCRDB; GCR.1405; -
 DR GCRDB; GCR.1524; -
 DR InterPro; IPR000057; -
 DR InterPro; IPR000174; -
 DR InterPro; IPR000276; -
 DR Pfam; PF00001; 7tm1.1;
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PRINTS; PR00427; INTRLEUKIN8R.
 DR PRINTS; PR00573; INTRLEUKIN8R.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Chemotaxis.
 FT DOMAIN 1 47 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 48 74 1 (POTENTIAL).
 FT DOMAIN 75 83 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 84 104 2 (POTENTIAL).
 FT DOMAIN 105 119 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 120 141 3 (POTENTIAL).
 FT DOMAIN 142 162 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 163 182 4 (POTENTIAL).
 FT DOMAIN 183 207 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 208 230 5 (POTENTIAL).
 FT DOMAIN 231 250 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 251 272 6 (POTENTIAL).
 FT DOMAIN 273 296 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 297 314 7 (POTENTIAL).
 FT DOMAIN 315 359 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 23 23 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 202 201 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 118 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 359 AA; 40532 MW; EF547326A074ABDD CRC64;

Query Match 58.8%; Score 70; DB 1; Length 359;
 Best Local Similarity 70.0%; Pred. No. 0.0064;
 Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIIAVVLVFLACOIPHNVL 20
 II ||||| | : : : : :
 Db 251 VIFAVVLVFLCWPYNVL 270

RESULT 15
 IL8B_MACMU STANDARD; PRT; 353 AA.
 AC Q28519;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (FRAGMENT).
 GN IL8RB OR CXCR2.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopitheciinae; Macaca.
 OX NCBI_TaxID=9544;

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RN  SEQUENCE FROM N.A.
RP  MEDLINE=96175151; PubMed=9110929;
RA  Alvarez V., Coto E., Setien F., Gonzalez S., Gonzalez-Roces S.,
RA  Lopez-Larrea C.;
RL  "Characterization of interleukin-8 receptors in non-human primates.";
CC  Immunogenetics 43:261-267(1996).
CC  -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC  NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC  CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC  G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC  MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
CC  AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
CC  -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC  -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC  -----
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CC  -----
DR  EMBL; X91116; CAA62565.1; -.
DR  HSSP; P34996; 1DDD.
DR  InterPro: IPR000276; -.
DR  Pfam; PF00001; 7tm1.1.
DR  PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
DR  PROSITE; PS00262; G_PROTEIN_RECEPTOR_F1_2; 1.
KW  G-protein coupled receptor; Transmembrane; Glycoprotein;
KW  Chemotaxis.
FT  NON_TER 1 45
FT DOMAIN <1 45 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 46 72 1 (POTENTIAL).
FT DOMAIN 73 81 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 82 102 2 (POTENTIAL).
FT DOMAIN 103 117 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 118 139 3 (POTENTIAL).
FT DOMAIN 140 160 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 161 180 4 (POTENTIAL).
FT DOMAIN 181 205 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 206 228 5 (POTENTIAL).
FT DOMAIN 229 248 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 249 270 6 (POTENTIAL).
FT DOMAIN 271 291 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 292 312 7 (POTENTIAL).
FT DOMAIN 313 >353 CYTOPLASMIC (POTENTIAL).
FT DISULFID 116 193 BY SIMILARITY.
FT CARBOHYD 19 19 N-LINKED (GLCNAC... ) (POTENTIAL).
FT NON_TER 353 353
SQ  SEQUENCE 353 AA; 39947 MW; EC8B38130657C713 CRC64;

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Query Match      58.0%; Score 69; DB 1; Length 353;
Best Local Similarity 61.9%; Pred. No. 0.0088;
Matches 13; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy 1 VIIAVVLVFLACQIPHNMYLL 21
   |||:|:|:|:|:|:|:|:|:|
Db 249 VIFAVVLIFLLCWLPLSLVLL 269

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Search completed: May 23, 2001, 15:36:20
Job time: 651 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:35:16 ; Search time 189.03 Seconds
(without alignments)
15.501 Million cell updates/sec

Title: US-08-887-977-10_COPY_246_270

Perfect score: 119
Sequence: 1 VIIAVLVFLACQIPHNMLLVTA 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPTREMBL_15:*
- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_unclassified:*
- 13: sp_vertebrate:*
- 14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	114	95.8	367	11	Q9R1V0	Q9R1V0 mus musculus
2	74	62.2	79	4	Q9P2U2	Q9P2U2 homo sapien
3	74	62.2	111	4	Q9P2T6	Q9P2T6 homo sapien
4	70	58.8	380	4	Q9UNW8	Q9UNW8 homo sapien
5	68	57.1	174	6	Q9TU48	Q9TU48 bos taurus
6	68	57.1	174	6	Q9TQ57	Q9TQ57 bos taurus
7	67	56.3	382	11	Q9Z282	Q9Z282 mus musculus
8	61	51.3	361	6	O46685	O46685 bos taurus
9	60	50.4	368	13	O42444	O42444 oncorhynchus
10	59	49.6	375	4	O43494	O43494 homo sapien
11	58	48.7	342	13	Q93239	Q93239 cyprinus ca
12	57	47.9	360	11	Q9JL20	Q9JL20 mus musculus
13	57	47.9	362	11	Q9JL21	Q9JL21 mus musculus
14	57	47.9	362	11	Q9JF1	Q9JF1 mus musculus
15	56	47.1	350	4	Q9NPB9	Q9NPB9 homo sapien
16	55	46.2	346	13	Q9PUA9	Q9PUA9 bufo japoni
17	55	46.2	354	14	Q9IP69	Q9IP69 human cytom
18	55	46.2	354	14	Q9IP68	Q9IP68 human cytom
19	55	46.2	354	14	Q9IP67	Q9IP67 human cytom

20	55	46.2	354	14	Q9IP66	Q9IP66 human cytom
21	55	46.2	354	14	Q9IP65	Q9IP65 human cytom
22	55	46.2	361	4	Q9NZG2	Q9NZG2 homo sapien
23	55	46.2	362	11	O89039	O89039 rattus norv
24	55	46.2	362	11	Q9JL20	Q9JL20 rattus norv
25	54	45.4	336	5	Q9Y073	Q9Y073 lymnaea sta
26	54	45.4	369	4	Q9UQ06	Q9UQ06 homo sapien
27	53	44.5	385	11	Q9JK40	Q9JK40 mus musculu
28	52	43.7	296	6	Q9TTY6	Q9TTY6 canis famil
29	52	43.7	367	11	Q9JL19	Q9JL19 rattus norv
30	51	42.9	336	14	Q9JSH4	Q9JSH4 fowlpox vir
31	51	42.9	415	4	O15185	O15185 homo sapien
32	51	42.9	678	5	Q94736	Q94736 stomoxys ca
33	50	42.0	106	5	O9W4R0	O9W4R0 drosophila
34	50	42.0	263	5	O76873	O76873 drosophila
35	50	42.0	351	6	Q9MYJ9	Q9MYJ9 oryctolagus
36	50	42.0	367	11	O88410	O88410 mus musculu
37	50	42.0	367	11	Q9QWN6	Q9QWN6 mus musculu
38	50	42.0	394	5	O9U721	Q9U721 drosophila
39	50	42.0	521	5	O9VAD2	O9VAD2 drosophila
40	49	41.2	343	6	O9XT45	O9XT45 macaca mula
41	49	41.2	343	6	Q9N0Z0	Q9N0Z0 cercopithec
42	49	41.2	359	13	Q9PVY7	Q9PVY7 anguilla an
43	49	41.2	360	4	Q9ULY7	Q9ULY7 homo sapien
44	49	41.2	360	4	Q9ULY6	Q9ULY6 homo sapien
45	49	41.2	384	13	Q9PUQ8	Q9PUQ8 fugu rubrip

ALIGNMENTS

RESULT 1					
Q9R1V0					
ID	Q9R1V0	PRELIMINARY;	PRT;	367	AA.
AC	Q9R1V0;				
DT	01-MAY-2000 (TrEMBLrel. 13, Created)				
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)				
DT	01-JUN-2000 (TrEMBLrel. 14, Last annotation update)				
DE	CC CHEMOKINE LARC SPECIFIC RECEPTOR.				
GN	MCCR6.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Tanaka Y.;				
RT	"Molecular Cloning of Murine Homologue of CCR6, the Specific Receptor for CC Chemokine LARC."				
RL	Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AB016031; BAA82443.1;				
DR	INTERPRO; IPR000190;				
DR	INTERPRO; IPR000276;				
DR	INTERPRO; IPR000355;				
DR	PFAM; PF00001; 7tm.1; 1.				
DR	PRINTS; PR00237; GPCRHHODOPSN.				
DR	PRINTS; PR00635; ANGIOTENSINR.				
DR	PRINTS; PR00657; CCEMOKINER.				
DR	PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.				
KW	Receptor.				
SQ	SEQUENCE 367 AA; 42082 MW; 207FD98B2F7A6DD3 CRC64;				

Query Match 95.8%; Score 114; DB 11; Length 367;
Best Local Similarity 95.8%; Pred. No. 6.5e-09;
Matches 23; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	VIIAVLVFLACQIPHNMLLVTA 24	
Db	247	VIIAVLVFLACQIPHNMLLVTA 270	

RESULT 2

Q9P2U2
ID Q9P2U2 PRELIMINARY; PRT; 79 AA.
AC Q9P2U2;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE IL-8 RECEPTOR TYPE A (FRAGMENT).
GN CXCR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kato H., Tsuchiya N., Tokunaga K.;
RT "Detection of single nucleotide polymorphisms in the coding region of
human CXCR1-chemokine receptor CXCR1, CXCR2, and CXCR3."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB032728; BAA92290.1; -
KW Receptor.
FT NON_TER 1 1
FT NON_TER 79 79
SQ SEQUENCE 79 AA; 9103 MW; D9393C53AA651564 CRC64;

Query Match 62.2%; Score 74; DB 4; Length 79;
Best Local Similarity 66.7%; Pred. No. 0.0011;
Matches 14; Conservative 4; Mismatches 4; Indels 3; Gaps 0;
QY 1 VTIIVLVFLACQIPHNMLVLL 21
DB 21 VIFAVVLFLCWLPLYNVLVLL 41

RESULT 3
Q9P2T6 PRELIMINARY; PRT; 111 AA.
AC Q9P2T6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE IL-8 RECEPTOR TYPE B (FRAGMENT).
GN CXCR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kato H., Tsuchiya N., Tokunaga K.;
RT "Detection of single nucleotide polymorphisms in the coding region of
human CXCR1-chemokine receptor CXCR1, CXCR2, and CXCR3."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB032734; BAA92296.1; -
KW Receptor.
FT NON_TER 1 1
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12947 MW; 1425DC123439A1BB CRC64;

Query Match 62.2%; Score 74; DB 4; Length 111;
Best Local Similarity 66.7%; Pred. No. 0.0014;
Matches 14; Conservative 4; Mismatches 4; Indels 3; Gaps 0;
QY 1 VTIIVLVFLACQIPHNMLVLL 21
DB 62 VIFAVVLFLCWLPLYNVLVLL 82

RESULT 4
Q9UNW8 PRELIMINARY; PRT; 380 AA.
ID Q9UNW8
AC Q9UNW8;

DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE G PROTEIN-COUPLED RECEPTOR.
GN G2A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Weng Z., Witte O.N.;
RT "A DNA damage and stress inducible G protein-coupled receptor blocks
cells in G2/M."
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF083955; AAD47380.1; -
DR INTERPRO; IPR000276; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 380 AA; 42499 MW; 6DE63D17275ECD74 CRC64;

Query Match 58.8%; Score 70; DB 4; Length 380;
Best Local Similarity 60.9%; Pred. No. 0.015;
Matches 14; Conservative 5; Mismatches 4; Indels 4; Gaps 0;
QY 3 TAVLVFLACQIPHNMLVLTAA 25
DB 245 TAVVFLVCFAPYHLLVLTAA 267

RESULT 5
Q9TU48 PRELIMINARY; PRT; 174 AA.
AC Q9TU48;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE INTERLEUKIN 8 RECEPTOR-LIKE PROTEIN (FRAGMENT).
GN IL8R.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Grosche W.M., Kappes S.M., Laegreid W.W., Keele J.W.,
Chitko-McKown C.G., Heaton M.P.;
RT "Single Nucleotide Polymorphism (SNP) Discovery and Linkage Mapping of
Bovine Cytokine Genes."
RL Mamm. Genome 10:1062-1069(1999).
DR EMBL; AF140650; AAF07867.1; -
DR INTERPRO; IPR000174; -
DR INTERPRO; IPR000276; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSIN.
DR PRINTS; PR00427; INTRLEUKIN8R.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 174 174
SQ SEQUENCE 174 AA; 20107 MW; D20E223B0FE8E836 CRC64;

Query Match 57.1%; Score 68; DB 6; Length 174;
Best Local Similarity 61.9%; Pred. No. 0.015;
Matches 13; Conservative 4; Mismatches 4; Indels 4; Gaps 0;
QY 1 VTIIVLVFLACQIPHNMLVLL 21
DB 100 VIFAVVLFLCWLPLYNVLVLI 120

```
RESULT 6
Q9TQ57 ID Q9TQ57 PRELIMINARY; PRT; 174 AA.
AC OQ57; 2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE INTERLEUKIN 8 RECEPTOR-LIKE PROTEIN (FRAGMENT).
GN IL8R.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
ON NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Grosse W.M., Kappes S.M., Laegreid W.W., Keele J.W.,
RA Chitko-McKown C.G., Heaton M.P.;
RT "Single Nucleotide Polymorphism (SNP) Discovery and Linkage Mapping of
RT Bovine Cytokine Genes.";
RL Mamm. Genome 10:1062-1069(1999).
DR EMBL; AF140652; AAF07869.1; -
DR EMBL; AF140648; AAF07865.1; -
DR EMBL; AF140649; AAF07866.1; -
DR EMBL; AF140651; AAF07868.1; -
DR INTERPRO; IPR000174; -
DR INTERPRO; IPR000276; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PRINTS; PR00427; INTRLEUKIN8R.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 174 174
SQ SEQUENCE 174 AA; 20116 MW; D21C877CE5BAFC6 CRC64;

Query Match 57.1%; Score 68; DB 6; Length 174;
Best Local Similarity 61.9%; Pred. No. 0.015;
Matches 13; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 VIIAVLVFLACQIPHNMLLV 21
Db 100 VIFAVLVFLXLCWLPYNLVLI 120

RESULT 7
Q9Z282 ID Q9Z282 PRELIMINARY; PRT; 382 AA.
AC Q9Z282;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE G PROTEIN-COUPLED RECEPTOR G2A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98445372; PubMed=9770487;
RA Weng Z., Fluckiger A.C., Nisitani S., Wahl M.I., Le L.Q., Hunter C.A.,
RA Fernal A.A., Le Beau M.M., Witte O.N.;
RT "A DNA damage and stress inducible G protein-coupled receptor blocks
RT cells in G2/M.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:12334-12339(1998).
DR EMBL; AF083442; AAC67542.1; -
DR INTERPRO; IPR000276; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
```

```
SQ SEQUENCE 382 AA; 42652 MW; D4F8CE0370CCD610 CRC64;

Query Match 56.3%; Score 67; DB 11; Length 382;
Best Local Similarity 60.9%; Pred. No. 0.041;
Matches 14; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 3 IAVVLVFLACQIPHNMLLVTA 25
Db 243 IAVVTIFLVCFAFYHVLLVKA 265

RESULT 8
O46685 ID O46685 PRELIMINARY; PRT; 361 AA.
AC O46685;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE ORPHAN G PROTEIN-COUPLED RECEPTOR BRGRIB.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
ON NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Ferrer-Martinez A., Felipe A., Casado J., Pastor-Anglada M.;
RA Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; U88367; AAC05612.1; -
DR EMBL; U88366; AAC05611.1; -
DR INTERPRO; IPR000276; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
SQ SEQUENCE 361 AA; 40905 MW; 4802E77C9A45DEE1 CRC64;

Query Match 51.3%; Score 61; DB 6; Length 361;
Best Local Similarity 40.9%; Pred. No. 0.29;
Matches 9; Conservative 11; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VIIAVLVFLACQIPHNMLLV 22
Db 229 LVLSVVIFLACFLPYHLLIV 250

RESULT 9
O42444 ID O42444 PRELIMINARY; PRT; 368 AA.
AC O42444;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE INTERLEUKIN-8-LIKE RECEPTOR.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
ON NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Zou J., Daniels G.D., Cunningham C., Secombes C.J.;
RA Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ003159; CAA05917.1; -
DR INTERPRO; IPR000276; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
```

SQ SEQUENCE 368 AA; 41523 MW; BE28E2D4C47E821A CRC64;

Query Match 50.4%; Score 60; DB 13; Length 368;
Best Local Similarity 50.0%; Pred. No. 0.4;
Matches 12; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 1 VIIAVLVFLACQIPHNNVLLVTA 24
II:IIIIII I:IIIIII I:
Db 255 VILVVAVFVLSQLPYNSVLVMEA 278

RESULT 10

O43494
ID O43494 PRELIMINARY; PRT; 375 AA.

AC O43494;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE G PROTEIN-COUPLED RECEPTOR.
GN GPR30.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=98140132; PubMed=9479505;

RA O'dowd B.F., Nguyen T., Marchese A., Cheng R., Lynch K.R.,
RA Heng H.H.Q., Kolakowski L.F. Jr., George S.R.;

RT "Discovery of three novel G-protein-coupled receptor genes.";
RL Genomics 47:310-313(1998).

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
DR EMBL: AF027956; AAC52027.1; -;
DR INTERPRO: IPR000276; -;

DR PFAM: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.

DR PROSITE: PS00237; G-PROTEIN RECEPTOR; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.

SQ SEQUENCE 375 AA; 42230 MW; 619CFLEAE65A912 CRC64;

Query Match 49.6%; Score 59; DB 4; Length 375;
Best Local Similarity 50.0%; Pred. No. 0.57;
Matches 11; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY 1 VIIAVLVFLACQIPHNNVLLV 22
II:IIIIII I:IIIIII I:
Db 260 MILAVLVVFFVCWLPENVFISV 281

RESULT 11

O93239
ID O93239 PRELIMINARY; PRT; 342 AA.

AC O93239;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE CXC CHEMOKINE RECEPTOR-2.

OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.

OX NCBI_TaxID=7962;
RN [1]

RP SEQUENCE FROM N.A.
RA Fujiki K., Nakao M., Shin D., Yano T.;

RT "cDNA cloning of a carp homologue-2 of mammalian interleukin-8
receptors.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL: AB010713; BAA31470.1; -;
DR INTERPRO: IPR000276; -;

DR PFAM: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G-PROTEIN RECEPTOR; UNKNOWN 1.
SQ SEQUENCE 342 AA; 38481 MW; 8946E5E5534B39 CRC64;

Query Match 48.7%; Score 58; DB 13; Length 342;
Best Local Similarity 45.5%; Pred. No. 0.74;
Matches 10; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

OY 1 VIIAVLVFLACQIPHNNVLLV 22
II:IIIIII I:IIIIII I:
Db 233 VILSVLAFIVCWLPFNILELI 254

RESULT 12

O9JL20
ID O9JL20 PRELIMINARY; PRT; 360 AA.

AC O9JL20;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CC CHEMOKINE RECEPTOR 10B (FRAGMENT).
GN CCR10.

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RP SEQUENCE FROM N.A.
RX STRAIN=BALB/C;
RX MEDLINE=20191997; PubMed=10725696;

RA Jarman D.I., Rits M., Bota D., Gerard N.P., Graham G.J.,
RA Clark-Lewis I., Gerard C.;

RT "Cutting edge: identification of the orphan receptor G-protein-coupled
receptor 2 as CCR10, a specific receptor for the chemokine ESKine.";
RL J. Immunol. 164:3460-3464(2000).

DR EMBL: AF215983; AAF63711.1; -;
DR NON-TER. 1 1
KW RECEPTOR.

FT NON-TER. 1 1
SQ SEQUENCE 360 AA; 38738 MW; 16CBFEF69F785BA23 CRC64;

Query Match 47.9%; Score 57; DB 11; Length 360;
Best Local Similarity 36.0%; Pred. No. 1.1;
Matches 9; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

Query Match 47.9%; Score 57; DB 11; Length 360;
Best Local Similarity 36.0%; Pred. No. 1.1;
Matches 9; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

OY 1 VIIAVLVFLACQIPHNNVLLVTA 25
II:IIIIII I:IIIIII I:
Db 246 VVALVAVFVVLQPLYSIALLLDTA 270

RESULT 13

O9JL21
ID O9JL21 PRELIMINARY; PRT; 362 AA.

AC O9JL21;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CC CHEMOKINE RECEPTOR 10A.
GN CCR10.

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=20191997; PubMed=10725696;

RA Jarman D.I., Rits M., Bota D., Gerard N.P., Graham G.J.,
RA Clark-Lewis I., Gerard C.;

RT "Cutting edge: identification of the orphan receptor G-protein-coupled
receptor 2 as CCR10, a specific receptor for the chemokine ESKine.";
RL J. Immunol. 164:3460-3464(2000).

DR EMBL: AF215983; AAF63711.1; -;
DR NON-TER. 1 1
KW RECEPTOR.

FT NON-TER. 1 1
SQ SEQUENCE 360 AA; 38738 MW; 16CBFEF69F785BA23 CRC64;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:28:32 ; Search time 184.73 Seconds
(without alignments)
6.189 Million cell updates/sec

Title: US-08-887-977-10_COPY_271_290

Perfect score: 105

Sequence: 1 NLGKNRSCQSEKLGITYTKT 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	105	100.0	365	19 W48086	Human dendritic ce
2	105	100.0	365	21 Y97077	Primate (human) ch
3	46	43.8	202	21 G07214	Arabidopsis thalia
4	46	43.8	202	21 G51812	Arabidopsis thalia
5	46	43.8	218	21 G31193	Arabidopsis thalia
6	46	43.8	250	21 G07213	Arabidopsis thalia
7	46	43.8	250	21 G51811	Arabidopsis thalia
8	46	43.8	266	21 G31192	Arabidopsis thalia
9	46	43.8	379	22 B49209	V.cholerae VPI pha
10	44	41.9	49	18 Y11212	S. pneumoniae 3-ox
11	44	41.9	140	21 B41413	Human ORFX ORF1177

12	44	41.9	186	19 W38474	S. pneumoniae 3-ox
13	44	41.9	243	19 W80670	S. pneumoniae fatt
14	44	41.9	243	21 B15706	Streptococcus pneu
15	42	40.0	349	21 G31207	Arabidopsis thalia
16	42	40.0	1198	20 Y29248	Amino acid sequenc
17	41	39.0	610	11 R05494	Endothelial leukoc
18	41	39.0	610	11 R05538	Endothelial-leukoc
19	41	39.0	610	11 R08116	Endothelial cell-1
20	41	39.0	610	18 W18839	E-selectin. Homo
21	41	39.0	610	19 W46733	Amino acid sequenc
22	41	39.0	610	21 Y94504	Human E-selectin p
23	41	39.0	610	21 Y59500	Human ELAM-1 prote
24	41	39.0	694	19 W56539	Chicken hedgehog i
25	41	39.0	700	19 W56537	Mouse hedgehog int
26	41	39.0	700	19 W56538	Human hedgehog int
27	40.5	38.6	727	17 R88390	Human neurotransmi
28	40	38.1	25	17 R99674	RHAMM gene exon 2A
29	40	38.1	38	17 R99676	RHAMM gene exon 2A
30	40	38.1	84	21 G02646	Human secreted pro
31	40	38.1	204	21 G28778	Arabidopsis thalia
32	40	38.1	258	21 G28777	Arabidopsis thalia
33	40	38.1	304	21 G28776	Arabidopsis thalia
34	40	38.1	315	17 R89523	Rape leaf beta-ket
35	40	38.1	315	17 R89322	Rape seed beta-ket
36	40	38.1	343	21 B43598	Human cancer assoc
37	40	38.1	368	20 Y60520	Human normal bladd
38	40	38.1	426	18 W09821	Mouse interleukin-
39	40	38.1	630	18 W39166	Mouse RHAMM protei
40	40	38.1	631	17 R99675	RHAMM 1-2a isoform
41	39	37.1	31	20 Y02849	Fragment of human
42	39	37.1	101	20 W98976	Alcaligenes sp. pr
43	39	37.1	187	20 Y02844	Fragment of human
44	39	37.1	235	21 G22781	Arabidopsis thalia
45	39	37.1	235	21 G50473	Arabidopsis thalia

ALIGNMENTS

RESULT 1
W48086
ID W48086 standard; Protein; 365 AA.
XX
AC W48086;
XX
DT 11-JUN-1998 (first entry)
XX
DE Human dendritic cell chemokine receptor.
DE Human; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta;
KW receptor; dendritic cell; macrophage; inflammation; asthma.
KW Homo sapiens.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 193
FT /note= "encoded by CAN"
FT
PN WO9801557-A2.
XX
XX 15-JAN-1998.
XX
PF 02-JUL-1997; 97WO-US10819.
XX
PR 04-JUN-1997; 97US-0048593.
PR 05-JUL-1996; 96US-0675814.
PR 11-OCT-1996; 96US-0028329.
XX
XX (SCHE) SCHERING CORP.
PA
XX Gish KC, Schall TJ, Vicari A, Wang W, Zlotnik A;
XX WPI; 1998-101054/09.
DR

DR N-PSDB; V15418.
XX Novel chemokines, e.g. thymus expressed chemokine - used for
PT treating inflammatory conditions including asthma.
XX
XX
PS Claim 3; Page 94-95; 202pp; English.
XX
CC The present sequence represents human dendritic cell chemokine receptor.
CC Antibodies which bind to the protein can be used in detecting or
CC diagnosing various immunological conditions related to expression
CC of the protein. The nucleic acid can be used for screening and
CC isolating DNA clones for the chemokines, especially from other
CC species. The chemokine can be used in the treatment of conditions
CC associated with abnormal physiology or development, including
CC inflammatory conditions such as asthma.
XX
XX
SQ Sequence 365 AA;

Query Match 100.0%; Score 105; DB 19; Length 365;
Best Local Similarity 100.0%; Pred. No. 3.5e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLGKNRSCQSEKLIQYTKT 20
Db 271 nlgkmrscqsekligytktt 290
|||||

RESULT 2
Y97077
ID Y97077 standard; Protein; 365 AA.
AC Y97077;
XX
XX
DT 04-DEC-2000 (first entry)
DE
DE
XX
XX
XX
KW MIP-3-alpha; chemokine; CCR6 receptor; ligand; cytostatic; agonist;
KW antagonist; anti-psoriatic; dermatological; immunosuppressive;
XX anti-inflammatory.
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 193 /note= "Encoded by CAN#"
FT
XX
XX
PN WO2000046248-A1.
PD 10-AUG-2000.
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XX
PF 02-FEB-2000; 2000WO-US00511.
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PR 03-FEB-1999; 99US-0244281.
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XX
PA (SCHE) SCHERING CORP.
XX
XX
PI Oldham ER, Honey B, Dieu-Nosjean M, Caux C, Zlotnik A;
XX
XX
DR WPI; 2000-543477/49.
XX
XX
XX N-PSDB; A51971.
XX
XX
PT Novel methods for modulating the migration of cells within or to the
PT skin using MIP-3-alpha or CCR6 agonists or antagonists, useful for
PT treating skin disorders, e.g. cancer
XX
XX
PS Disclosure; Page 53-54; 61pp; English.
XX
XX
XX The MIP-3-alpha chemokine is expressed in inflamed skin cells. This
CC chemokine is the ligand for the CCR6 receptor. MIP-3-alpha or CCR6
CC agonists or antagonists can be used to modulate the migration of a cell
CC within or to the skin of a mammal. MIP-3-alpha can be used to purify a

CC population of cells expressing a MIP-3-alpha receptor. The methods are
CC useful for treating a mammalian subject with a skin disease or condition,
CC e.g. cancer, metastasis, psoriasis, atopic or contact dermatitis,
CC systemic lupus erythematosus and lichen ruber planus, or for treating
CC skin transplants or grafts.
XX
XX
SQ Sequence 365 AA;

Query Match 100.0%; Score 105; DB 21; Length 365;
Best Local Similarity 100.0%; Pred. No. 3.5e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLGKNRSCQSEKLIQYTKT 20
Db 271 nlgkmrscqsekligytktt 290
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RESULT 3
G07214
ID G07214 standard; Protein; 202 AA.
XX
XX
AC G07214;
XX
XX
DT 17-OCT-2000 (first entry)
XX
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4283.

XX
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
XX
OS Arabidopsis thaliana.
XX
XX
PN EP1033405-A2.
XX
XX
PD 06-SEP-2000.
XX
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PF 25-FEB-2000; 2000EP-0301439.

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Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
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RESULT 4
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ID G51812 standard; Protein; 202 AA.
AC G51812;
XX
XX
DF 18-OCT-2000 (first entry)
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65796.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
PN EP1033405-A2.
XX
PD 06-SEP-2000.
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Best Local Similarity

Matches

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Conservative

1;

Mismatches

8;

Indels

0;

Gaps

0;

Length

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XX	KW	hybridisation assay; genetic mapping; gene expression control; promoter;
XX	KW	termination sequence.
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PR 29-OCT-1999; 99US-0162142.

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Best Local Similarity 50.0%; Pred. No. 7.7;

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KW hybridisation assay; genetic mapping; gene expression control; promoter;
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Query Match 43.8%; Score 46; DB 21; Length 250;
Best Local Similarity 50.0%; Pred. No. 9;
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
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XX DT 18-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 65795.
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
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OS Arabidopsis thaliana.
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PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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PR 18-JUN-1999; 99US-0139458.
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PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
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PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 18-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.

PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 43.8%; Score 46; DB 21; Length 250;
Best Local Similarity 50.0%; Pred. No. 9;
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 3 GKMNRSCQSEKLGITYTKT 20
Db 85 gsinnlqlnkqygltkk 102

RESULT 8
G31192
ID G31192 standard; Protein; 266 AA.
XX
AC G31192;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 37418.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
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XX PD 06-SEP-2000. 99US-0142055.
XX PF 25-FEB-2000; 2000EP-0301439. 99US-0142390.
XX PR 25-FEB-1999; 99US-0121825. 99US-0142803.
PR 05-MAR-1999; 99US-0123180. 99US-0142920.
PR 09-MAR-1999; 99US-0123548. 99US-0142977.
PR 23-MAR-1999; 99US-0125788. 99US-0143542.
PR 25-MAR-1999; 99US-0126264. 99US-0143624.
PR 29-MAR-1999; 99US-0126785. 99US-0144005.
PR 01-APR-1999; 99US-0127462. 99US-0144085.
PR 06-APR-1999; 99US-0128234. 99US-0144086.
PR 08-APR-1999; 99US-0128714. 99US-0144325.
PR 16-APR-1999; 99US-0129845. 99US-0144331.
PR 19-APR-1999; 99US-0130077. 99US-0144332.
PR 21-APR-1999; 99US-0130449. 99US-0144333.
PR 23-APR-1999; 99US-0130510. 99US-0144335.
PR 28-APR-1999; 99US-0130891. 99US-0144352.
PR 30-APR-1999; 99US-0131449. 99US-0144632.
PR 30-APR-1999; 99US-0132048. 99US-0144884.
PR 04-MAY-1999; 99US-0132407. 99US-0144814.
PR 05-MAY-1999; 99US-0132484. 99US-0145086.
PR 06-MAY-1999; 99US-0132485. 99US-0145088.
PR 06-MAY-1999; 99US-0132486. 99US-0145085.
PR 07-MAY-1999; 99US-0132487. 99US-0145087.
PR 11-MAY-1999; 99US-0132863. 99US-0145089.
PR 14-MAY-1999; 99US-0134256. 99US-0145192.
PR 14-MAY-1999; 99US-0134218. 99US-0145145.
PR 14-MAY-1999; 99US-0134219. 99US-0145218.
PR 14-MAY-1999; 99US-0134221. 99US-0145224.
PR 14-MAY-1999; 99US-0134370. 99US-0145226.
PR 18-MAY-1999; 99US-0134768. 99US-0145913.
PR 19-MAY-1999; 99US-0134941. 99US-0145918.
PR 20-MAY-1999; 99US-0135124. 99US-0145919.
PR 21-MAY-1999; 99US-0135353. 99US-0145951.
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PR 25-MAY-1999; 99US-0136021. 99US-0146388.
PR 27-MAY-1999; 99US-0136392. 99US-0146389.
PR 28-MAY-1999; 99US-0136782. 99US-0147038.
PR 01-JUN-1999; 99US-0137222. 99US-0147204.
PR 03-JUN-1999; 99US-0137528. 99US-0147302.
PR 04-JUN-1999; 99US-0137502. 99US-0147192.
PR 07-JUN-1999; 99US-0137724. 99US-0147260.
PR 08-JUN-1999; 99US-0138094. 99US-0147303.
PR 10-JUN-1999; 99US-0138540. 99US-0147416.
PR 10-JUN-1999; 99US-0138847. 99US-0147493.
PR 14-JUN-1999; 99US-0139119. 99US-0147935.
PR 16-JUN-1999; 99US-0139452. 99US-0148171.
PR 16-JUN-1999; 99US-0139453. 99US-0148319.
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PR 18-JUN-1999; 99US-0139492. 99US-0148565.
PR 18-JUN-1999; 99US-0139454. 99US-0148684.
PR 18-JUN-1999; 99US-0139455. 99US-0149368.
PR 18-JUN-1999; 99US-0139456. 99US-0149375.
PR 18-JUN-1999; 99US-0139457. 99US-0149426.
PR 18-JUN-1999; 99US-0139458. 99US-0149722.
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PR 18-JUN-1999; 99US-0139460. 99US-0149929.
PR 18-JUN-1999; 99US-0139461. 99US-0149902.
PR 18-JUN-1999; 99US-0139462. 99US-0149930.
PR 18-JUN-1999; 99US-0139463. 99US-0150566.
PR 18-JUN-1999; 99US-0139750. 99US-0150884.
PR 18-JUN-1999; 99US-0139763. 99US-0151065.
PR 21-JUN-1999; 99US-0139817. 99US-0151066.
PR 22-JUN-1999; 99US-0139899. 99US-0151080.
PR 23-JUN-1999; 99US-0140353. 99US-0151303.
PR 23-JUN-1999; 99US-0140354. 99US-0151338.
PR 24-JUN-1999; 99US-0140695. 99US-0151930.
PR 28-JUN-1999; 99US-0140823. 99US-0152363.
PR 29-JUN-1999; 99US-0140991. 99US-0153070.
PR 30-JUN-1999; 99US-0141287. 99US-0153758.
PR 01-JUL-1999; 99US-0141842. 99US-0154018.
PR 01-JUL-1999; 99US-0142154. 99US-0154039.
PR 99US-0154779.

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PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 43.8%; Score 46; DB 21; Length 266;
Best Local Similarity 50.0%; Pred. No. 9.6;
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 3 CKMNRSCQSEKLGITYTKT 20
Db 85 gslnnlcqlnkqyltkt 102

RESULT 9
B49209
ID B49209 standard; Protein; 379 AA.
AC B49209;
XX AC
XX XX
DT 12-MAR-2001 (first entry)
XX
DE V.cholerae VPI phage VPI orf3 protien.
XX
KW Bacteriophage; pathogenicity island; vaccine; allergy.
XX
OS Unidentified.
XX
PN WO200067784-A1.
XX
PD 16-NOV-2000.
XX
PF 10-MAY-2000; 2000WO-US12580.
XX
PR 10-MAY-1999; 99US-0133373.
XX
PA (UYMA-) UNIV MARYLAND BALTIMORE.
XX
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PI Karaolis DKR;
XX
DR WPI; 2001-122703/13.
XX
PT Isolated bacteriophage encoded by a pathogenicity island of a
PT pathogenic bacterium, useful for generating bacteriophage-base vaccines
PT or vectors, e.g. to treat allergies -
XX
PS Disclosure; Fig 5; 59pp; English.
XX
CC The present invention relates to an isolated bacteriophage encoded by
CC a pathogenicity island of a pathogenic bacterium. The bacteriophage may
CC be used in pharmaceuticals e.g. for generating an immune response,
CC especially to produce antibodies, as a bacteriophage-based vaccine
CC against pathogenic bacteria expressing virulence factors, as a
CC vaccine vector, e.g. to prevent or treat allergies, diseases or
CC other pathological conditions.
XX
SQ Sequence 379 AA;

Query Match 43.8%; Score 46; DB 22; Length 379;
Best Local Similarity 45.0%; Pred. No. 14;
Matches 9; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

Qy 1 NLGKMNRSCQSEKLGITYTKT 20
Db 198 nkgksgneslnrkiigtnt 217

RESULT 10
Y11212
ID Y11212 standard; Protein; 49 AA.
XX
AC Y11212;
XX
DT 20-MAY-1999 (first entry)
XX
DE S. pneumoniae 3-oxoacyl-(acyl carrier protein) reductase.
XX
KW Streptococcus pneumoniae strain 0100993; vaccine; immune response;
KW streptococcal infection; pneumococcal.
XX
OS Streptococcus pneumoniae.
XX
PN WO9737026-A1.
XX
PD 09-OCT-1997.
XX
PF 01-APR-1997; 97WO-US05306.
XX
PR 22-AUG-1996; 96US-0025788.
PR 02-APR-1996; 96US-0014690.
XX
PA (SMIK ) SMITHKLINE BEECHAM CORP.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Black MT, Hodgson JE, Knowles DJC, Nicholas RO;
PI Stodola RK;
XX
DR WPI; 1997-503111/46.
DR N-PSDB; X30801.
XX
XX Nucleic acids encoding pneumococcal polypeptide(s) - useful in
PT vaccines, drug screening, etc
XX
PS Claim 6; Page 253; 354pp; English.
XX
CC X30724 to X30946 represent genomic DNA sequences isolated from
CC Streptococcus pneumoniae strain 0100993. These genomic DNA sequences
CC encode the novel proteins given in Y11114 to Y11367. The proteins,
CC isolated from Streptococcus pneumoniae, can be used in vaccines against
CC streptococcal infections and in assays for identifying compounds that
```

CC inhibit or activate the activity of the proteins. The antagonists can
 CC be used to treat an individual having need to inhibit a bacterial
 CC protein. Vectors expressing the proteins can be used to induce a
 CC protective immune response in mammals.

XX Sequence 49 AA;

Query Match 41.9%; Score 44; DB 18; Length 49;

Best Local Similarity 40.0%; Pred. No. 3-2; Mismatches 0; Gaps 0;

Matches 8; Conservative 5; Indels 7; Indels 0; Gaps 0;

QY 1 NLGKMRSCQSEKLIGYTKT 20

I: I: I: III: III:

Db 10 nigqanyaaskagligftks 29

RESULT 11

B41413

ID B41413 standard; Protein: 140 AA.

XX AC B41413;

XX DT 08-FEB-2001 (first entry)

DE Human ORFX ORE1177 polypeptide sequence SEQ ID NO:2354.

XX KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;

XX KW vulnary; antiparotatic; antiparkinsonian; nootropic; neuroprotective;

XX KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;

XX KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;

XX KW hypotensive; dermatological; immunosuppressive; antiinflammatory;

XX KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;

XX KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;

XX KW neurodegenerative disorder; osteoarthritis; graft vs host disease;

XX KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;

XX KW cholesterol ester storage; systemic lupus erythematosus; infection;

XX KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;

XX KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;

XX KW bone damage; cartilage damage; antiinflammatory disease; coagulation;

XX KW thrombosis; contraceptive.

XX OS Homo sapiens.

XX PN WO200058473-A2.

XX PD 05-OCT-2000.

XX PF 31-MAR-2000; 2000WO-US08621.

XX PR 31-MAR-1999; 99US-0127607.

XX PR 02-APR-1999; 99US-0127636.

XX PR 05-APR-1999; 99US-0127728.

XX PR 30-MAR-2000; 2000US-0540763.

XX PA (CURA-) CURAGEN CORP.

XX PI Shimkets RA, Leach M;

XX PI WPI; 2000-60362/57.

XX DR N-PSDB; C75622.

XX PT Novel nucleic acids and peptides derived from open reading frame X,

XX PT useful for treating e.g. cancers, proliferative disorders,

XX PT neurodegenerative disorders and cardiovascular disease -

XX PS Claim 11; Page 1718; 5507pp; English.

XX PS C74446 to C77606 encode the proteins given in B40237 to B43397, which

XX CC represent the human ORFX open reading frames 1 to 3161. The ORFX

XX CC sequences have activities such as: cytostatic; hepatotropic; vulnary;

XX CC antiparotatic; antiparkinsonian; nootropic; neuroprotective; osteopathic;

XX CC anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;

CC cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;

CC dermatological; immunosuppressive; antiinflammatory; antibacterial;

CC antiviral; antifungal; antirheumatic; antithyroid; and antianemic. The

CC sequences can be used for determining the presence of or predisposition

CC to, or preventing or treating pathological conditions associated with an

CC ORFX-associated disorder. The nucleic acids can be used to express ORFX

CC proteins in gene therapy vectors. The proteins and nucleic acids may be

CC used to treat cancers, proliferative disorders, neurodegenerative

CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,

CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester

CC storage, systemic lupus erythematosus, severe combined immunodeficiency

CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune

CC disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and

CC cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to

CC enhance coagulation; to inhibit thrombosis; and as a contraceptive.

XX Sequence 140 AA;

Query Match 41.9%; Score 44; DB 21; Length 140;

Best Local Similarity 40.0%; Pred. No. 10;

Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 NLGKMRSCQSEKLIGYTKT 20

I: I: I: III: III:

Db 110 nigqanyaaskagligftks 129

RESULT 12

W38474

ID W38474 standard; Protein: 186 AA.

XX AC W38474;

XX DT 06-NOV-1998 (first entry)

XX DE S. pneumoniae 3-oxoacyl reductase precursor protein.

XX DE Streptococcus pneumoniae protein; genetic immunisation; antagonist;

XX KW immunological response; inoculation; antibody production; inhibitor;

XX KW T cell immune response; antimicrobial compound; bacterial adhesion;

XX KW extracellular matrix protein; protein-mediated cell invasion; wound;

XX KW pathogenesis.

XX OS Streptococcus pneumoniae.

XX PN WO9743303-A1.

XX PD 20-NOV-1997.

XX PF 14-MAY-1997; 97WO-US07950.

XX PR 14-MAY-1996; 96US-0017670.

XX PA (SMIK) SMITHKLINE BEECHAM CORP.

XX PA (SMIK) SMITHKLINE BEECHAM PLC.

XX PI Black MT, Hodgson JE, Knowles DJC, Nicholas RO;

XX PI Stodola RK;

XX DR WPI; 1998-008793/01.

XX DR N-PSDB; T98542.

XX PT Novel Streptococcus pneumoniae proteins and related DNA - useful for

XX PT diagnosing anti-microbial agents for treatment of bacterial

XX PT infections

XX PS Claim 12; Page 268; 483pp; English.

XX PS This sequence represents a Streptococcus pneumoniae protein that, based

XX CC on homology with a Cuphea lanceolata protein is a 3-oxoacyl reductase

XX CC precursor protein, and is encoded by a DNA sequence of the invention.

XX CC The DNA sequences were isolated from Streptococcus pneumoniae strain

CC 0100993 (NCIMB 40794). The Streptococcus pneumoniae proteins of the
 CC invention can be used to identify compounds which interact with and
 CC inhibit or activate the activity of the proteins. Antagonists can be
 CC used to treat diseases caused by S. pneumoniae proteins, through genetic
 CC immunisation. They can also be used to induce an immunological response
 CC in a mammal by inoculation with the S. pneumoniae proteins or delivery
 CC of the encoding nucleic acids in a vector adequate to produce antibody
 CC and/or T cell immune responses to protect the animal from disease. The
 CC proteins can also be used to identify antimicrobial compounds which are
 CC capable of inhibiting their bioactivity. In particular the proteins of
 CC the invention can be used to prevent adhesion of bacteria to mammalian
 CC extracellular matrix proteins on in-dwelling devices or in wounds, to
 CC block protein-mediated mammalian cell invasion, and to block the normal
 CC progression of pathogenesis in infections initiated other than by the
 CC implantation of in-dwelling devices or other surgical techniques.

XX SQ Sequence 186 AA;
 Query Match 41.9%; Score 44; DB 19; Length 186;
 Best Local Similarity 40.0%; Pred. No. 14;
 Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 NLGNRSCQSEKLGITYTKT 20
 I:|:|:|:|:|:|:
 Db 147 nigqanyaaskagligftks 166

RESULT 13

W80670
 ID W80670 standard; Protein; 243 AA.

XX AC W80670;

XX DT 24-DEC-1998 (first entry)

XX DE S. pneumoniae fatty acid biosynthesis protein.

XX KW Streptococcus pneumoniae protein; recombinant; gene expression; DNA chip;
 XX KW virulence; antibody; infection; detection; treatment; hypothetical;
 XX KW cell wall biosynthetic, external target; minimal gene set protein.

XX OS Streptococcus pneumoniae.

XX PN W09826072-A1.

XX PD 18-JUN-1998.

XX PF 09-DEC-1997; 97WO-US22578.

XX PR 13-DEC-1996; 96US-0036281.

XX PA (ELIL) LILLY & CO ELI.

XX PI Baltz RH, Burret SG, Dehoff BS, Hoskins JA, Jaskunas SR;

XX PI Mills BJ, Norris FH, Peery RB, Rockey PK, Rostock PR;

XX PI Skatrud PL, Smith MC, Solenberg PJ, Treadway PJ;

XX PI Young Bellido ML;

XX DR WPI; 1998-348529/30.

XX ST Streptococcus pneumoniae nucleic acid sequences - used in DNA chips
 PT for evaluating gene expression, and identification of virulence
 PT genes

XX PS Claim 3; Page 270; 333pp; English.

XX CC This sequence represents a S. pneumoniae fatty acid biosynthesis
 CC protein. The invention provides DNA sequences (V65201 to V65304) from
 CC the Streptococcus pneumoniae genome and corresponding protein sequences
 CC (W80605 to W80728). The protein sequences are classified as hypothetical,
 CC cell wall biosynthetic, external target, or minimal gene set proteins. A
 CC recombinant host containing a vector comprising any of the above nucleic

CC acids can be used for the recombinant expression of the proteins. The
 CC invention also provides a DNA chip having arrayed on it at least 15 base
 CC pair fragment of any one or more of these DNA sequences. The DNA chip can
 CC be used methods for evaluating gene expression in S. pneumoniae and for
 CC identifying virulence genes in S. pneumoniae. Antibodies that selectively
 CC bind to the above proteins or peptide fragments can be used to treat
 CC S. pneumoniae infection. The antibodies can also be used to detect
 CC S. pneumoniae cells.

XX SQ Sequence 243 AA;

Query Match 41.9%; Score 44; DB 19; Length 243;
 Best Local Similarity 40.0%; Pred. No. 18;
 Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 NLGNRSCQSEKLGITYTKT 20
 I:|:|:|:|:|:|:
 Db 147 nigqanyaaskagligftks 166

RESULT 14

B15706
 ID B15706 standard; Protein; 243 AA.

XX AC B15706;

XX DT 07-DEC-2000 (first entry)

XX DE Streptococcus pneumoniae FabG polypeptide.

XX KW Streptococcus pneumoniae; FabG; 3-oxoacyl-acyl carrier protein reductase;
 XX KW antibacterial; cytostatic; antiulcer; cancer; gastric ulcer; gastritis;
 XX KW Helicobacter pylori infection; microbial infection.

XX OS Streptococcus pneumoniae.

XX PN W0200044885-A1.

XX PD 03-AUG-2000.

XX PF 19-JAN-2000; 2000WO-US01131.

XX PR 27-JAN-1999; 99US-0239052.

XX PA (SMIK) SMITHKLINE BEECHAM CORP.

XX PI Holmes DJ, Mooney J, Zhong YY, Debouck C, Jaworski DD, Wang M;
 XX PI Warren RL, Kosmatka AL, Mcdevitt D, Ingraham KA, Chaliker AF;
 XX PI So CY, Wallis NG, Pearson SC;

XX DR WPI; 2000-482971/42.

XX DR N-PSDB; A74684.

XX ST FabG polypeptide, isolated from Streptococcus pneumoniae, is used to
 PT treat microbial diseases, identify agonists and antagonists for
 PT treating microbial infections and to detect diseases associated with
 PT microbial infections -

XX Claim 1; Page 3; 40pp; English.

XX CC The present sequence is a FabG (2-oxoacyl-acyl carrier protein
 CC reductase) polypeptide. A full length FabG gene was isolated from a
 CC Streptococcus pneumoniae 0100993 DNA library in E. coli. FabG
 CC polynucleotides and polypeptides are used for detection and treatment of
 CC microbial diseases. They may also be used to identify antagonists and
 CC agonists which can then be used to treat microbial diseases. Compounds
 CC that interfere with the initial physical interaction between a pathogen
 CC and a host have been identified. The compounds are able to prevent the
 CC adhesion of bacteria to mammalian extracellular proteins in wounds,
 CC prevent adhesion between mammalian extracellular proteins and bacterial
 CC FabG proteins which mediate tissue damage and/or to block normal
 CC progression of pathogenesis in infections mediated by implantation of

PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.

PR 29-OCT-1999; 99US-0162142.

Query Match 40.0%; Score 42; DB 21; Length 349;
Best Local Similarity 64.3%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 LGKMNRCQSEKLI 15
||| ||||| ||
Db 27 lgsmnrscslcsvli 40

Search completed: May 23, 2001, 15:28:33
Job time: 410 sec


```
QY 3 GKNRSCQSEKLG 16
    ||:| || |.:|
Db 500 GKNMCSGEPVFG 513

RESULT 2
US-09-209-668-19
; Sequence 19, Application US/09209668A
; Patent No. 6114517
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
; FILE REFERENCE: ISPH-0336
; CURRENT FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 19
; LENGTH: 610
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-209-668-19

Query Match 39.0%; Score 41; DB 4; Length 610;
Best Local Similarity 50.0%; Pred. No. 49;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 GKNRSCQSEKLG 16
    ||:| || |.:|
Db 500 GKNMCSGEPVFG 513

RESULT 3
5217870-2
; Patent No. 5217870
; APPLICANT: HESSION, CATHERINE A.; LOBB, ROY R.; GOELZ, SUSAN E.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST CDX
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/345,151
; FILING DATE: 28-APR-1989
; SEQ ID NO: 2;
; LENGTH: 610
5217870-2

Query Match 39.0%; Score 41; DB 6; Length 610;
Best Local Similarity 50.0%; Pred. No. 49;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 GKNRSCQSEKLG 16
    ||:| || |.:|
Db 500 GKNMCSGEPVFG 513

RESULT 4
US-08-424-424B-2
; Sequence 2, Application US/08424424B
; Patent No. 5759854
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Neurotransmitter Transporter
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA

QY 3 GKNRSCQSEKLG 16
    ||:| || |.:|
Db 500 GKNMCSGEPVFG 513

RESULT 5
PCT-US94-05363A-2
; Sequence 2, Application PC/TUS9405363A
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Neurotransmitter Transporter
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05363A
; FILING DATE: SUBMITTED HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
```

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; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,424B
; FILING DATE: APRIL 21, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05363
; FILING DATE: MAY 25, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-308
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 727 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-424-424B-2

Query Match 38.6%; Score 40.5; DB 1; Length 727;
Best Local Similarity 42.1%; Pred. NO. 71;
Matches 8; Conservative 3; Mismatches 5; Indels 3; Gaps 1;

QY 5 MNRSC---QSEKLGTYKT 20
    || | :||:| |
Db 362 MNKCVVNAEKILGYLNT 380

RESULT 5
PCT-US94-05363A-2
; Sequence 2, Application PC/TUS9405363A
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Neurotransmitter Transporter
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05363A
; FILING DATE: SUBMITTED HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
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;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 727 AMINO ACIDS
;; TYPE: AMINO ACID
;; STRANDEDNESS:
;; TOPOLOGY: LINEAR
;; MOLECULE TYPE: PROTEIN
PCT-US94-05363A-2

Query Match 38.6%; Score 40.5; DB 5; Length 727;
Best Local Similarity 42.1%; Pred. No. 71;
Matches 8; Conservative 3; Mismatches 5; Indels 3; Gaps 1;

Oy 5 MNRSC---QSEKLIYTKT 20
|| | :||:| |
Db 362 MNEKCVVENAEKILGYLNT 380

RESULT 6
US-08-793-035-9
; Sequence 9, Application US/08793035
; Patent No. 6011201
; GENERAL INFORMATION:
; APPLICANT: Slabas, Antoni R.
; APPLICANT: White, Andrew
; APPLICANT: Chase, Dianne
; APPLICANT: Elborough, Keiran
; APPLICANT: Fentem, Phillip A.
; TITLE OF INVENTION: B-Ketoacyl ACP Reductase Genes From
; TITLE OF INVENTION: Brassica Napus
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: US
; ZIP: 77210-4433
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,035
; FILING DATE: 28-JUL-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9414622.2
; FILING DATE: 20-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB95/01678
; FILING DATE: 17-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kammerer, Patricia A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: MOBT:132
; TELEPHONE: 713.787.1400
; TELEFAX: 713.787.1440
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 315 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-793-035-9

Query Match 38.1%; Score 40; DB 3; Length 315;
Best Local Similarity 35.0%; Pred. No. 36;
Matches 7; Conservative 6; Mismatches 7; Indels 7; Gaps 0;

Oy 1 NLGKMNRSQCSEKLIYTKT 20
|:|: | :||:| |
Db 216 NIGQANYAAKAGVIGFSKT 235

RESULT 7
US-08-793-035-10
; Sequence 10, Application US/08793035
; Patent No. 6011201
; GENERAL INFORMATION:
; APPLICANT: Slabas, Antoni R.
; APPLICANT: White, Andrew
; APPLICANT: Chase, Dianne
; APPLICANT: Elborough, Keiran
; APPLICANT: Fentem, Phillip A.
; TITLE OF INVENTION: B-Ketoacyl ACP Reductase Genes From
; TITLE OF INVENTION: Brassica Napus
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: US
; ZIP: 77210-4433
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,035
; FILING DATE: 28-JUL-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9414622.2
; FILING DATE: 20-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB95/01678
; FILING DATE: 17-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kammerer, Patricia A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: MOBT:132
; TELEPHONE: 713.787.1400
; TELEFAX: 713.787.1440
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 315 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-793-035-10

Query Match 38.1%; Score 40; DB 3; Length 315;
Best Local Similarity 35.0%; Pred. No. 36;
Matches 7; Conservative 6; Mismatches 7; Indels 7; Gaps 0;

Oy 1 NLGKMNRSQCSEKLIYTKT 20
|:|: | :||:| |
Db 216 NIGQANYAAKAGVIGFSKT 235

RESULT 8
US-08-467-948A-29
; Sequence 29, Application US/08467948A
; Patent No. 5998164
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: CAO, LIANG

APPLICANT: NI, JIAN
APPLICANT: GENTZ, CAROL J.
APPLICANT: BULT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR2
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,948A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-467-948A-29

Query Match 35.2%; Score 37; DB 2; Length 325;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 8 SCQSEKLGITYK 19
|||||: |
Db 265 SCQSEKILRYMK 276

RESULT 9
US-08-467-947A-29
Sequence 29, Application US/08467947A
Patent No. 6090575
GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: CAO, LIANG
APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: BULT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR1
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC

COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,947A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-467-947A-29

Query Match 35.2%; Score 37; DB 3; Length 325;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 8 SCQSEKLGITYK 19
|||||: |
Db 265 SCQSEKILRYMK 276

RESULT 10
US-08-988-876-8
Sequence 8, Application US/08988876
Patent No. 6063596
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
TITLE OF INVENTION: WITH IMMUNE RESPONSE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,876
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, Seventh Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/847,007A
FILING DATE: 01-MAY-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 6083480nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 97,209
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1..6
OTHER INFORMATION: /label= Cyclic
OTHER INFORMATION: /note= "The amino terminus and the side chain sulfur
OTHER INFORMATION: atom of homomocysteine are covalently linked via
OTHER INFORMATION: a acetyl group."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: /label= Variant residues
OTHER INFORMATION: /note= "The residue is homomocysteine."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 13
OTHER INFORMATION: /label= BAT
OTHER INFORMATION: /note= "The side chain sulfur atom of the cysteine is
OTHER INFORMATION: covalently linked to a BAT chelating moiety."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 31
OTHER INFORMATION: /label= Amide
OTHER INFORMATION: /note= "The carboxyl terminus is modified to an
OTHER INFORMATION: amide"
US-08-847-007A-4

Query Match 34.3%; Score 36; DB 3; Length 31;
Best Local Similarity 47.4%; Pred. NO. 15;
Matches 9; Conservative 3; Mismatches 5; Indels 2; Gaps 1;
QY 2 LGKMRSCQSEKLGITYTKT 20
|||: ||: ||: |:
Db 8 LGKL--SCELHKLQTYPT 24

RESULT 14
US-08-847-007A-5
; Sequence 5, Application US/08847007A
; Patent No. 6083480
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T

APPLICANT: Bush, Larry R
APPLICANT: Pearson, Daniel P
APPLICANT: Lister-James, John
TITLE OF INVENTION: Radiolabeled peptides
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, Seventh Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/847,007A
FILING DATE: 01-MAY-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 6083480nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 97,209
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1..6
OTHER INFORMATION: /label= Cyclic
OTHER INFORMATION: /note= "The amino terminus and the side chain sulfur
OTHER INFORMATION: atom of homomocysteine are covalently linked via
OTHER INFORMATION: a acetyl group."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: /label= Variant residues
OTHER INFORMATION: /note= "The residue is homomocysteine."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 31
OTHER INFORMATION: /label= Amide
OTHER INFORMATION: /note= "The carboxyl terminus is modified to an
OTHER INFORMATION: amide"
US-08-847-007A-5

Query Match 34.3%; Score 36; DB 3; Length 31;
Best Local Similarity 47.4%; Pred. NO. 15;
Matches 9; Conservative 3; Mismatches 5; Indels 2; Gaps 1;
QY 2 LGKMRSCQSEKLGITYTKT 20
|||: ||: ||: |:
Db 8 LGKL--SCELHKLQTYPT 24

RESULT 15
US-08-847-007A-6
; Sequence 6, Application US/08847007A
; Patent No. 6083480
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Bush, Larry R
; APPLICANT: Pearson, Daniel P

APPLICANT: Lister-James, John
 TITLE OF INVENTION: Radiolabeled Peptides
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: McDonnell Boenhen Hulbert & Berghoff
 STREET: 300 South Wacker Drive, Seventh Floor
 CITY: Chicago
 STATE: IL
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/847,007A
 FILING DATE: 01-MAY-1997
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 6083480nan, Kevin E
 REGISTRATION NUMBER: 35,303
 REFERENCE/DOCKET NUMBER: 97,209
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-913-0001
 TELEFAX: 312-913-0002
 TELEX:

INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 31 amino acids
 TYPE: amino acid
 TOPOLOGY: circular
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 1..6
 OTHER INFORMATION: /label= Cyclic
 OTHER INFORMATION: /note= "The amino terminus and the side chain sulfur
 OTHER INFORMATION: atom of homohomocysteine are covalently linked via
 OTHER INFORMATION: a acetyl group."
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 6
 OTHER INFORMATION: /label= Variant residues
 OTHER INFORMATION: /note= "The residue is homohomocysteine."
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 31
 OTHER INFORMATION: /label= Amide
 OTHER INFORMATION: /note= "The carboxyl terminus is modified to an
 OTHER INFORMATION: amide"

US-08-847-007A-6

Query Match 34.3%; Score 36; DB 3; Length 31;
 Best Local Similarity 47.4%; Pred. No. 15;
 Matches 9; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

QY 2 LGKMRSCQSEKLGTYTKT 20
 ||| ||| |||
 Db 8 LGKL--SCELHKLQTYPT 24

Search completed: May 23, 2001, 15:30:08
 Job time: 415 sec

Query Match 42.9%; Score 45; DB 2; Length 3071;
Best Local Similarity 53.3%; Pred. No. 63;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NLGKNRSCQSEKLI 15
||||:| |||
Db 473 NLGKLSVTCYPEKII 487

RESULT 7

S22450
3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) precursor, NADPH-dependent [va
N:Alternate names: beta-ketoacyl-ACP reductase
C:Species: Cuphea lanceolata
C:Date: 16-Feb-1995 #sequence_revision 23-Feb-1996 #text_change 17-Mar-2000
C:Accession: S22450; S19832
R:Klein, B.; Pawlowski, K.; Hoerick-Grandpierre, C.; Schell, J.; Toepfer, R.
Mol. Gen. Genet. 233, 122-128, 1992
A:Title: Isolation and characterization of a cDNA from Cuphea lanceolata encoding a beta
A:Reference number: S22450; MUID:92293104
A:Accession: S22450
A:Molecule type: mRNA
A:Residues: 1-320 <KLE>
A:Cross-references: EMBL:X64566; NID:g18045; PIDN:CAA45866.1; PID:g18046
A:Experimental source: immature embryo
C:Genetics:
A:Gene: Ckr27
A:Genome: nuclear
C:Function:
A:Description: EC 1.1.1.100 [validated; MUID:92293104]
A:Pathway: fatty acid biosynthesis
A:Note: integral part of the fatty acid synthase type II
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C:Keywords: chloroplast; fatty acid biosynthesis; NADP; oxidoreductase
F:1-63/Domain: transit peptide (chloroplast) #status predicted <TNP>
F:64-320/Product: 3-oxoacyl-[acyl-carrier-protein] reductase #status predicted <MAT>
F:78-258/Domain: short-chain alcohol dehydrogenase homology <SADH>
F:227/Active site: Tyr #status predicted

Query Match 41.9%; Score 44; DB 2; Length 320;
Best Local Similarity 45.0%; Pred. No. 11;
Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 1 NLGKNRSCQSEKLIQYTKT 20
| | | | | : |||||
Db 221 NAGQANYSAKAGVICFTKT 240

RESULT 8

C36769
13R protein - human herpesvirus 6 (strain Uganda-1102)
C:Species: human herpesvirus 6
C:Date: 26-Jul-1991 #sequence_revision 26-Jul-1991 #text_change 02-Jun-2000
C:Accession: C36769
R:Lawrence, G.L.; Chee, M.; Craxton, M.A.; Gompels, U.A.; Honess, R.W.; Barrrell, B.G.
J. Virol. 64, 287-299, 1990
A:Title: Human herpesvirus 6 is closely related to human cytomegalovirus.
A:Reference number: A33560; MUID:90080132
A:Accession: C36769
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-350 <LAW>
A:Cross-references: GB:M28243
C:Superfamily: human herpesvirus 4 BGLF3 protein

Query Match 41.0%; Score 43; DB 2; Length 350;
Best Local Similarity 58.3%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 9 CQSEKLIQYTKT 20
|||: |||
Db 181 CQSDSCFGYSKT 192

RESULT 9

T44027
hypothetical protein U67 [imported] - human herpesvirus 6
C:Species: human herpesvirus 6
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C:Accession: T44027; T44212
R:Isegawa, Y.; Mukai, T.; Nakano, K.; Kagawa, M.; Chen, J.; Mori, Y.; Sunagawa, T.; K
J. Virol. 73, 8053-8063, 1999
A:Title: Comparison of the complete DNA sequences of human herpesvirus 6 variants A a
A:Reference number: 222732; MUID:99412319
A:Accession: T44027
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-353 <ISE>
A:Cross-references: EMBL:AB021506; NID:g4995977; PIDN:BAA78288.1; PID:g4996055
A:Experimental source: strain HST; pop. variant B
R:Dominguez, G.; Dambaugh, T.R.; Stamey, F.R.; Dewhurst, S.; Inoue, N.; Pellett, P.E.
J. Virol. 73, 8040-8052, 1999
A:Title: Human herpesvirus 6B genome sequence: coding content and comparison with hum
A:Reference number: 222734; MUID:99412318
A:Accession: T44212
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-353 <DOM>
A:Cross-references: EMBL:AF157706; PIDN:AAD49668.1
A:Experimental source: strain 429; variant B
C:Genetics:
A:Gene: U67
C:Superfamily: human herpesvirus 4 BGLF3 protein

Query Match 41.0%; Score 43; DB 2; Length 353;
Best Local Similarity 58.3%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 9 CQSEKLIQYTKT 20
|||: |||
Db 184 CQSDSCFGYSKT 195

RESULT 10

T49479
hypothetical protein B14D6.310 [imported] - Neurospora crassa
C:Species: Neurospora crassa
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000
C:Accession: T49479
R:Schulte, U.; Algn, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu
submitted to the Protein Sequence Database, May 2000
A:Reference number: 225022
A:Accession: T49479
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-102 <SCH>
A:Cross-references: EMBL:AL356173; GSPDB:GN00116; NCSP:B14D6.310
A:Experimental source: BAC clone B14D6; strain OR74A
C:Genetics:
A:Gene: NCSP:B14D6.310
A:Map position: 6
C:Superfamily: Neurospora crassa hypothetical protein B14D6.310

Query Match 40.0%; Score 42; DB 2; Length 102;
Best Local Similarity 53.8%; Pred. No. 8.2;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 6 NRSCQSEKLIQYTKT 18
||||: |||
Db 5 NRSCNSQLISFT 17

RESULT 11
S77280
3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) - *Synechocystis* sp. (strain PC
N/Alternate names: protein sir0886
C:Species: *Synechocystis* sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
A:Accession: S77280
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
S.
A:Reference number: S74322; MUID:97061201
A:Accession: S77280
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-247 <KAN>
A:Cross-references: EMBL:D90907; GB:AB001339; NID:g1652618; PIDN:BAAL7614.1; PID:g165269
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Genetics:
A:Gene: fabG
C:Function:
A:Pathway: fatty acid biosynthesis
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C:Keywords: fatty acid biosynthesis; NADP; oxidoreductase
F:7-187/Domain: short-chain alcohol dehydrogenase homology <SADH>
F:156/Active site: Tyr #status predicted

Query Match 40.0%; Score 42; DB 2; Length 247;
Best Local Similarity 45.0%; Pred. No. 19;
Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 NLGKNRSCQSEKLGITYTKT 20
| | | | | | | | | |
DB 150 NPGQANYSAKAGVIGFTKT 169

RESULT 12
C83188
Probable ATP-binding component of ABC transporter PA3672 [imported] - *Pseudomonas aerugi*
C:Species: *Pseudomonas aeruginosa*
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: C83188
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337
A:Accession: C83188
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-307 <STO>
A:Cross-references: GB:AE004786; GB:AE004091; NID:g9949822; PIDN:AAG07060.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA3672
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 40.0%; Score 42; DB 2; Length 307;
Best Local Similarity 58.3%; Pred. No. 23;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 6 NRSCQSEKLG 17
| | | | | | | | | |
DB 67 NRTLQQRLLGY 78

RESULT 13
T04549
hypothetical protein F28J12.190 - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 15-Sep-2000
C:Accession: T04549
R:Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancro
submitted to the Protein Sequence Database, February 1998
A:Reference number: 215377
A:Accession: T04549
A:Molecule type: DNA
A:Residues: 1-349 <BEV>
A:Cross-references: EMBL:AL021710
A:Experimental source: cultivar Columbia; BAC clone F28J12
C:Genetics:
A:Map position: 4
A:Introns: 27/3; 62/3; 90/3; 118/3; 224/2; 246/3; 264/3; 306/3
A:Note: F28J12.190
C:Superfamily: *Arabidopsis thaliana* hypothetical protein T20K18.190

Query Match 40.0%; Score 42; DB 2; Length 349;
Best Local Similarity 64.3%; Pred. No. 26;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 LGKNRSCQSEKLI 15
| | | | | | | | | |
DB 27 LGSMNRSLCSVLI 40

RESULT 14
S52472
cell fusion protein precursor - mumps virus
C:Species: mumps virus
C:Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 24-Nov-1999
C:Accession: S52472
R:Cusi, M.G.
submitted to the EMBL Data Library, November 1994
A:Reference number: S52472
A:Accession: S52472
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-538 <CUS>
A:Cross-references: EMBL:X82887; NID:g683483; PIDN:CAA58060.1; PID:g683484
C:Superfamily: parainfluenza virus cell fusion protein

Query Match 40.0%; Score 42; DB 2; Length 538;
Best Local Similarity 35.0%; Pred. No. 39;
Matches 7; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 NLGKNRSCQSEKLGITYTKT 20
| | | | | | | | | |
DB 56 NIQPIDNSCESKSVTQYNTK 75

RESULT 15
S28313
hypothetical protein F02A9.5 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S28313
R:Barks, M.
submitted to the EMBL Data Library, December 1992
A:Reference number: S28296
A:Accession: S28313
A:Molecule type: DNA
A:Residues: 1-608 <BER>
A:Cross-references: EMBL:Z19555; NID:g6705; PID:g6711
C:Genetics:
A:Introns: 19/1; 55/2; 152/3; 352/1; 453/3; 505/2; 584/3
C:Superfamily: propionyl-CoA carboxylase beta chain

Query Match 40.0%; Score 42; DB 1; Length 608;
 Best Local Similarity 44.0%; Pred. NO. 44;
 Matches 11; Conservative 2; Mismatches 6; Indels 6; Gaps 1;

Qy 1 NLGKXNRSCQSEKLI-----GYTK 19
 Db 8 NLGSRNTSIQSYVLLRTRWERYLK 32

Search completed: May 23, 2001, 15:32:03
 Job time: 510 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 23, 2001, 15:36:20 ; Search time 62.39 Seconds
(without alignments)

10.981 Million cell updates/sec

Title: US-08-887-977-10_COPY_271_290
Perfect score: 105
Sequence: 1 NLGKNRSCQSEKLGTYTKT 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	105	100.0	374	1 CKR6_HUMAN	P51684 homo sapien
2	63	60.0	367	1 CKR6_MOUSE	O54689 mus musculu
3	46	43.8	248	1 FABG_AOUAE	O67610 aquifex aeo
4	44	41.9	320	1 FABG_CUPLA	P28643 cuphea lanc
5	43	41.0	353	1 UL95_HSV6U	P24444 human herpe
6	42.5	40.5	730	1 KDGA_MOUSE	O88673 mus musculu
7	42	40.0	247	1 FAG1_SYNY3	P73574 synechocyst
8	42	40.0	414	1 YLPD_CAEEL	P34384 caenorhabdi
9	42	40.0	608	1 YLPC_CAEEL	P34385 caenorhabdi
10	41.5	39.5	411	1 RAPS_CHICK	O42393 gallus gall
11	41	39.0	164	1 HIT1_YEAST	P46973 saccharomyc
12	41	39.0	485	1 LEM2_BOVIN	P98107 bos taurus
13	41	39.0	551	1 LEM2_RABIT	P27113 oryctolagus
14	41	39.0	610	1 LEM2_HUMAN	P16581 homo sapien
15	40	38.1	201	1 FABG_BRANA	P27582 brassica na
16	40	38.1	340	1 ENDR_PAEPO	P27871 paenibacill
17	40	38.1	424	1 I131_MOUSE	O09030 mus musculu
18	40	38.1	794	1 HMMR_MOUSE	Q00547 mus musculu
19	40	38.1	865	1 CPN_DROME	Q02910 drosophila
20	40	38.1	937	1 PAC4_RAT	O63415 rattus norv
21	40	38.1	1149	1 ATL1_MOUSE	P07004 mus musculu
22	40	38.1	1164	1 ATL1_HUMAN	Q9Y290 homo sapien
23	39.5	37.6	362	1 HIS7_HAEIN	P44327 haemophilus
24	39.5	37.6	411	1 RAPS_HUMAN	Q13702 homo sapien
25	39.5	37.6	411	1 RAPS_MOUSE	P12672 mus musculu
26	39.5	37.6	745	1 NSF1_DROME	P46461 drosophila
27	39	37.1	153	1 YNZ5_YEAST	P53849 saccharomyc
28	39	37.1	227	1 TYSA_BACAT	O30394 bacillus at
29	39	37.1	230	1 TYSA_BACAM	O30397 bacillus am
30	39	37.1	244	1 FABG_BUCAI	P57432 buchnera ap
31	39	37.1	279	1 TYSA_BACSU	P42326 bacillus su
32	39	37.1	279	1 TYSY_BPPT	P07606 bacterioph
33	39	37.1	342	1 CGGR_BACME	P35168 bacillus me

34 39 37.1 515 1 VAC1_YEAST P32609 saccharomyc
35 39 37.1 549 1 LEM2_RAT P98105 rattus norv
36 39 37.1 612 1 LEM2_MOUSE Q00590 mus musculu
37 39 37.1 677 1 YD64_MYCPN P75417 mycoplasma
38 39 37.1 681 1 MP10_HUMAN O00566 homo sapien
39 39 37.1 794 1 YC84_MYCPN P75493 mycoplasma
40 39 37.1 894 1 FOX2_NEUCR Q01373 neurospora
41 38.5 36.7 212 1 MAD2_PETHY Q07474 petunia hyb
42 38.5 36.7 419 1 PFTB_PEA Q04903 pium sativ
43 38 36.2 102 1 YN12_METTL P05410 methanococc
44 38 36.2 266 1 CD82_MOUSE P40237 mus musculu
45 38 36.2 314 1 M1AA_BACHD Q9KAC3 bacillus ha

ALIGNMENTS

RESULT 1
CKR6_HUMAN STANDARD; PRT; 374 AA.
AC P51684; Q92846 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 40, Last annotation update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CCR-6) (LARC
DE RECEPTOR) (GPR-CY4) (GPCY4) (CHEMOKINE RECEPTOR-LIKE 3) (CKR-L3)
DE (DRY6).
GN CKR6 OR CMKBR6 OR STRL22 OR GPR29 OR CKRL3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND FUNCTION.
RX MEDLINE=973113465; PubMed=9169459;
RA Baba M., Imai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K.,
RA Nomiyama H., Yoshie O.;
RT Identification of CKR6, the specific receptor for a novel
RT lymphocyte-directed CC chemokine LARC.;
RL J. Biol. Chem. 272:14893-14898(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Lautens L.L., Modi W., Bonner T.I.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97040707; PubMed=8886020;
RA Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G.;
RT Molecular cloning and RNA expression of two new human chemokine
RT receptor-like genes.;
RL Biochem. Biophys. Res. Commun. 227:846-853(1996).
RN [4]
RP SEQUENCE FROM N.A.
RA McCoy R., Perlmutter D.H.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=97224503; PubMed=9070937;
RA Liao F., Lee H.-H., Farber J.M.;
RT Cloning of STRL22, a new human gene encoding a G-protein-coupled
RT receptor related to chemokine receptors and located on chromosome
RT 6q27.;
RL Genomics 40:175-180(1997).
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-
CC ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE
CC INTRACELLULAR CALCIUM IONS LEVEL.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: SPLEEN, LYMPH NODES, APPENDIX, AND FETAL
CC NATURAL KILLER CELLS, MONOCYTES, OR GRANULOCYTES.
CC -!- INDUCTION: INTERLEUKIN-2.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-6 IS THE INITIATOR.


```

RESULT 3
FABG_AQUAE
ID FABG_AQUAE STANDARD; PRT; 248 AA.
AC O67610;
DT 15-DEC-1998 (Rel. 37, Created)
DT 13-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) (3-KETOACYL-
DE ACYL CARRIER PROTEIN REDUCTASE).
GN FABG OR AQ_1716.
OS Aquifex aeolicus.
OC Bacteria; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus.";
RL Nature 392:353-358(1998).
CC -1- CATALYTIC ACTIVITY: (3R)-3-HYDROXYACYL-[ACYL-CARRIER PROTEIN] +
CC NADP(+) = 3-OXOACYL-[ACYL-CARRIER PROTEIN] + NADPH.
CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
CC PATHWAY.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AE000752; AAC07575.1;
DR InterPro: IPR002198;
DR InterPro: IPR002347;
DR Pfam: PF00106; adh_short; 1.
DR Pfam: PF00678; adh_short_C2; 1.
DR PRINTS: PR00080; SDRFAMILY.
DR PRINTS: PR00081; GDRDH.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Fatty acid biosynthesis; Oxidoreductase; NADP.
FT NP_BIND 12 36 NADP (BY SIMILARITY).
FT ACT_SITE 157 157 BY SIMILARITY.
SQ SEQUENCE 248 AA; 26867 MW; 5CFD9EB9AD83F2C5 CRC64;

Query Match 43.8%; Score 46; DB 1; Length 248;
Best Local Similarity 45.0%; Pred. No. 1.6;
Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 NLGKMNRCQSEKLGITYTKT 20
|:|:| | | | | | | | | |
DB 151 NVGQVNTTKAGLIGFTKS 170

RESULT 4
FABG_CUPLA
ID FABG_CUPLA STANDARD; PRT; 320 AA.
AC P28643;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE PRECURSOR (EC 1.1.1.100)
DE (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE).
GN CLKR27.
OS Cuphea lanceolata.

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OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Myrtales; Lythraceae; Cuphea.
OX NCBI_TaxID=3930;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92293104; PubMed=1376402;
RA Klein B., Pawlowski K., Hoerick-Grandpierre C., Schell J.,
RA Toepfer R.;
RT "Isolation and characterization of a cDNA from Cuphea lanceolata
RT encoding a beta-ketoacyl-ACP reductase.";
RL Mol. Gen. Genet. 233:122-128(1992).
CC -1- CATALYTIC ACTIVITY: (3R)-3-HYDROXYACYL-[ACYL-CARRIER PROTEIN] +
CC NADP(+) = 3-OXOACYL-[ACYL-CARRIER PROTEIN] + NADPH.
CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
CC PATHWAY.
CC -1- SUBUNIT: HOMOTETRAMER (PROBABLE).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST AND NON-PHOTOSYNTHETIC
CC PLASTIDS.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X64566; CAA45866.1;
DR PIR: S19832; S19832.
DR HSP: Q12634; 1YBV.
DR InterPro: IPR002198;
DR InterPro: IPR002347;
DR Pfam: PF00106; adh_short; 1.
DR Pfam: PF00678; adh_short_C2; 1.
DR PRINTS: PR00080; SDRFAMILY.
DR PRINTS: PR00081; GDRDH.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Fatty acid biosynthesis; Oxidoreductase; NADP; Chloroplast;
FT TRANSIT 1 61 CHLOROPLAST (BY SIMILARITY).
FT CHAIN 62 320 3-OXOACYL-[ACYL-CARRIER PROTEIN]
FT NP_BIND 82 106 REDUCTASE.
FT ACT_SITE 227 227 NADP (BY SIMILARITY).
SQ SEQUENCE 320 AA; 33103 MW; 06BAF0522B2B8C87 CRC64;

Query Match 41.9%; Score 44; DB 1; Length 320;
Best Local Similarity 45.0%; Pred. No. 4.3;
Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 NLGKMNRCQSEKLGITYTKT 20
|:|:| | | | | | | | | |
DB 221 NAGQANYSAAKAGVIGFTKT 240

RESULT 5
UL95_HSV6U
ID UL95_HSV6U STANDARD; PRT; 353 AA.
AC P24444;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PROTEIN U67.
GN U67 OR 13R.
OS Human herpesvirus (type 6 / strain Uganda-1102) (HHV6).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Roseolovirus.
OX NCBI_TaxID=10370;
RN [1]

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RP SEQUENCE FROM N.A.
 RX MEDLINE=9080132; PubMed=2152817;
 RA Lawrence G.L., Chee M., Craxton M.A., Gompels U.A., Honess R.W.,
 RA Barrall B.G.;
 RT "Human herpesvirus 6 is closely related to human cytomegalovirus.";
 RL J. Virol. 64:287-299(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95266321; PubMed=7747482;
 RA Gompels U.A., Nicholas J., Lawrence G., Jones M., Thomson B.J.,
 RA Martin M.E., Efstathiou S., Craxton M., Macaulay H.A.;
 RT "The DNA sequence of human herpesvirus-6: structure, coding content,
 RT and genome evolution.";
 RL Virology 209:29-51(1995).
 CC -!- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS TOGETHER EBV BGLF3,
 CC HVS-1 34, HSV-6 U67, AND HCMV UL95.
 CC -----
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 CC -----
 DR EMBL; M68963; AAA65575.1; -;
 DR EMBL; X83413; CAA58359.1; -;
 DR PIR; C36769; C36769.
 SQ SEQUENCE 353 AA; 39531 MW; E30E73D5D0ACEBA7 CRC64;

 Query Match 41.0%; Score 43; DB 1; Length 353;
 Best Local Similarity 58.3%; Pred. No. 7;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 9 CQSEKLIQYTKT 20
 ||| ||||
 DB 184 CQSDSCFGYSKT 195

 RESULT 6
 KDGA_MOUSE STANDARD; PRT; 730 AA.
 ID AC 088673;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE DIACYLGLYCEROL KINASE, ALPHA (EC 2.7.1.107) (DIGLYCERIDE KINASE) (DGK-
 DE ALPHA) (DAG KINASE ALPHA) (80 KDA DIACYLGLYCEROL KINASE).
 GN DGKA OR DAGK1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sanjuan M.A., Carrera A.C., Merida I.;
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: UPON CELL STIMULATION CONVERTS THE SECOND MESSENGER
 CC DIACYLGLYCEROL INTO PHOSPHATIDATE, INITIATING THE RESYNTHESIS
 CC OF PHOSPHATIDYLINOSITOLS AND ATTENUATING PROTEIN KINASE C
 CC ACTIVITY (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: ATP + 1,2-DIACYLGLYCEROL = ADP +
 CC 1,2-DIACYLGLYCEROL 3-PHOSPHATE.
 CC -!- ENZYME REGULATION: STIMULATED BY CALCIUM AND PHOSPHATIDYLSELINE.
 CC PHOSPHORYLATED BY PROTEIN KINASE C (BY SIMILARITY).
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE EUKARYOTIC DIACYLGLYCEROL KINASE
 CC FAMILY.
 CC -!- SIMILARITY: CONTAINS 2 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
 CC BINDING DOMAINS.
 CC -!- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
 CC -----

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 CC -----
 DR EMBL; AF085219; AAC33483.1; -;
 DR MGD; MGI:102952; Dagk1.
 DR InterPro; IPR000756; -;
 DR InterPro; IPR001206; -;
 DR InterPro; IPR002048; -;
 DR InterPro; IPR002219; -;
 DR Pfam; PF00609; DAGKA; 1.
 DR Pfam; PF00781; DAGKC; 1.
 DR Pfam; PF00130; DAG-PE-bind; 2.
 DR Pfam; PF00036; ehand; 2.
 DR PROSITE; PS00479; DAG-PE_BIND_DOM_1; 2.
 DR PROSITE; PS00081; DAG-PE_BIND_DOM_2; 2.
 DR PROSITE; PS00018; EF_HAND; 2.
 KW Transferase; Kinase; Calcium-binding; Phorbol-ester binding;
 KW Multigene family.
 FT CA_BIND 124 135 SITE 1 (PROBABLE).
 FT CA_BIND 169 180 SITE 2 (PROBABLE).
 FT DOMAIN 207 254 PHORBOL-ESTER AND DAG BINDING (BY
 FT SIMILARITY).
 FT DOMAIN 271 320 PHORBOL-ESTER AND DAG BINDING (BY
 FT SIMILARITY).
 FT DOMAIN 370 495 CATALYTIC-A (POTENTIAL).
 FT DOMAIN 515 696 CATALYTIC-B (POTENTIAL).
 SQ SEQUENCE 730 AA; 82791 MW; 277D8975961599DE CRC64;

 Query Match 40.5%; Score 42.5; DB 1; Length 730;
 Best Local Similarity 60.0%; Pred. No. 17;
 Matches 9; Conservative 2; Mismatches 3; Indels 1; Gaps 1;
 QY 3 GRMNRSCQSEKLIGY 17
 |::| |::| |::|
 DB 37 GEMNREFCQGD-AIGY 50

 RESULT 7
 FAG1_SYNY3 STANDARD; PRT; 247 AA.
 ID FAG1_SYNY3
 AC P73574;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE 1 (EC 1.1.1.100) (3-
 DE KETOACYL-ACYL CARRIER PROTEIN REDUCTASE 1).
 GN FAG1 OR SILR0886.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_TaxID=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hirose M., Sugita M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
 RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
 RA Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-136(1996).
 CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC -----
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OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Adrenal gland;
 RX MEDLINE=93382537; PubMed=7690465;
 RA Nguyen M., Strubel N.A., Bischoff J.;
 RT "A role for sialyl Lewis-X/A glycoconjugates in capillary
 RT morphogenesis";
 RL Nature 365:267-269(1993).
 CC -!- FUNCTION: EXPRESSED ON CYTOKINE INDUCED ENDOTHELIAL CELLS AND
 CC MEDIATES THEIR BINDING TO LEUKOCYTES. THE LIGAND RECOGNIZED BY
 CC ELAM-1 IS SIALYL-LEWIS X (ALPHA(1->3)FUCOSYLATED DERIVATIVES OF
 CC POLYLACTOSAMINE THAT ARE FOUND AT THE NONREDUCING TERMINI OF
 CC GLYCOLIPIDS).
 CC -!- FUNCTION: INVOLVED IN CAPILLARY MORPHOGENESIS BY BINDING TO A
 CC BOVINE CAPILLARY ENDOTHELIAL (BCE) CELL SIALYL LEWIS-X AND/OR
 CC SIALYL LEWIS A-CONTAINING LIGAND (PROBABLY).
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -!- SIMILARITY: TO OTHER SELECTINS/LECAMS.
 CC -!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
 CC -!- SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS; BOVINE E-LECTIN LACKS
 CC THE HUMAN SUSHI-4 AND 5 EQUIVALENTS.
 CC -----
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 CC -----
 CC EMBL; L12039; AAA02991.1; -
 DR HSP; P16581; IESL.
 DR InterPro: IPR000436; -
 DR InterPro: IPR000561; -
 DR InterPro: IPR001304; -
 DR InterPro: IPR002396; -
 DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00059; lectin_c; 1.
 DR Pfam; PF00084; sush1; 4.
 DR PRINTS; PR00343; SELECTIN.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS00615; C-TYPE LECTIN_1; 1.
 DR PROSITE; PS50041; C-TYPE LECTIN_2; 1.
 DR Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;
 KW Selectin; Signal; Sush1; Repeat.
 FT SIGNAL 1 22 BY SIMILARITY.
 FT CHAIN 1 485
 FT DOMAIN 23 430 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 431 453 POTENTIAL.
 FT DOMAIN 454 485 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 39 139 C-TYPE LECTIN (SHORT FORM).
 FT DOMAIN 140 176 EGF-LIKE.
 FT DOMAIN 180 422 4 X SUSHI (SCR) REPEATS.
 FT DOMAIN 180 238 SUSHI 1.
 FT DOMAIN 241 300 SUSHI 2.
 FT DOMAIN 303 363 SUSHI 3.
 FT DOMAIN 366 422 SUSHI 4.
 FT DISULFID 41 139 BY SIMILARITY.
 FT DISULFID 112 131 BY SIMILARITY.
 FT DISULFID 144 155 BY SIMILARITY.
 FT DISULFID 149 164 BY SIMILARITY.
 FT DISULFID 166 175 BY SIMILARITY.
 FT DISULFID 181 224 BY SIMILARITY.
 FT DISULFID 210 237 BY SIMILARITY.
 FT DISULFID 242 286 BY SIMILARITY.
 FT DISULFID 272 299 BY SIMILARITY.
 FT DISULFID 304 349 BY SIMILARITY.
 FT DISULFID 335 362 BY SIMILARITY.
 FT DISULFID 367 408 BY SIMILARITY.

FT DISULFID 394 421 BY SIMILARITY.
 FT CARBOHYD 61 79 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 79 79 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 161 161 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 203 203 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 265 265 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 312 312 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 316 316 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 379 379 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 401 401 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 485 AA; 53200 MW; AE931C9B521E3904 CRC64;
 Query Match 39.0%; Score 41; DB 1; Length 485;
 Best Local Similarity 42.9%; Pred. No. 21;
 Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 3 GKNRSCQSEKLG 16
 ||:|:| |::|
 Db 374 KLNWNCSEPVLG 387
 RESULT 13
 LEM2_RABIT
 ID LEM2_RABIT STANDARD; PRT; 551 AA.
 AC P27113;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1)
 DE (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2)
 DE (CD62E).
 GN SELE.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=92189729; PubMed=1372169;
 RA Larian J.D., Tsang T.C., Rumberger J.M., Burns D.K.;
 RT "Characterization of cDNA and genomic sequences encoding rabbit
 RT ELAM-1: conservation of structure and functional interactions with
 RT leukocytes";
 RL DNA Cell Biol. 11:149-162(1992).
 CC -!- FUNCTION: EXPRESSED ON CYTOKINE INDUCED ENDOTHELIAL CELLS AND
 CC MEDIATES THEIR BINDING TO LEUKOCYTES. THE LIGAND RECOGNIZED BY
 CC ELAM-1 IS SIALYL-LEWIS X (ALPHA(1->3)FUCOSYLATED DERIVATIVES OF
 CC POLYLACTOSAMINE THAT ARE FOUND AT THE NONREDUCING TERMINI OF
 CC GLYCOLIPIDS).
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -!- INDUCTION: BY CYTOKINES.
 CC -!- SIMILARITY: TO OTHER SELECTINS/LECAMS.
 CC -!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
 CC -!- SIMILARITY: CONTAINS 5 SUSHI (SCR) REPEATS.
 CC -----
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 CC -----
 CC EMBL; M91004; AAA31243.1; -
 DR EMBL; M91005; AAA31244.1; -
 DR HSP; P16581; IKJA.
 DR InterPro: IPR000436; -
 DR InterPro: IPR000561; -
 DR InterPro: IPR001304; -

DR InterPro: IPR002396; --
 DR Pfam: PF00008; EGF_1;
 DR Pfam: PF00059; lectin_c; 1.
 DR Pfam: PF00084; sushi; 5.
 DR PRINTS: PR00343; SELECTIN.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS00615; C-TYPE_LECTIN_1; 1.
 DR PROSITE: PS00041; C-TYPE_LECTIN_2; 1.
 DR Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;
 KW Selectin; Signal; Sushi; Repeat.
 FT SIGNAL 1 23
 FT CHAIN 24 551
 FT DOMAIN 24 495
 FT TRANSMEM 496 517
 FT DOMAIN 518 551
 FT DOMAIN 518 551
 FT DOMAIN 518 551
 FT DOMAIN 141 177
 FT DOMAIN 181 487
 FT DOMAIN 181 487
 FT DOMAIN 181 487
 FT DOMAIN 243 302
 FT DOMAIN 305 365
 FT DOMAIN 368 428
 FT DOMAIN 431 487
 FT DOMAIN 431 487
 FT DISULFID 42 140
 FT DISULFID 113 132
 FT DISULFID 145 156
 FT DISULFID 150 165
 FT DISULFID 167 176
 FT DISULFID 182 226
 FT DISULFID 212 239
 FT DISULFID 244 288
 FT DISULFID 274 301
 FT DISULFID 306 351
 FT DISULFID 337 364
 FT DISULFID 369 414
 FT DISULFID 400 427
 FT DISULFID 432 473
 FT DISULFID 459 486
 FT CARBOHYD 32 32
 FT CARBOHYD 45 45
 FT CARBOHYD 162 162
 FT CARBOHYD 194 194
 FT CARBOHYD 201 201
 FT CARBOHYD 205 205
 FT CARBOHYD 267 267
 FT CARBOHYD 314 314
 FT CARBOHYD 321 321
 FT CARBOHYD 334 334
 FT CARBOHYD 442 442
 FT CARBOHYD 466 466
 FT CARBOHYD 308 308
 FT CONFLICT 328 328
 FT CONFLICT 491 491
 SQ SEQUENCE 551 AA; 60346 MW; 239C8A883B23240E CRC64;
 Query Match 39.0%; Score 41; DB 1; Length 551;
 Best Local Similarity 53.3%; Pred. No. 23;
 Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 Oy 2 LGKMNRCQSEKLG 16
 ||| ||| | | | | |
 Db 438 LGKTNVSCSGEPVFC 452
 RESULT 14
 LEM2_HUMAN STANDARD; PRT; 610 AA.
 ID LEM2_HUMAN
 AC P1658L; P16111;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE B-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1)
 DE (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2)
 DE (CD62E).
 GN SELE OR ELAM1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90175359; PubMed=1689848;
 RA Hession C., Osborn L., Goff D., Chi-Rosso G., Vassallo C.,
 RA Pasek M., Pittack C., Tizard R., Goelz S., McCarthy K., Hopple S.,
 RA Lobb R.;
 RT "Endothelial leukocyte adhesion molecule 1: direct expression cloning
 RT and functional interactions.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:1673-1677(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89162047; PubMed=2466335;
 RA Bevilacqua M.P., Stengelin S., Gimbrone M.A. Jr., Seed B.;
 RT "Endothelial leukocyte adhesion molecule 1: an inducible receptor for
 RT neutrophils related to complement regulatory proteins and lectins.";
 RL Science 243:1160-1165(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91115870; PubMed=1703529;
 RA Collins T., Williams A., Johnston G.I., Kim J., Eddy R., Shows T.,
 RA Gimbrone M.A. Jr., Bevilacqua M.P.;
 RT "Structure and chromosomal location of the gene for endothelial-
 RT leukocyte adhesion molecule 1.";
 RL J. Biol. Chem. 266:2466-2473(1991).
 RN [4]
 RP LIGAND.
 RX MEDLINE=91068005; PubMed=1701274;
 RA Phillips M.L., Nudelma E., Gaeta F.C., Perez M., Singhal A.K.,
 RA Hakomori S., Paulson J.C.;
 RT "ELAM-1 mediates cell adhesion by recognition of a carbohydrate
 RT ligand, sialyl-Lex.";
 RL Science 250:1130-1132(1990).
 RN [5]
 RP 3D-STRUCTURE MODELING OF LECTIN DOMAIN.
 RX MEDLINE=93202275; PubMed=7681016;
 RA Mills A.;
 RT "Modelling the carbohydrate recognition domain of human E-selectin.";
 RL FEBS Lett. 319:5-11(1993).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 22-178.
 RX MEDLINE=94150646; PubMed=7509040;
 RA Graves B.J., Crowther R.L., Chandran C., Rumberger J.M., Li S.,
 RA Huang K.-S., Presky D.H., Familletti P.C., Wolitzky B.A., Burns D.K.;
 RT "Insight into E-selectin/ligand interaction from the crystal
 RT structure and mutagenesis of the lec/EGF domains.";
 RL Nature 367:532-538(1994).
 RN [7]
 RP VARIANT ARG-149.
 RX MEDLINE=95179107; PubMed=7533025;
 RA Wenzel K., Felix S., Kleber F.X., Brachold R., Menke T., Schattke S.,
 RA Schulte K.L., Glaser C., Rohde K., Baumann G., Speer A.;
 RT "E-selectin polymorphism and atherosclerosis: an association study.";
 RL Hum. Mol. Genet. 3:1935-1937(1994).
 RN [8]
 RP VARIANT ARG-149.
 RX MEDLINE=99134508; PubMed=9933738;
 RA Ye S.Q., Usher D., Virgil D., Zhang L.Q., Yochim S.E., Gupta R.;
 RT "A PstI polymorphism detects the mutation of serine-128 to arginine in
 RT CD 62E gene - a risk factor for coronary artery disease.";
 RL J. Biomed. Sci. 6:18-21(1999).
 CC -!- FUNCTION: EXPRESSED ON CYTOKINE INDUCED ENDOTHELIAL CELLS AND
 CC MEDIATES THEIR BINDING TO LEUKOCYTES. THE LIGAND RECOGNIZED BY
 CC ELAM-1 IS SIALYL-LEWIS X (ALPHA(1->3)FUCOSYLATED DERIVATIVES OF
 CC POLYLACTOSAMINE THAT ARE FOUND AT THE NONREDUCING TERMINI OF
 CC GLYCOLIPIDS).

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- POLYMORPHISM: A POLYMORPHISM IN POSITION 149 IS ASSOCIATED WITH A
 CC HIGHER RISK OF CORONARY ARTERY DISEASE (CAD). A SIGNIFICANTLY
 CC HIGHER MUTATION FREQUENCY (ARG-149) IS OBSERVED IN PATIENTS WITH
 CC ANGIOGRAPHICALLY PROVEN SEVERE ATHEROSCLEROSIS COMPARED WITH AN
 CC UNSELECTED POPULATION (SER-149).
 CC -1- SIMILARITY: TO OTHER SELECTINS/LECTINS.
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 6 SUSHI (SCR) REPEATS.
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD62e entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd62e.htm".
 CC -----
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 CC -----
 CC EMBL; M30640; AAA52377.1; -;
 CC EMBL; M61893; AAA52375.1; -;
 CC EMBL; M61895; AAA52375.1; JOINED.
 CC EMBL; M61887; AAA52375.1; JOINED.
 CC EMBL; M61888; AAA52375.1; JOINED.
 CC EMBL; M61890; AAA52375.1; JOINED.
 CC EMBL; M61891; AAA52375.1; JOINED.
 CC EMBL; M61892; AAA52375.1; JOINED.
 CC EMBL; M24736; AAA52376.1; -;
 CC PIR; A32606; A32606.
 CC PIR; A35046; A35046.
 CC PIR; A38615; A38615.
 CC PDB; 1ESL; 31-AUG-94.
 CC PDB; 1KJA; 03-APR-96.
 CC MIM; 131210; -;
 CC InterPro; IPR000436; -;
 CC InterPro; IPR000561; -;
 CC InterPro; IPR001304; -;
 CC InterPro; IPR002396; -;
 CC Pfam; PF00008; EGF_1;
 CC Pfam; PF00059; lectin_c; 1.
 CC Pfam; PF00084; sush1; 6.
 CC PRINTS; PR00343; SELECTIN.
 CC PROSITE; PS00022; EGF_1; 1.
 CC PROSITE; PS01186; EGF_2; 1.
 CC PROSITE; PS00615; C-TYPE LECTIN_1; 1.
 CC PROSITE; PS00041; C-TYPE LECTIN_2; 1.
 CC Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;
 CC Selectin; Signal; Sush1; Repeat; Polymorphism; 3D-structure.
 CC SIGNAL 1 21
 CC CHAIN 22 610
 CC DOMAIN 22 556
 CC TRANSMEM 557 578
 CC DOMAIN 579 610
 CC DOMAIN 38 138
 CC DOMAIN 139 175
 CC DOMAIN 179 548
 CC DOMAIN 179 238
 CC DOMAIN 241 300
 CC DOMAIN 303 363
 CC DOMAIN 366 426
 CC DOMAIN 429 489
 CC DOMAIN 492 548
 CC DISULFID 40 138
 CC DISULFID 111 130
 CC DISULFID 143 154
 CC DISULFID 148 163
 CC DISULFID 165 174
 CC DISULFID 180 224
 CC DISULFID 210 237
 CC DISULFID 242 286
 CC DISULFID 272 299
 CC BY SIMILARITY.
 CC BY SIMILARITY.
 CC BY SIMILARITY.
 CC BY SIMILARITY.

FT DISULFID 304 349 BY SIMILARITY.
 FT DISULFID 335 362 BY SIMILARITY.
 FT DISULFID 367 412 BY SIMILARITY.
 FT DISULFID 398 425 BY SIMILARITY.
 FT DISULFID 430 475 BY SIMILARITY.
 FT DISULFID 461 488 BY SIMILARITY.
 FT DISULFID 493 534 BY SIMILARITY.
 FT DISULFID 520 547 BY SIMILARITY.
 FT CARBOHYD 25 25 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 145 145 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 160 160 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 179 179 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 199 199 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 203 203 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 265 265 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 312 312 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 332 332 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 503 503 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 527 527 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT VARIANT 149 149 S -> R (ASSOCIATED WITH A RISK FACTOR FOR
 FT CAD).
 FT FTFTId=VAR_004191.
 FT H -> Y (IN REF. 2).
 SQ SEQUENCE 610 AA; 66655 MW; 7D43E3C0D1229229 CRC64;
 Query Match 39.0%; Score 41; DB 1; Length 610;
 Best Local Similarity 50.0%; Pred. No. 26;
 Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 3 GKMNRSCQSEKILIG 16
 ||:||||:
 Db 500 GKINMSCGEPVFG 513
 RESULT 15
 FABG_BRANA
 ID FABG_BRANA STANDARD; PRT; 201 AA.
 AC P27582;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) (3-KETOACYL-
 DE ACYL CARRIER PROTEIN REDUCTASE) (FRAGMENTS).
 OS Brassica napus (rape).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Brassica.
 OX NCBI_TaxID=3708;
 RN [1]
 RP SEQUENCE OF 35-62 AND 81-84.
 RC TISSUE=Seed;
 RX MEDLINE=92223071; PubMed=1562581;
 RA Sheldon P.S., Kekwick R.G.O., Smith C.G., Sidebottom C.M.,
 RA Slabas A.R.;
 RT "3-oxoacyl-[ACP] reductase from oilseed rape (Brassica napus).";
 RL Biochim. Biophys. Acta 1120:151-159(1992).
 RN [2]
 RP SEQUENCE OF 63-201 FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Seed;
 RX MEDLINE=92246853; PubMed=1575676;
 RA Slabas A.R., Chase D., Nishida I., Murata N., Sidebottom C.,
 RA Safford R., Kekwick R.G., Sheldon P.S., Hardie D.G., Mackintosh R.W.;
 RT "Molecular cloning of higher-plant 3-oxoacyl-(acyl carrier protein)
 RT reductase. Sequence identities with the nodg-gene product of the
 RT nitrogen-fixing soil bacterium Rhizobium meliloti.";
 RL Biochem. J. 283:321-326(1992).
 EC -1- CATALYTIC ACTIVITY: (3R)-3-HYDROXYACYL-[ACYL-CARRIER PROTEIN] +
 CC NADPH(+) = 3-OXOACYL-[ACYL-CARRIER PROTEIN] + NADPH.
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
 CC PATHWAY.
 CC -1- SUBUNIT: HOMOTETRAMER (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST AND NON-PHOTOSYNTHETIC

CC PLASTIDS.
CC -!- TISSUE SPECIFICITY: EMBRYO AND LEAF TISSUES.
CC -!- MISCELLANEOUS: EXHIBITS A MARKED PREFERENCE FOR ACYL-CARRIER
CC PROTEIN DERIVATIVES OVER COA DERIVATIVES AS SUBSTRATES.
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
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CC -----
DR EMBL; X64463; CAA45793.1; -
DR HSSP; P19992; 2HSD.
DR InterPro; IPR002198; -
DR Pfam; PF00106; adh_short; 1.
DR Pfam; PF00678; adh_short_C2; 1.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Fatty acid biosynthesis; Oxidoreductase; NADP; Chloroplast.
FT NON_CONS 27 28
FT NON_CONS 34 35
FT NON_CONS 62 63
FT ACT_SITE 108 108 BY SIMILARITY.
SQ SEQUENCE 201 AA; 21042 MW; FD51B2E369D2D967 CRC64;

Query Match 38.1%; Score 40; DB 1; Length 201;
Best Local Similarity 35.0%; Pred. No. 13;
Matches 7; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Oy 1 NLGKMNRCQSEKLGITYTKT 20
|.:|.:|.:|
Db 102 NIGQANYAAKAGVIGFSKT 121

Search completed: May 23, 2001, 15:36:21
Job time: 652 sec

RESULT	3
Q9SZS0	
ID	PRELIMINARY;
AC	Q9SZS0; PRT; 266 AA.
DT	Q9SZS0;
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE	01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE	HYPOTHETICAL 29.5 KDA PROTEIN.
GN	F27G19.50 OR AT4G27450.
OS	Arabidopsis thaliana (Mouse-ear cress).
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC	Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC	Brassicales; Brassicaceae; Arabidopsids.
OX	NCBI_TaxID=3702;
[1]	
RN	SEQUENCE FROM N.A.
RA	Bavan M., Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
RA	Rancroft I., Mewes H.W., Mayer K.F.X., Lemcke K., Mannhaupt G.,
RA	Schuelter C.;
RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
[2]	
RN	SEQUENCE FROM N.A.
RA	EU Arabidopsis sequencing project;
RL	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
[3]	
RN	SEQUENCE FROM N.A.
RA	Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
RA	Mewes H.W., Lemcke K., Mayer K.F.X.;

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Query Match      43.8%;   Score 46;   DB 2;   Length 379;
Best Local Similarity 45.0%;   Pred. No. 5.5;
Matches 9;   Conservative 2;   Mismatches 9;   Indels 0;   Gaps 0;

Qy  1  NLGRMNRSCQSEKLIQYTKT  20
      |||  : ||||| |
Db  198  NKGKSGNESLRKIIQYTN  217

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Query Match 43.8%; Score 46; DB 2; Length 379;
Best Local Similarity 45.0%; Pred. No. 5.5;
Matches 9; Conservative 2; Mismatches 9; Indels

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RESULT 5
Q9ZQS4 ID Q9ZQS4 PRELIMINARY; PRT; 620 AA.
AC Q9ZQS4;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE MYC-RP.
GN MYC-RP.
OS Perilla frutescens.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
OC Lamiales; Lamiales; Perilla.
OX NCBI_TaxID=48386;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LEAF;
RA Gong Z., Yamagishi E., Yamazaki M., Saito K.;
RT "A constitutively expressed myc-like gene is involved in the
RT regulation of anthocyanin biosynthesis in the leaves of Perilla
RT frutescens.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB024050; BAA75513.1; -.
DR HSSP; P25912; 1HLO.
DR INTERPRO; IPR001092; -.
DR INTERPRO; IPR003015; -.
DR PFAM; PF00010; HLH; 1.
DR PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
SQ SEQUENCE 620 AA; 68702 MW; F9B6EBBD377DCF14 CRC64;

Query Match 42.9%; Score 45; DB 10; Length 620;
Best Local Similarity 44.4%; Pred. No. 14;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 2 LGKMRSCQSEKLIGYTK 19
|| :|| :|| :||
Db 514 LGNKRKSCDTERMAGENK 531

RESULT 6
Q9SLX2 ID Q9SLX2 PRELIMINARY; PRT; 620 AA.
AC Q9SLX2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE MYC-GP.
GN MYC-GP.
OS Perilla frutescens.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
OC Lamiales; Lamiales; Perilla.
OX NCBI_TaxID=48386;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LEAF OF GREEN P. FRUTESCENS;
RA Gong Z., Yamagishi E., Yamazaki M., Saito K.;
RT "A constitutively expressed Myc-like gene involved in anthocyanin
RT biosynthesis from Perilla frutescens: molecular characterization,
RT heterologous expression in transgenic plants and transactivation in
RT yeast cells.";
RL Plant Mol. Biol. 41:33-44(1999).
DR EMBL; AB024051; BAA75514.1; -.
DR HSSP; P25912; 1HLO.
DR INTERPRO; IPR001092; -.
DR INTERPRO; IPR003015; -.
DR PFAM; PF00010; HLH; 1.
DR PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
SQ SEQUENCE 620 AA; 68718 MW; B0FD91AA9607D8B5 CRC64;

Query Match 42.9%; Score 45; DB 10; Length 620;

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Best Local Similarity 44.4%; Pred. No. 14;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 2 LGKMRSCQSEKLIGYTK 19
|| :|| :|| :||
Db 514 LGNKRKSCDTERMAGENK 531

RESULT 7
Q9SND0 ID Q9SND0 PRELIMINARY; PRT; 3071 AA.
AC Q9SND0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE HYPOTHETICAL 343.7 KDA PROTEIN.
GN FilCi.220.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bagues M., Collado M.C., Navarro P., Terol J., Perez-Alonso M.,
RA Mewes H.W., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RA Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL132976; CAB62317.1; -.
DR INTERPRO; IPR000005; -.
DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 3071 AA; 343689 MW; 4A3F7C9F71C92A25 CRC64;

Query Match 42.9%; Score 45; DB 10; Length 3071;
Best Local Similarity 53.3%; Pred. No. 69;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 NLGKMRSCQSEKLI 15
||||:|:|:|
Db 473 NLGKLSVTCYPEKII 487

RESULT 8
Q9YCX9 ID Q9YCX9 PRELIMINARY; PRT; 260 AA.
AC Q9YCX9;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CALBINDIN D28K.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=INTESTINE;
RX MEDLINE=98232071; PubMed=9572360;
RA Anano T., Noro N., Kawabata H., Kobayashi Y., Yoshizato K.;
RT "Metamorphosis-associated and region-specific expression of calbindin
RT gene in the posterior intestinal epithelium of xenopus laevis larva.";
RL Dev. Growth Differ. 40:177-188(1998).
DR EMBL; U76636; AAD00259.1; -.
DR HSSP; P02618; 1CDP.
DR INTERPRO; IPR002048; -.
DR PFAM; PF00036; efhand; 4.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.

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SQ SEQUENCE 260 AA; 29939 MW; 794F7ED14CAC9CD0 CRC64;

Query Match 41.9%; Score 44; DB 13; Length 260;
Best Local Similarity 47.4%; Pred. No. 8.4;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 2 LGKMNRCQSEKLGITYTKT 20
| | | | | | | | | |
Db 130 LKANKPCESKLEYYTHT 148

RESULT 9

ID Q9WT06 PRELIMINARY; PRT; 353 AA.
AC Q9WT06;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE U67 PROTEIN.
GN U67.
OS Human herpesvirus 6, and Human herpesvirus 6B.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Roseolovirus.
OX NCBI_TaxID=10368, 32604;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Human herpesvirus 6; STRAIN=HST;
RA Isegawa Y., Mukai T., Nakano K., Kagawa M., Chen J., Mori Y.,
RA Sunagawa T., Sashihara J., Zou P., Kosuge H., Yamaniishi K.;
RT "A comparison of the complete DNA sequences between human herpesvirus-
6 variant A and B.";
RL J. Virol. 0:0-0(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=Human herpesvirus 6B; STRAIN=Z29;
RX MEDLINE=99412319; Pubmed=10482553;
RA Dominguez G., Dambaugh T.R., Stamey F.R., Dewhurst S., Inoue N.,
RA Pellett P.E.;
RT "Human herpesvirus 6B genome sequence: coding content and comparison
with human herpesvirus 6A.";
RL J. Virol. 73:8040-8052(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=Human herpesvirus 6B; STRAIN=Z29;
RA Pellett P.E., Dominguez G., Dambaugh T.R., Stamey F.R., Dewhurst S.,
RA Inoue N.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB021506; BAA78288.1; -;
DR EMBL; AF157706; AAD49668.1; -;
SQ SEQUENCE 353 AA; 39616 MW; 81E41323E16EF47F CRC64;

Query Match 41.0%; Score 43; DB 14; Length 353;
Best Local Similarity 58.3%; Pred. No. 17;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 9 CQSEKLGITYTKT 20
| | | | | | | | | |
Db 184 CQSDCFGYSKT 195

RESULT 10

ID Q9U9C1 PRELIMINARY; PRT; 522 AA.
AC Q9U9C1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE CYTOCHROME P450 (FRAGMENT).
GN CYP9A4.
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Sphingioidea; Sphingidae; Sphinginae; Manduca.
OX NCBI_TaxID=71130;
RN [1]
RP SEQUENCE FROM N.A.
RA Stevens J.L., Snyder M.J., Koener J.F., Feyereisen R.;
RT "Inducible P450s of the CYP9 family from larval Manduca sexta
midgut.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF172279; AAD51036.1; -;
DR INTERPRO; IPR001128; -;
DR INTERPRO; IPR002401; -;
DR INTERPRO; IPR002402; -;
DR INTERPRO; IPR002403; -;
DR PFAM; PF00067; P450; 1.
DR PRINTS; PR00385; P450.
DR PRINTS; PR00463; EP450I.
DR PRINTS; PR00464; EP450II.
DR PRINTS; PR00465; EP450IV.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 522 AA; 59951 MW; D2951BB872591E29 CRC64;

Query Match 41.0%; Score 43; DB 5; Length 522;
Best Local Similarity 46.7%; Pred. No. 25;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 NLGKMNRSCQSEKLI 15
| | | | | | | | | |
Db 398 NLGRANRKCKKDFII 412

RESULT 11

ID Q93000 PRELIMINARY; PRT; 556 AA.
AC Q93000;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
DE CHLI PROTEIN (FRAGMENT).
GN CHLRI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ouellette M.M., Wright W.E., Shay J.W.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U75969; AAB18751.1; -;
FT NON_TER 1
SQ SEQUENCE 556 AA; 61643 MW; 1357F45F750756B2 CRC64;

Query Match 41.0%; Score 43; DB 4; Length 556;
Best Local Similarity 43.5%; Pred. No. 27;
Matches 10; Conservative 4; Mismatches 5; Indels 4; Gaps 1;

Qy 1 NLGKMNRSCQ----SEKLGITYTK 19
| | | | | | | | | |
Db 216 NLFKVQRYCEKSMISRKLFQFTE 238

RESULT 12

ID Q92498 PRELIMINARY; PRT; 680 AA.
AC Q92498;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE CHLI PROTEIN.
GN HCHLI-1/KRG-2.

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 23, 2001, 15:28:33 ; Search time 184.73 Seconds
(without alignments)
8.974 Million cell updates/sec

Title: US-08-887-977-10_COPY_291_319

Perfect score: 158

Sequence: 1 VTEVLAFLHCLNPVLYAFIGKFRNYFL 29

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_0401.*
1: /SID56/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID56/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID56/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SID56/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SID56/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SID56/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SID56/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SID56/gcgdata/geneseq/geneseq/AA1987.DAT.*
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11: /SID56/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SID56/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SID56/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SID56/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SID56/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SID56/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SID56/gcgdata/geneseq/geneseq/AA1996.DAT.*
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19: /SID56/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SID56/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID56/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID56/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	158	100.0	365	19 W48086	Human dendritic ce
2	158	100.0	365	21 Y97077	Primate (human) ch
3	124	78.5	332	18 W26766	Human chemokine re
4	124	78.5	352	18 W27407	Human CCR5, Homo
5	124	78.5	352	18 W27123	Human chemokine re
6	124	78.5	352	18 W27125	Macaque chemokine
7	124	78.5	352	18 W07602	Human G-protein ch
8	124	78.5	352	19 W23835	Human CC chemokine
9	124	78.5	352	20 W88232	HIV-1 co-receptor
10	124	78.5	352	21 Y80128	Human G-protein ch
11	124	78.5	371	19 W23834	Human CC chemokine

12	124	78.5	439	20	Y41280	Fusion protein con
13	121	76.6	354	15	R53932	Interleukin 8 (IL-
14	121	76.6	355	13	R28272	Sequence in a high
15	121	76.6	355	16	R80950	Recombinant high a
16	121	76.6	360	17	R99274	Chemokine receptor
17	121	76.6	360	21	B07498	A human CCR4 chemo
18	120	75.9	209	21	B58414	Lung cancer associ
19	120	75.9	355	15	R52749	C-C chemokine rece
20	120	75.9	355	17	W03376	CC-chemokine recep
21	120	75.9	355	17	W03377	CC-chemokine recep
22	120	75.9	355	17	W03378	CC-chemokine recep
23	120	75.9	355	18	W31850	Human eosinophil e
24	120	75.9	355	18	W26588	Human MIP-1 alpha/
25	120	75.9	355	18	W27124	Human chemokine re
26	120	75.9	355	18	W25751	Human MIP-1alpha/R
27	120	75.9	355	18	W10100	Human C-C chemokin
28	120	75.9	355	19	W51744	Human C-C chemokin
29	120	75.9	355	19	W51745	Human C-C chemokin
30	120	75.9	355	19	W51746	Human C-C chemokin
31	120	75.9	355	21	B20571	Human CC-chemokine
32	116	73.4	350	13	R27791	Interleukin-8 rece
33	116	73.4	350	16	R68811	Interleukin-8 rece
34	116	73.4	350	16	R80756	Interleukin 8 rece
35	116	73.4	350	16	R80951	Recombinant high a
36	116	73.4	350	17	R09989	Human IL-8 recepto
37	116	73.4	355	15	R53748	Seven transmembran
38	116	73.4	355	19	W48722	Human V28 seven tr
39	116	73.4	355	21	B21692	Human 7TM receptor
40	116	73.4	355	21	B21693	Human 7TM receptor
41	116	73.4	355	21	Y90642	Human G protein-co
42	116	73.4	355	21	Y90677	Human mutant G pro
43	116	73.4	1060	16	R70123	IL8-R type 1-GBP 1
44	115	72.8	355	18	W29179	Rat CC chemokine r
45	115	72.8	359	19	W64778	A murine CXC chemo

ALIGNMENTS

RESULT 1

W48086
ID W48086 standard; Protein; 365 AA.

XX
AC W48086;

XX
DT 11-JUN-1998 (first entry)

XX
DE Human dendritic cell chemokine receptor.

XX
DE Human; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta;
receptor; dendritic cell; macrophage; inflammation; asthma.

XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers

FT Misc-difference 193 /note= "encoded by CAN"

XX
XX WO9801557-A2.

XX
XX 15-JAN-1998.

XX
XX 02-JUL-1997; 97WO-US10819.

XX
XX 04-JUN-1997; 97US-0048593.

PR
XX 05-JUL-1996; 96US-0675814.

PR
XX 11-OCT-1996; 96US-0028329.

XX
XX (SCHE) SCHERING CORP.

XX
XX Gish KC, Schall TJ, Vicari A, Wang W, Zlotnik A;

XX
XX WPI; 1998-101054/09.

DR

DR N-PSDB; V15418.
 XX Novel chemokines, e.g. thymus expressed chemokine - used for
 PT treating inflammatory conditions including asthma.
 XX
 PS Claim 3; Page 94-95; 202pp; English.
 XX
 CC The present sequence represents human dendritic cell chemokine receptor.
 CC Antibodies which bind to the protein can be used in detecting or
 CC diagnosing various immunological conditions related to expression
 CC of the protein. The nucleic acid can be used for screening and
 CC isolating DNA clones for the chemokines, especially from other
 CC species. The chemokine can be used in the treatment of conditions
 CC associated with abnormal physiology or development, including
 CC inflammatory conditions such as asthma.
 XX
 SQ Sequence 365 AA;

Query Match 100.0%; Score 158; DB 19; Length 365;
 Best Local Similarity 100.0%; Pred. No. 7.6e-17;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCCCLNPVLYAFIGQKFRNYFL 29
 |||||
 DB 291 vtevlafhlhccclnpvlyafigqkfrnyfl 319

RESULT 2
 Y97077
 ID Y97077 standard; Protein; 365 AA.
 XX
 AC Y97077;
 XX
 DT 04-DEC-2000 (first entry)
 XX
 DE Primate (human) chemokine receptor CCR6.
 KW MIP-3-alpha; chemokine; CCR6 receptor; ligand; cytostatic; agonist;
 KW antagonist; anti-psoriatic; dermatological; immunosuppressive;
 KW anti-inflammatory.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 193
 FT Misc-difference 193 /note= "Encoded by CAN#"

XX WO2000046248-A1.
 XX
 XX 10-AUG-2000.
 XX
 XX 02-FEB-2000; 2000WO-US00511.
 XX
 XX 03-FEB-1999; 99US-0244281.
 XX (SCHE) SCHERING CORP.
 XX
 XX Oldham ER, Homey B, Dieu-Nosjean M, Caux C, Zlotnik A;
 XX
 XX WPI; 2000-543477/49.
 DR N-PSDB; A51971.

PT Novel methods for modulating the migration of cells within or to the
 PT skin using MIP-3-alpha or CCR6 agonists or antagonists, useful for
 PT treating skin disorders, e.g. cancer
 XX
 PS Disclosure; Page 53-54; 61pp; English.

XX The MIP-3-alpha chemokine is expressed in inflamed skin cells. This
 CC chemokine is the ligand for the CCR6 receptor. MIP-3-alpha or CCR6
 CC agonists or antagonists can be used to modulate the migration of a cell
 CC within or to the skin of a mammal. MIP-3-alpha can be used to purify a

CC population of cells expressing a MIP-3-alpha receptor. The methods are
 CC useful for treating a mammalian subject with a skin disease or condition,
 CC e.g. cancer, metastasis, psoriasis, atopic or contact dermatitis,
 CC systemic lupus erythematosus and lichen ruber planus, or for treating
 CC skin transplants or grafts.

XX Sequence 365 AA;

Query Match 100.0%; Score 158; DB 21; Length 365;
 Best Local Similarity 100.0%; Pred. No. 7.6e-17;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCCCLNPVLYAFIGQKFRNYFL 29
 |||||
 DB 291 vtevlafhlhccclnpvlyafigqkfrnyfl 319

RESULT 3
 W26766
 ID W26766 standard; Protein; 332 AA.
 XX
 AC W26766;

XX
 DT 21-MAY-1998 (first entry)
 XX
 DE Human chemokine receptor MMLR-CCR.

XX Mammalian mixed lymphocyte receptor; chemokine receptor; MMLR-CCR;
 KW human; monocyte; macrophage; chemotaxis; haematopoiesis; infection;
 KW inflammation; proliferative disease; cardiovascular disease;
 KW tumour; rheumatoid arthritis; alveolitis; atherosclerosis;
 KW chronic granulomatous disease; asthma; myasthenia gravis;
 KW diabetes; inflammatory bowel disease; toxic shock syndrome;
 KW septic shock; Chediak-Higashi syndrome; therapy; diagnosis.

XX OS Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 107..128
 FT /note= "conserved peptide"
 FT Misc-difference 121
 FT /note= "a claimed polypeptide has isoleucine at
 residue 121"

XX WO9741225-A2.
 XX
 XX 06-NOV-1997.
 XX
 XX 25-APR-1997; 97WO-US06993.
 XX
 XX 26-APR-1996; 96US-0638081.
 XX (INCY-) INCYTE PHARM INC.
 XX
 XX Au-Young J, Bandman O, Coleman R, Wilde CG;
 XX
 XX WPI; 1997-549729/50.
 DR N-PSDB; T99542.

PT Polynucleotide encoding MMLR-CCR or MPHG-CCR chemokine receptor -
 PT useful to study, diagnose and treat, e.g. infection, inflammation,
 PT solid tumour and proliferative and cardiovascular disease

XX Claim 8; Page 37-38; 59pp; English.

XX This protein comprises human MMLR-CCR, a novel C-C chemokine
 CC receptor associated with monocyte/macrophage infiltration and
 CC chemotaxis and haematopoiesis. The amino acid sequence was deduced
 CC from a cDNA clone (see T99542) obtained from a cDNA library made
 CC from mononuclear cells collected on day 2 of a mixed lymphocyte
 CC culture, i.e. cells associated with inflammation and
 CC immunomodulation. Another novel chemokine receptor, MPHG-CCR

CC (see W36767), is also claimed. MMLR-CCR contains 7 transmembrane
CC spanning segments connected by a series of intracellular and
CC extracellular loops. MMLR-CCR and MHPG-CCR can be used to study,
CC diagnose and treat disease states in which normal leukocyte
CC function is perturbed by normal leukopoiesis or inappropriate
CC activation via chemokine agonists or antagonists, such as infection,
CC inflammation, proliferative disease, tumorigenesis, autoimmune
CC disease, abnormal cell proliferation, solid tumours, cardiovascular
CC disease, rheumatoid arthritis, alveolitis, atherosclerosis, chronic
CC granulomatous disease, asthma, myasthenia gravis, diabetes,
CC inflammatory bowel disease, toxic shock syndrome, septic shock and
CC Chediak-Higashi syndrome.
XX
SQ Sequence 332 AA;

Query Match 78.5%; Score 124; DB 18; Length 332;
Best Local Similarity 65.5%; Pred. No. 1.5e-11;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCCLNPLVLYAFIGOKERNYFL 29
||| | |||:||||:||||:||||:|
Db 261 vtetgmthccinpiiyafvgekfnyll 289

RESULT 4
W27407
ID W27407 standard; Protein; 352 AA.
XX
AC W27407;
XX
DT 14-APR-1998 (first entry)
XX
DE Human CCR5.
XX
KW Human Cys-Cys chemokine receptor 5; CCR5;
KW human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2;
KW diagnosis; treatment; prevention;
KW inflammatory disease; rheumatoid arthritis; glomerulonephritis;
KW asthma; idiopathic pulmonary fibrosis; psoriasis; viral infection;
KW cancer; atherosclerosis; autoimmune disorder.
XX
OS Homo sapiens.
XX
PN WO9732019-A2.
XX
PD 04-SEP-1997.
XX
PF 28-FEB-1997; 97WO-BE00023.
XX
PR 06-AUG-1996; 96EP-0870102.
PR 01-MAR-1996; 96EP-0870021.
XX
PA (EURO-) EUROSREEN SA.
XX
PI Libert F, Parmentier M, Samson M, Vassart G;
XX
XX WPI; 1997-479829/44.
DR N-PSDB; T90117.
XX
XX Active and inactive forms of human CC chemokine receptor CCR-5 -
PT useful to diagnose, prevent and/or treat inflammatory disorders,
PT autoimmune disease and viral infection
XX
XX Claim 4; Fig 1b-c; 94pp; English.
XX
XX The present sequence is human CC (Cys-Cys) chemokine receptor
CC 5 (CCR5), which is stimulated by MIP-1 alpha, MIP-1 beta or RANTES
CC chemokines, but not by monocyte chemoattractant protein 1 (MCP-1),
CC MCP-3, interleukin-8 (IL-8) or growth related gene product
CC alpha (GRO alpha) chemokines. Active CCR-5 is also a receptor of
CC human immunodeficiency virus type 1 or type 2 (HIV-1 or HIV-2).
CC CCR5 or its cDNA can be used to diagnose, treat and/or prevent

CC inflammatory diseases, e.g. rheumatoid arthritis,
CC glomerulonephritis, asthma, idiopathic pulmonary fibrosis and
CC psoriasis, viral infections, especially HIV-1 or HIV-2 infection,
CC cancer, atherosclerosis and autoimmune disorders.
XX
SQ Sequence 352 AA;

Query Match 78.5%; Score 124; DB 18; Length 352;
Best Local Similarity 65.5%; Pred. No. 1.6e-11;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCCLNPLVLYAFIGOKERNYFL 29
||| | |||:||||:||||:||||:|
Db 281 vtetgmthccinpiiyafvgekfnyll 309

RESULT 5
W27123
ID W27123 standard; Protein; 352 AA.
XX
AC W27123;
XX
DT 14-DEC-1997 (first entry)
XX
DE Human chemokine receptor 88C.
XX

KW Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis;
KW tumour; asthma; viral infection; AIDS; inflammation;
KW autoimmune disease; therapy; diagnosis; leukocyte trafficking;
KW G protein coupled receptor; ligand; modulator; antibody; human.
XX
OS Homo sapiens.
XX

Key	Location/Qualifiers
FT Domain	1..32
FT Domain	/label= Extracellular_domain
FT Domain	56..67
FT Domain	/label= Intracellular_domain
FT Domain	89..112
FT Domain	/label= Extracellular_domain
FT Domain	125..145
FT Domain	/label= Intracellular_domain
FT Domain	166..191
FT Domain	/label= Extracellular_domain
FT Domain	213..235
FT Domain	/label= Intracellular_domain
FT Domain	259..280
FT Domain	/label= Extracellular_domain
FT Domain	301..352
FT Domain	/label= Intracellular_domain

PN WO9722698-A2.
XX
XX 26-JUN-1997.
XX
XX 20-DEC-1996; 96WO-US20759.
XX
XX 07-JUN-1996; 96US-0661393.
XX 20-DEC-1995; 95US-0575967.
XX
XX (ICOS-) ICOS CORP.
XX
XX Gray PW, Raport CJ, Schweickart VL;
XX WPI; 1997-341689/31.
XX N-PSDB; T85161.

XX New nucleic acid encoding chemokine receptors 88-2B and 88C - used
PT to modulate leukocyte trafficking, e.g. for treatment of
PT inflammation, tumours, viral infections, autoimmune diseases, etc.
XX
XX Claim 16; Page 47-48; 65pp; English.
PS

XX This polypeptide sequence comprises novel human chemokine receptor
 CC 88C, a G protein coupled receptor that is involved in leukocyte
 CC trafficking. Its amino sequence was deduced from a cDNA clone
 CC (T85161) isolated from a macrophage library. It shows 62% identity
 CC to CCCKR1. Chemokine receptor 88-2B (see W27124) has also been
 CC identified. 88C and 88-2B receptors and their polypeptide fragments
 CC can be produced in transformed host cells. The receptors, peptides
 CC comprising one or more of the extracellular or intracellular
 CC domains, and anti-receptor antibodies can be used to modulate
 CC receptor activities, particularly ligand and G protein binding, and
 CC are potentially useful in the treatment of
 CC atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
 CC infection, AIDS, inflammatory conditions, pathological immune
 CC response, abnormal haematopoietic processes etc.
 XX
 SQ Sequence 352 AA;

Query Match 78.5%; Score 124; DB 18; Length 352;
 Best Local Similarity 65.5%; Pred. No. 1.6e-11;
 Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCLNPLVYAFIGOKFRNYFL 29
 ||| | |||:||||:||||| |
 Db 281 vtetlgtmthccinpiiyafvgekrnyll 309

RESULT 6
 W27125
 ID W27125 standard; Protein; 352 AA.

AC W27125;
 DT 14-DEC-1997 (first entry)
 XX Macaque chemokine receptor 88C.

XX Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis;
 KW tumour; asthma; viral infection; AIDS; inflammation;
 KW autoimmune disease; therapy; diagnosis; leukocyte trafficking;
 KW G protein coupled receptor; ligand; modulator; antibody.
 XX

OS Macaca sp.

XX W09722698-A2.

PD 26-JUN-1997.

XX 20-DEC-1996; 96WO-US20759.

XX 07-JUN-1996; 96US-0661393.

PR 20-DEC-1995; 95US-0575967.

XX (ICOS-) ICOS CORP.

PA Gray PW, Raport CJ, Schweickart VL;

PI WPI: 1997-341689/31.

DR N-PSDB; T85163.

XX New nucleic acid encoding chemokine receptors 88-2B and 88C - used
 PT to modulate leukocyte trafficking, e.g. for treatment of
 PT inflammation, tumours, viral infections, autoimmune diseases, etc.

XX Claim 36; Page 57-58; 65pp; English.

XX This polypeptide sequence comprises macaque chemokine receptor 88C,
 CC a G protein coupled receptor that is involved in leukocyte
 CC trafficking. Its amino sequence was deduced from a 88C DNA
 CC (T85163) isolated by PCR amplification. It shows 97% identity to
 CC human 88C (W27123). 88C receptors and their polypeptide fragments
 CC can be produced in transformed host cells. The receptors, peptides

CC comprising one or more of the extracellular or intracellular
 CC domains, and anti-receptor antibodies can be used to modulate
 CC receptor activities, particularly ligand and G protein binding, and
 CC are potentially useful in the treatment of
 CC atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
 CC infection, AIDS, inflammatory conditions, pathological immune
 CC response, abnormal haematopoietic processes etc. A hybridoma
 CC that produces an antibody that specifically binds to macaque 88C is
 CC claimed.
 XX
 SQ Sequence 352 AA;

Query Match 78.5%; Score 124; DB 18; Length 352;
 Best Local Similarity 65.5%; Pred. No. 1.6e-11;
 Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCLNPLVYAFIGOKFRNYFL 29
 ||| | |||:||||:||||| |
 Db 281 vtetlgtmthccinpiiyafvgekrnyll 309

RESULT 7
 W07602
 ID W07602 standard; Protein; 352 AA.

XX W07602;

XX 26-FEB-1997 (first entry)

XX Human G-protein chemokine receptor HDGNR10.

XX G-protein chemokine receptor; HDGNR10; signal transduction;
 KW haematopoiesis; leukaemia; inflammation; rheumatoid arthritis;
 KW diagnosis; therapy.

XX Homo sapiens.

XX W09639437-A1.

XX 12-DEC-1996.

XX 06-JUN-1995; 95WO-US07173.

XX 06-JUN-1995; 95WO-US07173.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Li Y, Ruben SM;

XX WPI: 1997-043072/04.

DR N-PSDB; T44042.

XX Human G-protein chemokine receptor, HDGNR10 - useful to identify
 PT (ant)agonists, for treatment of haematopoiesis, leukaemia, chronic
 PT and acute inflammation, rheumatoid arthritis, etc.

XX Claim 1; Page 44-46; 61pp; English.

XX Novel human mature G-protein chemokine receptor HDGNR10 (W07602)
 CC is a 7-transmembrane protein involved in signal transduction. Its
 CC amino acid sequence was deduced from a cDNA clone (T44042) isolated
 CC from a human monocyte library. Isolation of the cDNA allows
 CC prodn. of recombinant HDGNR10 in host, e.g. E. coli, COS or Sf9,
 CC cells. The recombinant receptor can be used to identify agonists
 CC or antagonists of the receptor; such cpds. can be used to treat
 CC conditions related to the under- and over-expression of G-protein
 CC chemokine receptors.

XX Sequence 352 AA;

Query Match 78.5%; Score 124; DB 18; Length 352;

Best Local Similarity 65.5%; Pred. No. 1.6e-11;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFHLHCLNPVLYAFIGQKFRNRYFL 29
||| | |||:||||:||||:|||| |
Db 281 vtetlgmthccinpiiyafvgekfnyll 309

RESULT 8

W23835
ID W23835 standard; Protein; 352 AA.

XX W23835;

XX 08-JUN-1998 (first entry)

XX Human CC chemokine receptor 5 (CCR5).

XX CC chemokine receptor 5; CCR5; G-protein coupled receptor;
KW human immunodeficiency virus; HIV; CD4; AIDS; therapy;
KW transgenic animal.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Domain 29..55

XX /label= I

XX /note= "transmembrane domain"

XX Region 109..120

XX /note= "extracellular loop-1 (Claim 19)"

XX Domain 104..126

XX /label= III

XX /note= "transmembrane domain"

XX Domain 143..171

XX /label= IV

XX /note= "transmembrane domain"

XX Region 187..210

XX /note= "extracellular loop-2 (Claim 19)"

XX Domain 194..219

XX /label= V

XX /note= "transmembrane domain"

XX Domain 238..258

XX /label= VI

XX /note= "transmembrane domain"

XX Region 261..276

XX /note= "extracellular loop-3 (Claim 19)"

XX Domain 277..300

XX /label= VII

XX /note= "transmembrane domain"

XX W09745543-A2.

XX 04-DEC-1997.

XX 28-MAY-1997; 97WO-US09586.

XX 28-MAY-1996; 96US-0018508.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Alkhatib G, Berger EA, Broder CC, Combadiere C;

XX Feng Y, Kennedy PE, Murphy PM;

XX WPI; 1998-032650/03.

XX N-PSDB; T76920.

XX CC chemokine receptor 5 polypeptide - used to inhibit membrane
XX fusion between HIV and a target cell

XX Claim 68; Fig 1C; 70pp; English.

XX This protein sequence comprises of a novel human macrophage-selective
XX CC chemokine receptor that has been designated CCR5. The sequence

CC was deduced from an isolated cDNA clone (see T76920). An Ala127Ieu
CC variant (see W238340 of CCR5 was also identified. The susceptibility
CC of human macrophages to HIV infection depends on cell surface
CC expression of CD4 and CCR5. CCR5 is a member of the 7-transmembrane
CC superfamily of G-protein coupled cell surface molecules. It plays
CC an essential role in the membrane fusion step of infection by some
CC HIV isolates. The establishment of stable, non-human cell lines
CC and transgenic mammals having cells that coexpress human CD4 and
CC CCR5 provides valuable tools for research of HIV infection.
CC Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding
CC agents capable of blocking membrane fusion between HIV and target
CC cells represent potential anti-HIV therapeutics for macrophage
XX tropic strains of HIV.

SQ Sequence 352 AA;

Query Match 78.5%; Score 124; DB 19; Length 352;

Best Local Similarity 65.5%; Pred. No. 1.6e-11;

Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFHLHCLNPVLYAFIGQKFRNRYFL 29
||| | |||:||||:||||:|||| |
Db 281 vtetlgmthccinpiiyafvgekfnyll 309

RESULT 9

W88232

ID W88232 standard; Protein; 352 AA.

XX W88232;

XX 15-MAR-1999 (first entry)

XX HIV-1 co-receptor CCR5.

XX HIV-1; CCR5; CCR5m303; co-receptor; infection; diagnosis; AIDS;

XX gene therapy; human.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Domain 32..56

XX /note= "transmembrane domain 1"

XX Domain 67..87

XX /note= "transmembrane domain 2"

XX Misc-difference 101

XX /note= "corresponds to TGT (CYS) in wild-type CCR5,

XX TGA (Stop) in Ccr5m303"

XX Domain 103..124

XX /note= "transmembrane domain 3"

XX Domain 142..167

XX /note= "transmembrane domain 4"

XX Domain 200..223

XX /note= "transmembrane domain 5"

XX Domain 236..260

XX /note= "transmembrane domain 6"

XX Domain 275..301

XX /note= "transmembrane domain 7"

XX W09854317-A1.

XX 03-DEC-1998.

XX 29-MAY-1998; 98WO-EP03437.

XX 30-MAY-1997; 97US-0048057.

XX (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.

XX Arenzana Siesdedos F, Beretta A, Braun J, Quillent C;

XX WPI; 1999-059835/05.

DR

DR N-PSDB; V84126.
XX New CCR5 variant protein of the HIV-1 co-receptor - useful in
PT developing resistance of CCR5-expressing cells to HIV-1 infection
XX
XX
XX
PS Disclosure; Page 34-35; 55pp; English.
XX
XX This is the amino acid sequence of wild-type human CCR5, which
CC serves as a co-receptor for infection by macrophage-tropic
CC (M-tropic) strains of HIV-1. The invention relates to the
CC identification of a CCR5 variant (see W88231), designated CCR5m303,
CC comprising the first two transmembrane domains of wild-type CCR5,
CC but lacking transmembrane domains 3-7. The presence of the
CC CCR5m303 variant with the wild type CCR5 allele shows a positive
CC correlation with resistance to infection with M-tropic HIV-1
CC strains, and may indicate slower progression of the disease. The
CC detection of CCR5 variants may be used to identify individuals at
CC lower risk of infection relative to the general population who, if
CC infected, may exhibit slower progression to AIDS. Probes and
CC primers (see V84127-36) are provided for use in diagnostic methods
CC for detecting the presence of such variants. A method is provided
CC for inhibiting HIV-1 infection of a cell expressing the CCR5
CC receptor. This involves introducing a nucleic acid encoding a CCR5
CC variant into the cell, thereby reducing the number of functional
CC CCR5 molecules present on the cell surface.
XX
XX
SQ Sequence 352 AA;

Query Match 78.5%; Score 124; DB 20; Length 352;
Best Local Similarity 65.5%; Pred. No. 1.6e-11;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCLNPVLYAFIGQKFRNYFL 29
||| | |||:||||:||||| |
Db 281 vtetlgtmthccinpiiyafvgekfnyll 309

RESULT 10
Y80128
ID Y80128 standard; Protein; 352 AA.
XX
XX AC Y80128;
XX
XX DT 19-MAY-2000 (first entry)
XX
XX DE Human G-protein chemokine receptor HDGNR10 SEQ ID NO:2.

XX Human; G-protein coupled receptor; G-protein chemokine receptor;
KW HDGNR10; diagnosis; haematopoiesis; wound healing; coagulation;
KW angiogenesis; tumour; infection; leukaemia; psoriasis; allergy;
KW T-cell mediated autoimmune disease; atherogenesis; anaphylaxis;
KW inflammation; allergic reaction; silicosis; sarcoidosis;
KW rheumatoid arthritis; hyper-eosinophilia syndrome.
XX
XX OS Homo sapiens.

XX US6025154-A.
XX
XX FN 15-FEB-2000.
XX
XX PD 06-JUN-1995; 95US-0466343.
XX
XX PF 06-JUN-1995; 95US-0466343.
XX
XX PR (HUMA-) HUMAN GENOME SCI INC.
XX
XX PA Li Y, Ruben SM;
XX
XX PI WPI; 2000-181807/16.
XX
XX DR N-PSDB; 291481.
XX
XX PT Isolated nucleic acid encoding human G-protein chemokine receptor

PT useful for diagnostic assays, scientific research and screening for
PT compounds which bind to and activate or inhibit activation of the
PT receptor polypeptides -
XX
XX Claim 1; Fig 1; 22pp; English.
XX
XX The present sequence represents a human G-protein chemokine receptor
CC designated HDGNR10. HDGNR10 polynucleotides are useful in methods of
CC screening for compounds which bind to and either: (1) activate the
CC HDGNR10 polypeptides causing stimulation of haematopoiesis, wound
CC healing, coagulation, and angiogenesis; treatment of solid tumours,
CC chronic infections, leukaemia, T-cell mediated autoimmune diseases,
CC parasitic infections, psoriasis, and to stimulate growth factor
CC activity; or (2) inhibit activation of the HDGNR10 polypeptides which
CC is useful for preventing and/or treating allergy, atherogenesis,
CC anaphylaxis, malignancy, chronic and acute inflammation, histamine and
CC immunoglobulin E-mediated allergic reactions, prostaglandin-independent
CC fever, bone marrow failure, silicosis, sarcoidosis, rheumatoid
CC arthritis shock and hyper-eosinophilia syndrome. The polynucleotides
CC are also useful for diagnostic assays for detecting diseases related to
CC mutations in the nucleic acid sequences encoding the polypeptides and
CC for detecting an altered level of the soluble form of the receptor
CC polypeptides. The polynucleotides are also useful for in vitro purposes
CC related to scientific research, synthesis of DNA and manufacture of
CC DNA vectors.
XX
XX
SQ Sequence 352 AA;

Query Match 78.5%; Score 124; DB 21; Length 352;
Best Local Similarity 65.5%; Pred. No. 1.6e-11;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCLNPVLYAFIGQKFRNYFL 29
||| | |||:||||:||||| |
Db 281 vtetlgtmthccinpiiyafvgekfnyll 309

RESULT 11
W23834
ID W23834 standard; Protein; 371 AA.
XX
XX AC W23834;
XX
XX DT 08-JUN-1998 (first entry)
XX
XX DE Human CC chemokine receptor 5 (CCR5) A127V variant.
XX
XX KW CC chemokine receptor 5; CCR5; G-protein coupled receptor;
KW human immunodeficiency virus; HIV; CD4; AIDS; therapy;
KW transgenic animal.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
FT Domain 48..74
FT /label= I
FT /note= "transmembrane domain"
FT Domain 123..145
FT /label= III
FT /note= "transmembrane domain"
FT Domain 162..190
FT /label= IV
FT /note= "transmembrane domain"
FT Domain 213..238
FT /label= V
FT /note= "transmembrane domain"
FT Domain 257..277
FT /label= VI
FT /note= "transmembrane domain"
FT Domain 296..319
FT /label= VII
FT /note= "transmembrane domain"

XX PN W09745543-A2.
 XX XX
 XX PD 04-DEC-1997.
 XX XX
 XX PF 28-MAY-1997; 97WO-US09586.
 XX XX
 XX PR 28-MAY-1996; 96US-0018508.
 XX XX
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX XX
 XX PI Alkhatib G, Berger EA, Broder CC, Combadiere C;
 XX PI Feng Y, Kennedy PE, Murphy PM;
 XX XX
 XX DR WPI; 1998-032650/03.
 XX DR N-PSDB; T76919.
 XX XX
 XX CC chemokine receptor 5 polypeptide - used to inhibit membrane
 XX PT fusion between HIV and a target cell
 XX XX
 XX PS Example 1; Fig 1B; 70pp; English.
 XX XX
 XX CC This protein sequence comprises an Alal27Leu variant of a novel
 XX CC human macrophage-selective CC chemokine receptor (see also
 XX CC W23835) that has been designated CCR5. The sequence was deduced
 XX CC from an isolated cDNA clone (see T76919). The conservative
 XX CC variation should not affect the activity of CCR5. The susceptibility
 XX CC of human macrophages to HIV infection depends on cell surface
 XX CC expression of CD4 and CCR5. CCR5 is a member of the 7-transmembrane
 XX CC superfamily of G-protein coupled cell surface molecules. It plays
 XX CC an essential role in the membrane fusion step of infection by some
 XX CC HIV isolates. The establishment of stable, non-human cell lines
 XX CC and transgenic mammals having cells that coexpress human CD4 and
 XX CC CCR5 provides valuable tools for research of HIV infection.
 XX CC Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding
 XX CC agents capable of blocking membrane fusion between HIV and target
 XX CC cells represent potential anti-HIV therapeutics for macrophage
 XX CC tropic strains of HIV.
 XX SQ Sequence 371 AA;

Query Match 78.5%; Score 124; DB 19; Length 371;
 Best Local Similarity 65.5%; Pred. No. 1.7e-11;
 Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Oy 1 VTEVLAFLHCLNPVLYAFIGQKFRNYFL 29
 ||| | |||:||||:||||:|
 Db 300 vtetlgtmthccinpiiyafvgekfrnyll 328

RESULT 12
 Y41280
 ID Y41280 standard; Protein; 439 AA.
 XX XX
 XX AC Y41280;
 XX XX
 XX DT 11-FEB-2000 (first entry)
 XX XX
 XX DE Fusion protein containing human chemokine receptor CCR-5.
 XX XX
 XX KW Prostaglandin; PG; E2EP3 receptor; E2EP2 receptor; CCR-5; human;
 XX KW chemokine receptor; ss2 adrenergic receptor; small G-protein rho;
 XX KW renal outer medullary potassium ion channel protein; ion-channel protein;
 XX KW lambda phage repressor protein; G-protein coupled receptor; bacteria;
 XX KW biochemical; vaccine; immunohistochemical; orphan receptor; HIV.
 XX OS Synthetic.
 XX OS Homo sapiens.
 XX XX
 XX PN W09953033-A1.
 XX XX
 XX PD 21-OCT-1999.

XX PF 16-APR-1999; 99WO-US08214.
 XX PR 16-APR-1998; 98US-0081989.
 XX XX
 XX PA (UYVA-) UNIV VANDERBILT.
 XX XX
 XX PI Breyer RM, Ma L, Kennedy C;
 XX XX
 XX XX WPI; 1999-620416/53.
 XX DR N-PSDB; Z24738.
 XX XX
 XX PT New nucleic acid constructs for high level expression of eukaryotic
 XX PT proteins in bacteria, for producing e.g. chemokine receptor CCR-5 for
 XX PT preventing HIV infection
 XX XX
 XX PS Disclosure; Page 49-53; 8lpp; English.
 XX XX
 XX CC The invention provides isolated nucleic acid sequences that encode rabbit
 XX CC prostaglandin (PG) E2EP3 receptor, human PG E2EP2 receptor, human
 XX CC chemokine receptor CCR-5, human ss2 adrenergic receptor, rat renal outer
 XX CC medullary potassium ion channel protein or human small G-protein rho,
 XX CC together with deduced protein sequences. Also provided is a method for
 XX CC the production of eukaryotic proteins by culturing bacteria transformed
 XX CC with vectors containing the above nucleic acid sequences or a nucleic
 XX CC acid (I) that comprises: (i) first sequence that encodes either a
 XX CC sequence comprising at least three positively charged amino acids, or a
 XX CC DNA-binding protein, or a lambda phage repressor protein, placed upstream
 XX CC of, and in frame with, (ii) a sequence encoding a protein. (I) are used
 XX CC for recombinant production of eukaryotic proteins, particularly membrane
 XX CC proteins, G-protein coupled receptors or ion-channel proteins, in
 XX CC bacteria. These proteins are useful for biochemical or structural
 XX CC studies; as therapeutic agents; in diagnostic and screening assays and as
 XX CC antigens for use in vaccines, and for raising antibodies that are useful
 XX CC as immunohistochemical markers, e.g. for orphan receptors or ion
 XX CC channels. Antibodies raised against the chemokine receptor CCR-5 can be
 XX CC used (when administered as antiserum or generated in vivo) to prevent
 XX CC entry of human immune deficiency virus (HIV) into cells.
 XX SQ Sequence 439 AA;

Query Match 78.5%; Score 124; DB 20; Length 439;
 Best Local Similarity 65.5%; Pred. No. 2e-11;
 Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Oy 1 VTEVLAFLHCLNPVLYAFIGQKFRNYFL 29
 ||| | |||:||||:||||:|
 Db 359 vtetlgtmthccinpiiyafvgekfrnyll 387

RESULT 13
 R53932
 ID R53932 standard; Protein; 354 AA.
 XX XX
 XX AC R53932;
 XX XX
 XX DT 23-FEB-1995 (first entry)
 XX XX
 XX DE Interleukin 8 (IL-8) receptor.
 XX XX
 XX KW Interleukin; receptor; antiinflammatory; psoriasis; reperfusion;
 XX KW rheumatoid arthritis; allograft; graft rejection.
 XX XX
 XX OS Homo sapiens.
 XX XX
 XX PN JP06100595-A.
 XX XX
 XX PD 12-APR-1994.
 XX XX
 XX PF 27-MAY-1991; 91JP-0149245.
 XX XX
 XX PR 27-MAY-1991; 91JP-0149245.

XX (UYBO-) UNIV BOSTON.
 XX WPI; 1994-156656/19.
 DR N-PSDB; 063919.
 XX Recombinant interleukin-8 receptor polypeptide - having
 PT antiinflammatory properties
 XX Claim 1; Figure 1; 13pp; Japanese.
 XX Anti-inflammatory agents containing the interleukin-8 receptor
 CC polypeptide can be used for the treatment of psoriasis, rheumatoid
 CC arthritis and other acute and chronic inflammatory diseases,
 CC including reperfusion and allograft rejection.
 XX Sequence 354 AA;

Query Match 76.6%; Score 121; DB 15; Length 354;
 Best Local Similarity 75.0%; Pred. No. 4.7e-11;
 Matches 21; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 TEVLAFHCCINPVLVAFIGOKERNYFL 29
 ||:| ||| ||||:||||| ||| ||
 Db 294 teilgfhscnlpilayafignfrngfl 321

RESULT 14
 R28272
 ID R28272 standard; Protein; 355 AA.
 XX R28272;
 XX 04-APR-1993 (first entry)
 DT Sequence in a high affinity recombinant rabbit interleukin-8
 DE (IL-8) receptor polypeptide in F3R.
 DE

XX IL-8 receptor polypeptide; G-protein-coupled receptor.

XX Oryctolagus cuniculus.
 XX W09218641-A.
 PN 29-OCT-1992.
 XX 10-APR-1992; 92WO-US02977.
 XX 10-APR-1991; 91US-0685101.
 PR 09-JUL-1991; 91US-0726606.
 PR 09-DEC-1991; 91US-0803842.

XX (REPK) REPLIGEN CORP..
 PA (UYBO-) UNIV BOSTON.
 XX Navarro J, Thomas KM, Witt DP;
 PI WPI; 1992-382123/46.
 DR N-PSDB; Q30011.

XX Recombinant mammalian interleukin-8 receptor - used for screening
 PT interleukin-8 binding antagonists, used to treat inflammation
 XX Claim 2; Fig 1; 71pp; English.

XX Rabbit high affinity IL-8 receptor gene was isolated from rabbit
 CC peritoneal neutrophils and used as a source of poly(A)+ RNA, to
 CC produce a rabbit neutrophil cDNA library. 250,000 recombinant
 CC plaques were screened for those which hybridized to an antisense
 CC oligonucleotide (Q30015). This probe was designed based on the
 CC sequence derived from the second transmembrane domain of G-protein-
 CC coupled receptors. After tertiary screening, six plaques were

CC isolated. The insert of one of these plaques, termed F3R was of 2.5
 CC kb in size. This insert was sequenced. The protein deduced from
 CC the F3R clone demonstrates that it belongs to the family of
 CC G-protein-coupled receptors. The deduced protein sequence
 CC indicates seven putative transmembrane segments.

XX Sequence 355 AA;

Query Match 76.6%; Score 121; DB 13; Length 355;
 Best Local Similarity 75.0%; Pred. No. 4.7e-11;
 Matches 21; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 2 TEVLAFHCCINPVLVAFIGOKERNYFL 29
 ||:| ||| ||||:||||| ||| ||
 Db 295 teilgfhscnlpilayafignfrngfl 322

RESULT 15
 R80950
 ID R80950 standard; Protein; 355 AA.
 XX R80950;
 XX 24-APR-1996 (first entry)
 DT Recombinant high affinity interleukin-8 receptor subtype A.
 DE
 XX IL-8A; IL-8B; receptor; monoclonal antibody; inflammatory disorder;
 KW anaphylaxis; systemic lupus erythematosus; rheumatoid arthritis;
 KW systemic necrotising vasculitis; psoriasis; asthma; allergy; ARDS;
 KW adult respiratory distress syndrome; neutrophil detection.

XX Oryctolagus cuniculus.

XX W09525126-A1.
 PN 21-SEP-1995.
 PD 09-MAR-1995; 95WO-US03032.
 PF 02-MAY-1994; 94US-0237937.
 PR 15-MAR-1994; 94US-0210250.

XX (REPK) REPLIGEN CORP..
 PA (UYBO-) UNIV BOSTON.

XX Greenfield EA, Larosa GJ, Navarro J, Thomas KM;
 PI Witt DT;

XX WPI; 1995-336945/43.
 DR N-PSDB; Q99949.

XX Monoclonal antibody against recombinant IL-8 receptor polypeptide -
 PT useful for treating inflammatory disorders, for detecting
 PT neutrophil(s) and for isolating IL-8 receptor from liq.mixt.

XX Claim 2; Fig 1A-B; 74pp; English.

XX Monoclonal antibodies were raised against recombinant interleukin-8
 CC (IL-8) receptor subtypes A and B from both human and rabbit sources
 CC (R80950-53 encoded by Q99949-52). The A subtype receptor (IL-8RA) is
 CC a high affinity receptor and the B subtype receptor (IL-8RB) is a
 CC low affinity receptor. The monoclonal antibody (mAb) pref. binds to
 CC the IL-8 binding domain thus blocking its activation. The mAbs are
 CC useful for treating inflammatory disorders (see key words) and for
 CC detecting the presence of neutrophils in a biological sample. The
 CC mAbs are also useful in the isolation of IL-8 receptors from a mixture.

XX Sequence 355 AA;

Query Match 76.6%; Score 121; DB 16; Length 355;

Best Local Similarity 75.0%; Pred. No. 4.7e-11;
Matches 21; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 2 TEVLAFHCCLNPNVLYAFIGQKERNYFL 29
||: ||| ||||: |||| ||| ||
Db 295 tellgflhsclnpliyafignfngfl 322

Search completed: May 23, 2001, 15:28:33
Job time: 410 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:30:08 ; Search time 95.91 Seconds
(without alignments)
5.809 Million cell updates/sec

Title: US-08-887-977-10_COPY_291_319

Perfect score: 158

Sequence: 1 VTEVLAFLHCLNPLVYAFIGQKERNYFL 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

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- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
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- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	124	78.5	352	3	US-08-466-343D-2
2	124	78.5	352	4	US-09-087-232A-13
3	121	76.6	354	1	US-07-759-568-2
4	121	76.6	360	4	US-08-875-573-20
5	120	75.9	355	1	US-08-012-988A-2
6	120	75.9	355	1	US-08-450-393A-5
7	120	75.9	355	4	US-08-446-669-5
8	120	75.9	355	5	PCT-US95-00476-5
9	116	73.4	350	1	US-08-202-056-1
10	116	73.4	350	1	US-08-076-093A-2
11	116	73.4	350	1	US-08-450-393A-7
12	116	73.4	350	1	US-08-410-453A-1
13	116	73.4	350	1	US-08-701-265-2
14	116	73.4	350	1	US-08-410-454A-1
15	116	73.4	350	2	US-08-284-586-2
16	116	73.4	350	2	US-08-410-456A-1
17	116	73.4	350	2	US-08-805-478-2
18	116	73.4	350	2	US-08-802-627A-2
19	116	73.4	350	2	US-08-801-238-2
20	116	73.4	350	2	US-08-801-228-2
21	116	73.4	350	3	US-09-104-296-2
22	116	73.4	350	4	US-08-446-669-7
23	116	73.4	350	5	PCT-US95-00476-7
24	116	73.4	355	1	US-08-153-848-28
25	116	73.4	355	1	US-08-153-848-32
26	116	73.4	355	3	US-09-299-843A-28
27	116	73.4	355	3	US-09-299-843A-32

28	116	73.4	355	5	PCT-US93-11153-28	Sequence 28, Appl
29	116	73.4	355	5	PCT-US93-11153-32	Sequence 32, Appl
30	114	72.2	337	1	US-08-153-848-46	Sequence 46, Appl
31	114	72.2	337	3	US-09-299-843A-46	Sequence 46, Appl
32	114	72.2	337	5	PCT-US93-11153-46	Sequence 46, Appl
33	114	72.2	347	1	US-08-461-244-3	Sequence 3, Appl
34	114	72.2	352	1	US-08-202-056-3	Sequence 3, Appl
35	114	72.2	352	1	US-08-076-093A-4	Sequence 4, Appl
36	114	72.2	352	1	US-08-450-393A-6	Sequence 6, Appl
37	114	72.2	352	1	US-08-701-265-4	Sequence 4, Appl
38	114	72.2	352	2	US-08-284-586-4	Sequence 4, Appl
39	114	72.2	352	2	US-08-805-478-4	Sequence 4, Appl
40	114	72.2	352	2	US-08-802-627A-4	Sequence 4, Appl
41	114	72.2	352	2	US-08-801-238-4	Sequence 4, Appl
42	114	72.2	352	2	US-08-801-228-4	Sequence 4, Appl
43	114	72.2	352	3	US-09-104-296-4	Sequence 4, Appl
44	114	72.2	352	4	US-08-446-669-6	Sequence 6, Appl
45	114	72.2	352	5	PCT-US95-00476-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-466-343D-2
; Sequence 2, Application US/08466343D
; Patent No. 6025154
; GENERAL INFORMATION:
; APPLICANT: LI, YI
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN
; TITLE OF INVENTION: CHEMOKINE RECEPTOR HDGNR10 (AS AMENDED)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,343D
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-466-343D-2

Query Match 78.5%; Score 124; DB 3; Length 352;
Best Local Similarity 65.5%; Pred. No. 2.4e-09;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 1 VTEVLAFLHCLNPLVYAFIGQKERNYFL 29
||| | |||:||||:|||||
Db 281 VTETLGLTHCCINPIIYAFVGEKERNYLL 309

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/759,568
; FILING DATE: 19910913
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Scott, Watson T.
; REGISTRATION NUMBER: 26581
; REFERENCE/DOCKET NUMBER: WTS/5683/91535/WBH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 cush
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 354 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-759-568-2

Query Match 76.6%; Score 121; DB 1; Length 354;
Best Local Similarity 75.0%; Pred. No. 5.9e-09;
Matches 21; Conservative 3; Mismatches 4; Indels 0;

QY 2 TEVLAFHLCCLPVLYAFVIGQKERNYFL 29
   ||| ||| ||| ||| ||| ||| ||| |||
DB 294 TEILGFHSLCLNPIIYAFVIGQFRNGFL 321

RESULT 4
US-08-875-573-20
; Sequence 20, Application US/08875573
; Patent No. 6150132
; GENERAL INFORMATION:
; APPLICANT: Wells, Timothy N.C.
; APPLICANT: Power, Christine A.
; TITLE OF INVENTION: A-CHEMOKINE RECEPTOR ABLE TO BIND TO
; TITLE OF INVENTION: MCP-1, MIP-1 ALPHA AND/OR RANTES. ITS USES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 No. 6150132th Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,573
; FILING DATE: 31-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/00143
; FILING DATE: 24-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9501683.8
; FILING DATE: 27-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mary J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1430-172
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:

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;
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-573-20

Query Match 76.6%; Score 121; DB 4; Length 360;
Best Local Similarity 67.9%; Pred. No. 6e-09;
Matches 19; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 TEVLAFHCLNPNVLYAFIGQKFRNYL 29
|||:|||||:|:|:|
Db 289 TETLAFVHCCLNPIIYFGLGKFRKYL 316

RESULT 5
US-08-012-988A-2
; Sequence 2, Application US/08012988A
; Patent No. 5652133
; GENERAL INFORMATION:
; APPLICANT: Murphy, Philip M.
; TITLE OF INVENTION: Cloning and Expression of Human
; TITLE OF INVENTION: Macrophage Inflammatory Protein-1 alpha (MIP-1
; TITLE OF INVENTION: alpha)/RANTES Receptor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/012,988A
; FILING DATE: 19930128
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 15280-118
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-012-988A-2

Query Match 75.9%; Score 120; DB 1; Length 355;
Best Local Similarity 66.7%; Pred. No. 8.1e-09;
Matches 18; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 VTEVLAFHCLNPNVLYAFIGQKFRNY 27
||||:||||:|:|:|
Db 285 VTEVIATHCCLNPNVLYAFVGERFRKY 311

RESULT 6
US-08-450-393A-5
; Sequence 5, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel

;
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cseri, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816COOLEYPA
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-450-393A-5

Query Match 75.9%; Score 120; DB 1; Length 355;
Best Local Similarity 66.7%; Pred. No. 8.1e-09;
Matches 18; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 VTEVLAFHCLNPNVLYAFIGQKFRNY 27
||||:||||:|:|:|
Db 285 VTEVIATHCCLNPNVLYAFVGERFRKY 311

RESULT 7
US-08-446-669-5
; Sequence 5, Application US/08446669
; Patent No. 6132987
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,669
; FILING DATE: May 25, 1995

;
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,669
; FILING DATE: May 25, 1995

Query Match 75.9%; Score 120; DB 1; Length 355;
Best Local Similarity 66.7%; Pred. No. 8.1e-09;
Matches 18; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 VTEVLAFHCLNPNVLYAFIGQKFRNY 27
||||:||||:|:|:|
Db 285 VTEVIATHCCLNPNVLYAFVGERFRKY 311

RESULT 6
US-08-450-393A-5
; Sequence 5, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel

```
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Neeley, Richard
;; REGISTRATION NUMBER: 30,092
;; REFERENCE/DOCKET NUMBER: UCAL-237/0105
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-843-5000
;; TELEFAX: 415-857-0663
;; TELEX: 380816COOLEYPA
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 355 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
US-08-446-669-5

Query Match 75.9%; Score 120; DB 4; Length 355;
Best Local Similarity 66.7%; Pred. No. 8.1e-09;
Matches 18; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCCCLNPVLYAFVIGQKFRNY 27
Db 285 VTEVIATHTCCVNPVIYAFVIGFRKY 311

RESULT 8
PCT-US95-00476-5
; Sequence 5, Application PC/TUS9500476
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 N. Figueroa Street, 5th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012-2628
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berliner, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-977-1001
; TELEFAX: 310-977-1003
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
PCT-US95-00476-5

Query Match 75.9%; Score 120; DB 5; Length 355;
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Best Local Similarity 66.7%; Pred. No. 8.1e-09;
Matches 18; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCCCLNPVLYAFVIGQKFRNY 27
Db 285 VTEVIATHTCCVNPVIYAFVIGFRKY 311

RESULT 9
US-08-202-056-1
; Sequence 1, Application US/08202056
; Patent No. 5440021
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Hebert, Caroline
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Lee, James
; TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,056
; FILING DATE: 25-FEB-1994
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/677211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 706P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-202-056-1

Query Match 73.4%; Score 116; DB 1; Length 350;
Best Local Similarity 71.4%; Pred. No. 2.7e-08;
Matches 20; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 TEVLAFLHCCCLNPVLYAFVIGQKFRNYEL 29
Db 290 TEILGLHCLNPVIYAFVIGQFRHGFL 317

RESULT 10
US-08-076-093A-2
; Sequence 2, Application US/08076093A
; Patent No. 5543503
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: Jin Kim, K.
; TITLE OF INVENTION: Antibodies to Human PF4A Receptors
```

NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/076.093A
FILING DATE: 11-Jun-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/952-9881
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-076-093A-2

Query Match 73.4%; Score 116; DB 1; Length 350;
Best Local Similarity 71.4%; Pred. No. 2.7e-08;
Matches 20; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 TEVLAFLHCLNPLVYAFIGOKERNYFL 29
Db 290 TEILGFLHCLNPLIYAFIGNFRHGFL 317

RESULT 11
US-08-450-393A-7
Sequence 7, Application US/08450393A
Patent No. 5707815
GENERAL INFORMATION:
APPLICANT: Charo, Israel
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450.393A
FILING DATE: May 25, 1995

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: UCAL-237/02US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5165
TELEFAX: 415-8857-0663
TELEX: 380816CooleyPA
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-450-393A-7

Query Match 73.4%; Score 116; DB 1; Length 350;
Best Local Similarity 71.4%; Pred. No. 2.7e-08;
Matches 20; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 TEVLAFLHCLNPLVYAFIGOKERNYFL 29
Db 290 TEILGFLHCLNPLIYAFIGNFRHGFL 317

RESULT 12
US-08-410-453A-1
Sequence 1, Application US/08410453A
Patent No. 5767063
GENERAL INFORMATION:
APPLICANT: Lee, James,
APPLICANT: Holmes, William E.,
APPLICANT: Woods, William I.,
TITLE OF INVENTION: Human PF4A Receptors and Their Use
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410.453A
FILING DATE: 24-Mar-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/234494
FILING DATE: 28-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0706C1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-08-410-453A-1

Query Match 73.4%; Score 116; DB 1; Length 350;
Best Local Similarity 71.4%; Pred. No. 2.7e-08;
Matches 20; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 TEVLAFLHCLNPNVLYAFIGQKFRNYFL 29
||:| ||| ||||:||||| ||: ||
Db 290 TEILGFLHCLNPIIYAFIQNFRHGFL 317

RESULT 13

US-08-701-265-2

; Sequence 2, Application US/08701265
; Patent No. 5776457

; GENERAL INFORMATION:

; APPLICANT: Chuntharapai, Anan

; APPLICANT: Lee, James

; APPLICANT: Hebert, Caroline

; APPLICANT: Jin Kim, K.

; TITLE OF INVENTION: Antibodies to Human PF4A Receptors

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/701,265

; FILING DATE: 22-AUG-1996

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/076093

; FILING DATE: 11-Jun-1993

; APPLICATION NUMBER: 07/810782

; FILING DATE: 19-DEC-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/677211

; FILING DATE: 29-MAR-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Love, Richard B.

; REGISTRATION NUMBER: 34,659

; REFERENCE/DOCKET NUMBER: 706P2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-5530

; TELEFAX: 415/952-9881

; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 350 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

US-08-701-265-2

Query Match 73.4%; Score 116; DB 1; Length 350;
Best Local Similarity 71.4%; Pred. No. 2.7e-08;
Matches 20; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 TEVLAFLHCLNPNVLYAFIGQKFRNYFL 29
||:| ||| ||||:||||| ||: ||
Db 290 TEILGFLHCLNPIIYAFIQNFRHGFL 317

RESULT 14

US-08-410-454A-1

; Sequence 1, Application US/08410454A

; Patent No. 5783415

; GENERAL INFORMATION:

; APPLICANT: Lee, James,

; APPLICANT: Holmes, William E.,

; APPLICANT: Woods, William I.

; TITLE OF INVENTION: Human PF4A Receptors and Their Use

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/410,454A

; FILING DATE: 24-Mar-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/234494

; FILING DATE: 28-APR-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/677211

; FILING DATE: 29-MAR-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Love, Richard B.

; REGISTRATION NUMBER: 34,659

; REFERENCE/DOCKET NUMBER: P0706C1D3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-5530

; TELEFAX: 415/952-9881

; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 350 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

US-08-410-454A-1

Query Match 73.4%; Score 116; DB 1; Length 350;

Best Local Similarity 71.4%; Pred. No. 2.7e-08;

Matches 20; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 TEVLAFLHCLNPNVLYAFIGQKFRNYFL 29

||:| ||| ||||:||||| ||: ||

Db 290 TEILGFLHCLNPIIYAFIQNFRHGFL 317

RESULT 15

US-08-284-586-2

; Sequence 2, Application US/08284586

; Patent No. 5840856

; GENERAL INFORMATION:

; APPLICANT: Chuntharapai, Anan

; APPLICANT: Lee, James

; APPLICANT: Hebert, Caroline

; APPLICANT: Jin Kim, K.

; TITLE OF INVENTION: Antibodies to Human PF4A Receptors

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,586
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/076,093A
FILING DATE: 11-Jun-1993
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P2
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
LENGTH: 350 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-284-586-2

Query Match 73.4%; Score 116; DB 2; Length 350;
Best Local Similarity 71.4%; Pred. No. 2.7e-08;
Matches 20; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 2 TEVLAFHCLNPVLYAFICQKERNYFL 29
||:| ||| ||||:||||| ||: ||
Db 290 TEILGELHCLNPPIYAFICQNERHGFL 317

Search completed: May 23, 2001, 15:30:09
Job time: 416 sec

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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:32:03 ; Search time 110.15 Seconds
(without alignments)
18.093 Million cell updates/sec

Title: US-08-887-977-10_COPY_291_319

Perfect score: 158
Sequence: 1 VTEVLAFLHCLNPVLYAFIGQKFRNYFL 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_67:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	158	100.0	369	JC5068	G protein-coupled
2	124	78.5	352	A43113	chemokine (C-C) re
3	121	76.6	354	A23669	interleukin-8 rece
4	121	76.6	355	JQ1231	interleukin-8 rece
5	121	76.6	360	A57160	chemokine (C-C) re
6	120	75.9	355	G02436	chemokine (C-C) re
7	120	75.9	355	A45177	chemokine (C-C) re
8	116	73.4	350	A39445	interleukin-8 rece
9	116	73.4	355	JC4304	orphan G protein-c
10	115	72.8	359	A48921	interleukin-8 rece
11	115	72.8	359	I49341	MIP-1 alpha recept
12	115	72.8	360	JC4587	chemokine (C-C) re
13	114	72.2	352	A45747	neuropeptide Y/pep
14	114	72.2	353	S28787	neuropeptide Y/pep
15	114	72.2	354	I58186	probable G protein
16	114	72.2	355	JC5067	G protein-coupled
17	114	72.2	360	JC2443	chemokine (C-C) re
18	113	71.5	358	A33752	interleukin-8 rece
19	113	71.5	374	I38450	chemokine (C-C) re
20	112	70.9	356	I49340	MIP-1 alpha recept
21	111	70.3	356	S42096	interleukin-8 rece
22	110	69.6	352	G00048	fusin (LESTRA) - c
23	109.5	69.3	323	Q08ED3	HHRF3 protein - hu
24	109	69.0	383	S55594	G protein-coupled
25	107	67.7	354	T09353	G protein-coupled
26	107	67.7	355	I49339	macrophage inflam
27	107	67.7	360	A53611	interleukin-8 rece
28	101	63.9	367	JE0349	interferon-inducib
29	100	63.3	350	JN0621	G protein-coupled

30	97	61.4	333	2	I65989	G protein-coupled
31	94	59.5	378	2	A45680	G protein-coupled
32	94	59.5	378	2	B55735	lymphocyte-specifi
33	92	58.2	359	2	S15403	angiotensin II rec
34	91	57.6	362	2	A39714	G protein-coupled
35	91	57.6	362	2	A30341	G protein-coupled
36	90	57.0	359	2	JC1104	angiotensin II rec
37	90	57.0	359	2	S44425	angiotensin II rec
38	90	57.0	359	2	JC1194	angiotensin II rec
39	90	57.0	359	2	A48857	angiotensin II rec
40	90	57.0	359	2	A42656	angiotensin II rec
41	90	57.0	359	2	JQ1516	angiotensin II rec
42	90	57.0	359	2	JH0621	angiotensin II rec
43	90	57.0	359	2	JC2134	angiotensin II rec
44	89	56.3	350	2	A42009	N-formyl peptide r
45	89	56.3	378	2	A55735	G protein-coupled

ALIGNMENTS

RESULT 1

JC5068
G protein-coupled receptor CKR-L3 - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
C:Accession: JC5068
R:Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
Biochem. Biophys. Res. Commun. 227, 846-853, 1996
A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-lik
A:Reference number: JC5067; MUID:97040707
A:Accession: JC5068
A:Molecule type: DNA
A:Residues: 1-369 <ZAB>
A:Cross-references: EMBL:279784; NID:gl668737; PIDN:CAB02144.1; PID:gl668738
C:Comment: This protein belongs to the family of alpha chemokine receptors.
C:Genetics:
A:Gene: GDB:CMKBR6; SURL22: GPR29; CCR6: CKR-L3; GPR-CY4
A:Cross-references: GDB:5370639; OMIM:601835
A:Map position: 6q27-6q27

C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein
F:42-68/Domain: transmembrane #status predicted <TM1>
F:79-99/Domain: transmembrane #status predicted <TM2>
F:115-136/Domain: transmembrane #status predicted <TM3>
F:160-180/Domain: transmembrane #status predicted <TM4>
F:212-233/Domain: transmembrane #status predicted <TM5>
F:250-271/Domain: transmembrane #status predicted <TM6>
F:292-315/Domain: transmembrane #status predicted <TM7>

Query Match 100.0%; Score 158; DB 2; Length 369;
Best Local Similarity 100.0%; Pred. No. 2.1e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VTEVLAFLHCLNPVLYAFIGQKFRNYFL 29
Db 295 VTEVLAFLHCLNPVLYAFIGQKFRNYFL 323

RESULT 2

A43113
chemokine (C-C) receptor 5 - human
N:Alternate names: C-C CKR-5; CCR5
C:Species: Homo sapiens (man)
C:Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 20-Jun-2000
C:Accession: A43113; S71808; A58834; A58832; G02653; A58833
R:Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.
Biochemistry 35, 3362-3367, 1996
A:Title: Molecular cloning and functional expression of a new human CC-chemokine rece
A:Reference number: A43113; MUID:96241590
A:Accession: A43113
A:Molecule type: mRNA

A:Residues: 1-352 <SAM1>
A:Cross-references: GB:X91492; NID:g1262810; PIDN:CAA62796.1; PID:g1262811
R:Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Saragost
M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Pa
Nature 382, 722-725, 1996
A:Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles of
A:Reference number: S71808; MUID:96345670
A:Accession: S71808
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 182-206; 207-230 <SAM2>
A:Accession: A58834
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-184; 'IKDSHLAGPAAACHGHLILGNPKNSASVSK' <SAM3>
A:Cross-references: GB:X99393; NID:g1524062; PIDN:CAA67767.1; PID:g1524063
A:Note: this frameshift mutation results in a non-functional receptor but confers a degra
nd may have had a selective advantage by conferring resistance to Yersinia plague infect
R:Combadere, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.
J. Leukoc. Biol. 60, 147-152, 1996
A:Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine rec
A:Reference number: A58832; MUID:96295970
A:Accession: A58832
A:Molecule type: mRNA
A:Residues: 1-352 <COM1>
A:Cross-references: GB:U57840; NID:g1502408; PIDN:AAB17071.1; PID:g1502409
A:Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes
R:Combadere, C.
submitted to the EMBL Data Library, May 1996
A:Reference number: H01541
A:Accession: G02653
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-89; 'L' 91-352 <COM2>
A:Cross-references: EMBL:U57840
R:Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
J. Biol. Chem. 271, 17161-17166, 1996
A:Title: Molecular cloning and functional characterization of a novel human CC chemokine
A:Reference number: A58833; MUID:96291862
A:Accession: A58833
A:Molecule type: mRNA
A:Residues: 1-352 <RAP>
A:Cross-references: GB:U54994; NID:g1457945; PIDN:AA050598.1; PID:g1457946
C:Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-1beta (see
C:Comment: Macrophage- and dual-tropic strains of HIV-1 bind to a complex of chemokine
C:Genetics:
A:Gene: GDB:CMKBR5; CCR5; CCR-5; CC-CCR-5; CCR5; ChemR13
A:Cross-references: GDB:1230510; OMIM:601373
A:Map position: 3p21-3p21
C:Function:
A:Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RANTR
A:Note: probably acts to control granulocyte proliferation and differentiation.
C:Superfamily: vertebrate rhodopsin
C:Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembran
F:32-56/Domain: transmembrane #status predicted <TM1>
F:67-87/Domain: transmembrane #status predicted <TM2>
F:103-124/Domain: transmembrane #status predicted <TM3>
F:142-166/Domain: transmembrane #status predicted <TM4>
F:193-218/Domain: transmembrane #status predicted <TM5>
F:236-257/Domain: transmembrane #status predicted <TM6>
F:285-300/Domain: transmembrane #status predicted <TM7>
F:260-269,101-178/Disulfide bonds: #status predicted
F:268/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:336,337,342/Binding site: phosphate (Ser) (covalent) #status predicted
F:340,343/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 78.5%; Score 124; DB 2; Length 352;
Best Local Similarity 65.5%; Pred. No. 1.7e-10;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCLNPVLYAFVGFQKFRNYFL 29
||| | |||:||||:||||| |

Db 281 VTETLGWTHCCINPIIYAFVGFQKFRNYLL 309

RESULT 3

A23669

interleukin-8 receptor, high affinity - rabbit

N:Alternate names: fMLP receptor

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 05-Nov-1999

C:Accession: A23669

R:Thomas, K.M.; Pyun, H.Y.; Navarro, J.

J. Biol. Chem. 265, 20661-20664, 1990

A:Title: Molecular cloning of the fMet-Leu-Phe receptor from neutrophils.

A:Reference number: A23669; MUID:91056034

A:Accession: A23669

A:Molecule type: mRNA

A:Residues: 1-354 <THO>

A:Cross-references: GB:M58021; GB:J05705; NID:g165442; PIDN:AAA31377.1; PID:g165443

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein; neutrophil

Query Match 76.6%; Score 121; DB 2; Length 354;

Best Local Similarity 75.0%; Pred. No. 4.7e-10;

Matches 21; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 TEVLAFLHCLNPVLYAFVGFQKFRNYFL 29

||| | |||:||||:||||| |

Db 294 TEILGFLHCLNPVLYAFVGFQKFRNGFL 321

RESULT 4

JQ1231

interleukin-8 receptor - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Nov-1999

C:Accession: JQ1231; A46483

R:Beckmann, M.P.; Munger, W.E.; Kozlosky, C.; VandenBos, T.; Price, V.; Lyman, S.; Ge

Biochem. Biophys. Res. Commun. 179, 784-789, 1991

A:Title: Molecular characterization of the interleukin-8 receptor.

A:Reference number: JQ1231; MUID:91378994

A:Accession: JQ1231

A:Molecule type: DNA

A:Residues: 1-355 <BEC>

A:Cross-references: GB:M74240; NID:g165438; PIDN:AAA31375.1; PID:g165439

R:Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.

J. Immunol. 148, 1261-1264, 1992

A:Title: Characterization of complementary DNA clones encoding the rabbit IL-8 recept

A:Reference number: A46483; MUID:92148149

A:Accession: A46483

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-355 <LEE>

A:Cross-references: GB:M82873; NID:g165440; PIDN:AAA31376.1; PID:g165441

A:Experimental source: neutrophils

A:Note: sequence extracted from NCBI backbone (NCBI:81526, NCBI:81530)

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 76.6%; Score 121; DB 2; Length 355;

Best Local Similarity 75.0%; Pred. No. 4.7e-10;

Matches 21; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 TEVLAFLHCLNPVLYAFVGFQKFRNYFL 29

||| | |||:||||:||||| |

Db 295 TEILGFLHCLNPVLYAFVGFQKFRNGFL 322

RESULT 5

A57160

chemokine (C-C) receptor 4 - human

N:Alternate names: C-C CKR-4

C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein

RESULT 8

A39445
Interleukin-8 receptor type A - human
N:Alternate names: interleukin-8 receptor, high-affinity
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1993 #sequence_revision 12-Apr-1996 #text_change 05-Nov-1999
C:Accession: I37449; I38710; I38711; A39445
R:Mollereau, C.; Muscatelli, F.; Mattei, M.G.; Vassart, G.; Parmentier, M.
Genomics 16, 248-251, 1993
A:Title: The high-affinity interleukin 8 receptor gene (IL8RA) maps to the 2q33-q36 region
A:Reference number: I37449; MUID:93252387
A:Accession: I37449

A:Molecule type: DNA
A:Residues: 1-350 <RES>
A:Cross-references: EMBL:X65858; NID:g312046; PIDN:CAA46688.1; PID:g312047
R:Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
J. Biol. Chem. 269, 26381-26389, 1994

A:Title: Comparison of the genomic organization and promoter function for human interleukin-8 receptor type A and B
A:Reference number: I37898; MUID:95014476
A:Accession: I38710

A:Molecule type: DNA
A:Residues: 1-350 <RE2>
A:Cross-references: EMBL:U11870; NID:g511804; PIDN:AAA64378.1; PID:g511805

A:Accession: I38711
A:Molecule type: mRNA
A:Residues: 1-16 <RE3>

A:Cross-references: EMBL:U11871; NID:g511806; PIDN:AAA64379.1; PID:g733002
R:Holmes, W.E.; Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.
Science 253, 1278-1280, 1991

A:Title: Structure and functional expression of a human interleukin-8 receptor.
A:Reference number: A39445; MUID:91368199
A:Accession: A39445

A:Molecule type: mRNA
A:Residues: 1-275, 'T', 277-350 <HOL>
A:Cross-references: GB:M68932; NID:g186369; PIDN:AAA59159.1; PID:g186370

C:Genetics:
A:Gene: GDB:IL8RA

A:Cross-references: GDB:135039; OMIM:146929
A:Map position: 2q35-2q35

C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein

Query Match

Best Local Similarity 73.4%; Score 116; DB 2; Length 350;
Matches 20; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 TEVLAFLHCLNPVLYAFIGQKFRNYFL 29
||| ||| |||||:||||| ||| |||

DB 290 TEILGLHCLNPVLYAFIGQKFRNYFL 317

RESULT 9

JC4304
Orphan G protein-coupled receptor - human

N:Alternate names: V28 protein
C:Species: Homo sapiens (man)

C:Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 19-May-2000
C:Accession: JC4304

R:Rapport, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.
Gene 163, 295-299, 1995

A:Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely related to G-protein-coupled receptor V28
A:Reference number: JC4304; MUID:96011651

A:Accession: JC4304
A:Molecule type: mRNA

A:Residues: 1-355 <RAP>
A:Cross-references: GB:U20350; NID:g665580; PIDN:AAA91783.1; PID:g665581

A:Experimental source: peripheral blood mononuclear cell
C:Comment: This protein is a cell-surface receptor which recognizes extracellular signal

C:Genetics:
A:Gene: V28

A:Map position: 3pter-p21

C:Superfamily: G protein-coupled receptor; lymphokine; transmembrane protein
F:35-57/Domain: transmembrane #status predicted <TM1>

F:66-88/Domain: transmembrane #status predicted <TM2>
F:104-125/Domain: transmembrane #status predicted <TM3>

F:146-165/Domain: transmembrane #status predicted <TM4>
F:197-217/Domain: transmembrane #status predicted <TM5>

F:230-254/Domain: transmembrane #status predicted <TM6>
F:275-296/Domain: transmembrane #status predicted <TM7>

Query Match 73.4%; Score 116; DB 2; Length 355;

Best Local Similarity 70.4%; Pred. No. 2.5e-09;

Matches 19; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCLNPVLYAFIGQKFRNY 27
||| ||| |||||:||||| ||| |||

DB 277 VTEVAFSHCLNPVLYAFIGQKFRNY 303

RESULT 10

A48921

N:Alternate names: G-protein coupled receptor Gpcrl6
C:Species: Mus musculus (house mouse)

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999
C:Accession: A48921; A53677; I49348; I59421; H48909; I53774

R:Cerretti, D.P.; Nelson, N.; Kozlosky, C.J.; Morrissey, P.J.; Copeland, N.G.; Gilber
Genomics 18, 410-413, 1993

A:Title: The murine homologue of the human interleukin-8 receptor type B maps near th
A:Reference number: A48921; MUID:94117014

A:Accession: A48921
A:Molecule type: DNA

A:Residues: 1-359 <CER>
A:Cross-references: GB:L12637; NID:g435093; PIDN:AAA39305.1; PID:g435094

R:Suzuki, H.; Prado, G.N.; Wilkinson, N.; Navarro, J.
J. Biol. Chem. 269, 18263-18266, 1994

A:Title: The N terminus of interleukin-8 (IL-8) receptor confers high affinity bindin
A:Reference number: A53677; MUID:94308043

A:Accession: A53677
A>Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: DNA
A:Residues: 1-359 <SUZ>

A:Cross-references: GB:L126549
A:Note: sequence extracted from NCBI backbone (NCBIP:149812)

R:Lee, J.; Cacalano, G.; Camerato, T.; Toy, K.; Moore, M.W.; Wood, W.I.
J. Immunol. 155, 2158-2164, 1995

A:Title: Chemokine binding and activities mediated by the mouse IL-8 receptor.
A:Reference number: I49348; MUID:95363183

A:Accession: I49348
A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-359 <RES>

A:Cross-references: EMBL:U31207; NID:g950174; PIDN:AAAC52239.1; PID:g950175
R:Bozic, C.R.; Gerard, N.P.; von Uexkull-Guldenband, C.; Kolakowski, L.F.

J. Biol. Chem. 269, 29355-29358, 1994
A:Title: The murine interleukin 8 type B receptor homologue and its ligands. Expressi

A:Reference number: I59421; MUID:95050766
A:Accession: I59421

A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:Residues: 1-359 <RE2>
A:Cross-references: GB:L13239; NID:g293665; PIDN:AAA62109.1; PID:g293666

R:Wilkie, T.M.; Chen, Y.; Gilbert, D.J.; Moore, K.J.; Yu, L.; Simon, M.I.; Copeland,
Genomics 18, 175-184, 1993

A:Title: Identification, chromosomal location, and genome organization of mammalian G
A:Reference number: A48909; MUID:94116980

A:Accession: H48909
A>Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA
A:Residues: 145-258 <WIL>

A:Cross-references: GB:L20337; NID:g438800; PIDN:AAA16853.1; PID:g438801

Search completed: May 23, 2001, 15:32:03
Job time: 510 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:36:21 ; Search time 62.39 Seconds
(without alignments)

15.923 Million cell updates/sec

Title: US-08-887-977-10_COPY_291_319

Perfect score: 158

Sequence: 1 VTEVLAFLHCLNPVLYAFIGKFRNYFL 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	158	100.0	374	1	CKR6_HUMAN
2	151	95.6	367	1	CKR6_MOUSE
3	124	78.5	352	1	CKR5_CERA
4	124	78.5	352	1	CKR5_CERTO
5	124	78.5	352	1	CKR5_GORGO
6	124	78.5	352	1	CKR5_HUMAN
7	124	78.5	352	1	CKR5_HYLLE
8	124	78.5	352	1	CKR5_MACMU
9	124	78.5	352	1	CKR5_PANTR
10	124	78.5	352	1	CKR5_PAPHA
11	124	78.5	352	1	CKR5_PONPY
12	124	78.5	352	1	CKR5_PYGHI
13	124	78.5	352	1	CKR5_PYGNE
14	124	78.5	352	1	CKR5_TRAFR
15	124	78.5	352	1	CKR5_TRAPH
16	123	77.8	354	1	CKR5_RAT
17	121	76.6	355	1	IL8A_RABIT
18	121	76.6	360	1	CKR1_HUMAN
19	120	75.9	355	1	CKR1_HUMAN
20	120	75.9	355	1	CKR3_HUMAN
21	119	75.3	355	1	CKR3_CERA
22	118	74.7	353	1	CKR8_MOUSE
23	116	73.4	350	1	IL8A_GORGO
24	116	73.4	350	1	IL8A_HUMAN
25	116	73.4	350	1	IL8A_PANTR
26	116	73.4	355	1	C3X1_HUMAN
27	115	72.8	349	1	CKR4_RAT
28	115	72.8	355	1	CKR3_MACMU
29	115	72.8	359	1	CKR4_MOUSE
30	115	72.8	359	1	CKR3_MOUSE
31	115	72.8	359	1	IL8B_MOUSE
32	115	72.8	359	1	IL8B_RAT
33	115	72.8	360	1	CKR4_MOUSE

34 115 72.8 373 1 CKR2_MOUSE
35 114 72.2 349 1 IL8A_RAT
36 114 72.2 352 1 CCR4_CERTO
37 114 72.2 352 1 CCR4_HUMAN
38 114 72.2 352 1 CCR4_MACMU
39 114 72.2 352 1 CCR4_PAPAN
40 114 72.2 353 1 CCR4_BOVIN
41 114 72.2 353 1 CCR4_FELCA
42 114 72.2 354 1 C3X1_MOUSE
43 114 72.2 354 1 C3X1_RAT
44 114 72.2 354 1 CKR5_MOUSE
45 114 72.2 355 1 CKR8_HUMAN

P51683 mus musculus
P70612 rattus norv
O62747 cercocobus
P30991 homo sapien
P79394 macaca mula
P56491 papio anubi
P25930 bos taurus
P56498 felis silve
Q920d9 mus musculus
P35411 rattus norv
P51682 mus musculus
P51685 homo sapien

ALIGNMENTS

RESULT 1
CKR6_HUMAN STANDARD; PRT; 374 AA.
AC P51684; Q92846; P78553;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CCR-6) (LARC
DE RECEPTOR) (GPR-CY4) (GPCY4) (CHEMOKINE RECEPTOR-LIKE 3) (CKR-L3)
DE (DRY6).
GN CCR6 OR CMKBR6 OR STRL22 OR GPR29 OR CKRL3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND FUNCTION.
RX MEDLINE=97313465; PubMed=9169459;
RA Baba M., Imai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K.,
RA Nomiya H., Yoshie O.;
RT "Identification of CCR6, the specific receptor for a novel
RT lymphocyte-directed CC chemokine LARC."
RL J. Biol. Chem. 272:14893-14898(1997).
[2]
RP SEQUENCE FROM N.A.
RX Lautens L.L., Modi W., Bonner T.I.;
RA Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97040707; PubMed=8886020;
RA Zaballios A., Varona R., Gutierrez J., Lind P., Marquez G.;
RT "Molecular cloning and RNA expression of two new human chemokine
RT receptor-like genes."
RL Biochem. Biophys. Res. Commun. 227:846-853(1996).
[4]
RP SEQUENCE FROM N.A.
RX McCoy R., Perlmutter D.H.;
RA Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
[5]
RP SEQUENCE FROM N.A.
RX MEDLINE=97224503; PubMed=9070937;
RA Liao F., Lee H.-H., Farber J.M.;
RT "Cloning of STRL22, a new human gene encoding a G-protein-coupled
RT receptor related to chemokine receptors and located on chromosome
RT 6q27".
RL Genomics 40:175-180(1997).
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-
CC ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE
CC INTRACELLULAR CALCIUM IONS LEVELS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: SPLEEN, LYMPH NODES, APPENDIX, AND FETAL
CC LIVER. EXPRESSED IN LYMPHOCYTES, T CELLS AND B CELLS BUT NOT IN
CC NATURAL KILLER CELLS, MONOCYTES, OR GRANULOCYTES.
CC -!- INDUCTION: INTERLEUKIN-2.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-6 IS THE INITIATOR.


```
RESULT 3
CKR5_CERAE
ID CKR5_CERAE STANDARD; PRT; 352 AA.
AC PS6493;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKR5.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=98001387; PubMed=9343222;
RA Kuhlmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT "Polymorphisms in the CKR5 genes of African green monkeys and mice
RT implicate specific amino acids in infections by simian and human
RT immunodeficiency viruses."
RL J. Virol. 71:8642-8656(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Murayama Y., Matsunaga S., Inoue-Murayama M.;
RT "cDNA sequence of African green monkey CKR-5 chemokine receptor
RT gene."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL; U83324; AAC51795.1; -
CC EMBL; U83325; AAC51796.1; -
CC EMBL; AB015944; BAA31328.1; -
CC GCRDb; GCR_2465; -
CC GCRDb; GCR_2466; -
CC InterPro; IPR000276; -
CC InterPro; IPR000355; -
CC InterPro; IPR002240; -
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PRINTS; PR00657; CCEHOKINER.
CC PRINTS; PRO1110; CHEMOKINER5.
CC PROSITE; PS00237; G_PROTEIN_RECF_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECF_F2_1; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.
CC DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 31 58 1 (POTENTIAL).
CC DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 69 89 2 (POTENTIAL).
CC DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 103 124 3 (POTENTIAL).
CC DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 142 166 4 (POTENTIAL).
CC DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 199 218 5 (POTENTIAL).
CC DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 236 260 6 (POTENTIAL).
```

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FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT VARIANT 14 14 N -> Y.
FT VARIANT 352 352 F -> L.
SQ SEQUENCE 352 AA; 40561 MW; 7F52E690C72EC29A CRC64;

Query Match. 78.5%; Score 124; DB 1; Length 352;
Best Local Similarity 65.5%; Pred. No. 5.3e-10;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLFLHCCCLNPVLYAFIGOKFENYFL 29
Db 281 VTETLGMTHCCINPIIYAFVGEKFRNYLL 309

RESULT 4
CKR5_CERTO
ID CKR5_CERTO STANDARD; PRT; 352 AA.
AC O62743; O62744; O62745; O62746;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKR5.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ISOLATE 079, 085, 087 AND 089;
RX MEDLINE=98321155; PubMed=9656999;
RA Chen Z., Gettie A., Ho D.D., Marx P.A.;
RT "Primary SIVsm isolates use the CKR5 coreceptor from sooty mangabey
RT naturally infected in west Africa: a comparison of coreceptor usage
RT of primary SIVsm, HIV-2, and SIVmac."
RL Virology 246:113-124(1998).
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC
CC EMBL; AF051902; AAC39830.1; -
CC EMBL; AF051903; AAC39831.1; -
CC EMBL; AF051904; AAC39832.1; -
CC EMBL; AF051905; AAC39833.1; -
CC InterPro; IPR000276; -
CC InterPro; IPR000355; -
CC InterPro; IPR002240; -
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PRINTS; PR00657; CCEHOKINER.
CC PROSITE; PS00237; G_PROTEIN_RECF_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECF_F2_1; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
CC DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 31 58 1 (POTENTIAL).
```

```
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT VARIANT 2 2 D -> E (IN ISOLATE 087).
FT VARIANT 3 3 Y -> D (IN ISOLATE 079).
FT VARIANT 25 25 V -> G (IN ISOLATE 087).
FT VARIANT 100 100 M -> K (IN ISOLATE 079).
FT VARIANT 107 107 L -> V (IN ISOLATE 089).
FT VARIANT 134 134 V -> G (IN ISOLATE 079).
FT VARIANT 146 146 V -> L (IN ISOLATES 085 AND 089).
FT VARIANT 340 340 T -> I (IN ISOLATE 079).
SQ SEQUENCE 352 AA; 40489 MW; 20A196E2D47B49CA CRC64;

Query Match 78.5%; Score 124; DB 1; Length 352;
Best Local Similarity 65.5%; Pred. No. 5.3e-10;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCLNPLVLYAFIGQKFRNYEL 29
DB 281 VTETLGTHCCINPIIYAFVGEKFRNYLL 309

RESULT 5
CKR5_GORGO STANDARD; PRT; 352 AA.
AC P56439;
AT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKBR5.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains."
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; AF005659; AAB62553.1; -
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DR GCRDb; GCR_1372; -.
DR InterPro; IPR000276; -.
DR InterPro; IPR000355; -.
DR InterPro; IPR002240; -.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHDOPSN.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01110; CHEMOKINER.
DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS00262; G-PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
SQ SEQUENCE 352 AA; 40515 MW; D0E6FCB9FE5EAC84 CRC64;
```

Query Match 78.5%; Score 124; DB 1; Length 352;
Best Local Similarity 65.5%; Pred. No. 5.3e-10;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCLNPLVLYAFIGQKFRNYEL 29
DB 281 VTETLGTHCCINPIIYAFVGEKFRNYLL 309

```
RESULT 6
CKR5_HUMAN STANDARD; PRT; 352 AA.
ID CKR5_HUMAN STANDARD; PRT; 352 AA.
AC P51881; O14692; O14693; O14695; O14697; O14698; O14699;
AC O14700; O14701; O14702; O14703; O14704; O14705; O14706; O14707;
AC O14708;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CCR-5) (CCR5)
DE (HIV-1 FUSION CO-RECEPTOR) (CHEMR13).
GN CKR5 OR CMKBR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96241590; PubMed=8639485;
RA Samson M., Labbe O., Mollereau C., Vassart G., Parmentier M.;
RT "Molecular cloning and functional expression of a new human
RT CC-chemokine receptor gene."
RL Biochemistry 35:3362-3367(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96291862; PubMed=8663314;
RA Raport C.J., Gosling J., Schweichart V.L., Gray P.W., Charo I.F.;
RT "Molecular cloning and functional characterization of a novel human
RT CC chemokine receptor (CCR5) for RANTES, MIP-1beta, and MIP-1alpha."
RL J. Biol. Chem. 271:17161-17166(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96295970; PubMed=8699119;
RA Combadiere C., Ahuja S.K., Tiffany H.L., Murphy P.M.;
```

RT "Cloning and functional expression of CC CKR5, a human monocyte CC
RT chemokine receptor selective for MIP-1(alpha), MIP-1(beta), and
RT RANTES";
RL J. Leukoc. Biol. 60:147-152(1996).
RN [4]
RP SEQUENCE FROM N.A.
RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
RA Nham M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
RA Goj L., la Bastide M., Kaplan N., Greco T., Touchman J.,
RA Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,
RA Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E.,
RA Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,
RA Watanabe M., Doggett N., Garcia D., Sagripanti J.L.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE-98001387; PubMed-9343222;
RA Kuhnmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
RT implicate specific amino acids in infections by simian and human
RT immunodeficiency viruses";
RL J. Virol. 71:8642-8656(1997).
RN [6]
RP SEQUENCE FROM N.A., AND POLYMORPHISMS.
RX MEDLINE-98022612; PubMed-9359654;
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA Ho D.D.;
RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism";
RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE-98049523; PubMed-9388201;
RA Mummidi S., Ahuja S.S., McDaniel B.L., Ahuja S.K.;
RT "The human CC chemokine receptor 5 (CCR5) gene. Multiple transcripts
RT with 5'-end heterogeneity, dual promoter usage, and evidence for
RT polymorphisms within the regulatory regions and noncoding exons.";
RL J. Biol. Chem. 272:30662-30671(1997).
RN [8]
RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION;
RX MEDLINE-96260017; PubMed-8649511;
RA Deng H., Liu R., Elmleier W., Choe S., Unutmaz D., Burkhardt M.,
RA di Marzio P., Marmon S., Sutton R.E., Hill C.M., Davis C.B.,
RA Peiper S.C., Schall T.J., Littman D.R., Landau N.R.;
RT "Identification of a major co-receptor for primary isolates of
RT HIV-1";
RL Nature 381:661-666(1996).
RN [9]
RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
RX MEDLINE-96260018; PubMed-8649512;
RA Draglic T., Litwin V., Allaway G.P., Martin S.R., Huang Y.,
RA Nagashima K.A., Cayan C., Maddon P.J., Koup R.A., Moore J.P.,
RA Paxton W.A.;
RT "HIV-1 entry into CD4+ cells is mediated by the chemokine receptor
RT CC-CKR-5";
RL Nature 381:667-673(1996).
CC -I- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION. ACTS AS CO-RECEPTOR WITH CD4 FOR PRIMARY NON-
CC SYNCTIUM-INDUCING STRAINS (NSI) (MACROPHAGE-TROPIC) OF HIV-1
CC VIRUS. IT PROMOTES ENV-MEDIATED FUSION OF THE VIRUS.
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -I- TISSUE SPECIFICITY: FOUND IN PROMYELOCYTIC CELLS.
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC EMBL; X91492; CAA62796.1; -
DR EMBL; U54994; AAC50598.1; -
DR EMBL; U57840; AAB17071.1; -
DR EMBL; U95626; AAB57793.1; -
DR EMBL; U83326; AAC51797.1; -
DR EMBL; AF011500; AAB65700.1; -
DR EMBL; AF011501; AAB65701.1; -
DR EMBL; AF011502; AAB65702.1; -
DR EMBL; AF011503; AAB65703.1; -
DR EMBL; AF011505; AAB65705.1; -
DR EMBL; AF011506; AAB65706.1; -
DR EMBL; AF011507; AAB65707.1; -
DR EMBL; AF011508; AAB65708.1; -
DR EMBL; AF011509; AAB65709.1; -
DR EMBL; AF011510; AAB65710.1; -
DR EMBL; AF011511; AAB65711.1; -
DR EMBL; AF011512; AAB65712.1; -
DR EMBL; AF011513; AAB65713.1; -
DR EMBL; AF011514; AAB65714.1; -
DR EMBL; AF011515; AAB65715.1; -
DR EMBL; AF011517; AAB65717.1; -
DR EMBL; AF011518; AAB65718.1; -
DR EMBL; AF011519; AAB65719.1; -
DR EMBL; AF011520; AAB65720.1; -
DR EMBL; AF011521; AAB65721.1; -
DR EMBL; AF011522; AAB65722.1; -
DR EMBL; AF011523; AAB65723.1; -
DR EMBL; AF011524; AAB65724.1; -
DR EMBL; AF011525; AAB65725.1; -
DR EMBL; AF011526; AAB65726.1; -
DR EMBL; AF011527; AAB65727.1; -
DR EMBL; AF011528; AAB65728.1; -
DR EMBL; AF011529; AAB65729.1; -
DR EMBL; AF011530; AAB65730.1; -
DR EMBL; AF011531; AAB65731.1; -
DR EMBL; AF011532; AAB65732.1; -
DR EMBL; AF011533; AAB65733.1; -
DR EMBL; AF011535; AAB65735.1; -
DR EMBL; AF011537; AAB65737.1; -
DR EMBL; AF031237; AAB94735.1; -
DR GCRDB; GCR_1923; -
DR GCRDB; GCR_1927; -
DR GCRDB; GCR_2116; -
DR GCRDB; GCR_2454; -
DR GCRDB; GCR_2497; -
DR MIM; 601373; -
DR InterPro; IPR000276; -
DR InterPro; IPR000355; -
DR InterPro; IPR002240; -
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.N.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01110; CHEMOKINER5.
DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS00262; G-PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULFID 101 178
BY SIMILARITY.

FT	CARBOHYD	268	268	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARIANT	10	10	Y -> D (IN INCCR5-71A).
FT	VARIANT	31	31	/FTid=VAR_003481.
FT	VARIANT	34	34	R -> H (IN INCCR5-72A).
FT	VARIANT	62	62	/FTid=VAR_003482.
FT	VARIANT	68	68	P -> L (IN TZCCR5-179).
FT	VARIANT	95	95	/FTid=VAR_003483.
FT	VARIANT	97	97	K -> R (IN UGCCR5-145B).
FT	VARIANT	122	122	/FTid=VAR_003484.
FT	VARIANT	158	158	Y -> H (IN ZWCCR5-7).
FT	VARIANT	176	176	/FTid=VAR_003485.
FT	VARIANT	177	177	D -> N (IN MKCCR5-107).
FT	VARIANT	315	315	/FTid=VAR_003486.
FT	VARIANT	316	316	G -> E (IN INCCR5-467).
FT	VARIANT	317	317	/FTid=VAR_003487.
FT	VARIANT	318	318	L -> P (IN ZWCCR5-7).
FT	VARIANT	319	319	/FTid=VAR_003488.
FT	VARIANT	320	320	F -> S (IN UGCCR5-145A).
FT	VARIANT	321	321	/FTid=VAR_003489.
FT	VARIANT	322	322	Y -> C (IN KECCR5-116).
FT	VARIANT	323	323	/FTid=VAR_003490.
FT	VARIANT	324	324	T -> A (IN INCCR5-45C).
FT	VARIANT	325	325	
FT	VARIANT	326	326	
FT	VARIANT	327	327	
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FT	VARIANT	402		

Pfam: PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR00241; ANGIOTENSINR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01106; CHEMOKINER1.
DR PRINTS; PR01107; CHEMOKINER2.
DR PRINTS; PR01109; CHEMOKINER5.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
EXTRACELLULAR (POTENTIAL).
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULFID 101 178
SQ SEQUENCE 352 AA; 40445 MW; 4F8E4F344CEB7C91 CRC64;

Query Match 78.5%; Score 124; DB 1; Length 352;
Best Local Similarity 65.5%; Pred. No. 5.3e-10;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCLNPVLXAFIGKERNYFL 29
||| | |||:::||:::||:::||::||
DB 281 VTETLGMTHCCINPIIYAFVGKEKNVLL 309

RESULT 8
CKR5_MACMU STANDARD; PRT; 352 AA.
ID CKR5_MACMU AC P79436; Q02746;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKR5.
OS Macaca mulatta (Rhesus macaque),
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
OC Eukaryota; Metazoa (Pig-tailed macaque).
OC Mammalia; Eutheria; Chordata; Craniata;
OC Cercopithecoidea; Primates; Catarrhini; Cercopithecidae;
OX NCBI_TaxID=9544, 9541, 9545;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta;
RX MEDLINE=97184592; PubMed=9032394;
RA Marcon L., Choe H., Martin K A., Farzan M., Ponath P.D., Wu L.,
RA Newman W., Gerard N., Gerard C., Soderosi J.;
RT "Utilization of C-C chemokine receptor 5 by the envelope
RT glycoproteins of a pathogenic simian immunodeficiency virus,
RT SIVmac239.";
RL J. Virol. 71:2522-2527(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta; STRAIN=INDIAN MACAQUE;
RX MEDLINE=97213934; PubMed=9060623;
RA Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.;
RT "Genetically divergent strains of simian immunodeficiency virus use
RT CCR5 as a coreceptor for entry";
RL J. Virol. 71:2705-2714(1997).
RN [3]

RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta; M.fascicularis, and M.nemestrina;
RA Hauer D.A., Margulies B.J., Clements J.E.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [4]

RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta, M.fascicularis, and M.nemestrina;
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
simian immunodeficiency virus strains."
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
DIFFERENTIATION.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----

DR EMBL; U77672; AAC51109.1; -
DR EMBL; U73739; AAC51158.1; -
DR EMBL; U96762; AAC34132.1; -
DR EMBL; AF005660; AAB62554.1; -
DR EMBL; AF005661; AAB62555.1; -
DR EMBL; AF005662; AAB62556.1; -
DR GCRDB; GCR_1296; -
DR GCRDB; GCR_1369; -
DR GCRDB; GCR_1370; -
DR GCRDB; GCR_1371; -
DR GCRDB; GCR_1639; -
DR GCRDB; GCR_1641; -
DR InterPro; IPR000276; -
DR InterPro; IPR000355; -
DR InterPro; IPR002240; -
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01110; CHEMOKINERS.
DR PROSITE; PS00237; G_PROTEIN_RECF_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECF_F2_1; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT CARBOHYD 268 268 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 241 292 M -> I (IN REF. 3).
FT CONFLICT 292 292 I -> M (IN REF. 3).
SQ SEQUENCE 352 AA; 40507 MW; 58B96C85909FACB2 CRC64;

Query Match 78.5%; Score 124; DB 1; Length 352;
Best Local Similarity 65.5%; Pred. No. 5.3e-10;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCCINPVLVAFIGQKFRNYEL 29
DB 281 VTETLGMTHCCINPIIYAFVGEKFRNYLL 309

RESULT 9
CKR5_PANTR STANDARD; PRT; 352 AA.
ID CKR5_PANTR
AC P56440; O02778;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-CR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKBR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
simian immunodeficiency virus strains."
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Zimmerman P.A., Buckler-White A., Alkhatib G.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=98022612; PubMed=9359654;
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA HO D.D.;
RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism."
RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97426118; PubMed=9282822;
RA Zacharova V., Zachar V., Goustin A.S.;
RT "Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural
HIV type 1 host."
RL AIDS Res. Hum. Retroviruses 13:1159-1161(1997).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=98090115; PubMed=9430250;
RA Pretet J.-L., Zerbib A., Girard M., Guillet J.-G., Butor C.;
RT "Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1."
RL AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
DIFFERENTIATION.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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DR EMBL; AF005663; AAB62557.1; -

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DR EMBL; U94329; AAB58446.1; -
DR EMBL; AF011542; AAB65742.1; -
DR EMBL; U97666; AAC51670.1; -
DR EMBL; AF011540; AAB65740.1; -
DR EMBL; U89797; AAC03717.1; -
DR GCRDb; GCR_1284; -
DR GCRDb; GCR_1367; -
DR GCRDb; GCR_2432; -
DR InterPro; IPR000276; -
DR InterPro; IPR000355; -
DR InterPro; IPR002240; -
DR Pfam; PF00001; 7tm.1.1;
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR00657; CCHEMOKINER5.
DR PRINTS; PR01110; CHEMOKINER5.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2;
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT CARBOHYD 268 268 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CONFLICT 123 123 T -> S (IN REF.1).
SQ SEQUENCE 352 AA; 40539 MW; 4A33E69B80FE34C CRC64;

Query Match 78.5%; Score 124; DB 1; Length 352;
Best Local Similarity 65.5%; Pred. No. 5.3e-10;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 VTEVIAFLHCCNLNPLYAFVIGKFRNYFL 29
    ||| | |||:||||:||||:|||||
Db 281 VTETLGTHCCINPIIYAFVGEKFRNYLL 309

RESULT 10
ID CKR5_PAPHA STANDARD; PRT; 352 AA.
AC P56441;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKBR5.
OS Papio hamadryas (Hamadryas baboon), and Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Papio.
OX NCBI_TaxID=9557, 9555;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=P.hamadryas;
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharton M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
RN [2]

SEQUENCE FROM N.A.
SPECIES=P.hamadryas;
MEDLINE=99210133; PubMed=10195758;
Saksena N.K., Wang B., Novembre F.J., Bolton W., Smit T.K., Lal R.B.;
"Species-specific changes in the CCR5 gene from African and Asian
nonhuman primates.";
AIDS Res. Hum. Retroviruses 15:479-483(1999).
[3]
SEQUENCE FROM N.A.
SPECIES=P.anubis;
Benton P.A., Timanus D.K., Shearer M.H., Lee D.R., Kennedy R.C.;
Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
DIFFERENTIATION.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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EMBL; AF005658; AAB62552.1; -
EMBL; AF105287; AAD20556.1; -
EMBL; AF105288; AAD20557.1; -
EMBL; AF105289; AAD20558.1; -
EMBL; AF105290; AAD20559.1; -
EMBL; AF023452; AAC63830.1; -
GCRDb; GCR_1373; -
GCRDb; GCR_2539; -
InterPro; IPR000276; -
InterPro; IPR000355; -
InterPro; IPR002240; -
Pfam; PF00001; 7tm.1.1;
PRINTS; PR00237; GPCRHHODPSN.
PRINTS; PR00657; CCHEMOKINER.
PRINTS; PR01110; CHEMOKINER5.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS0262; G_PROTEIN_RECEP_F1_2;
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT CARBOHYD 268 268 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CONFLICT 123 123 T -> S (IN REF.1).
SQ SEQUENCE 352 AA; 40489 MW; 5E1504A9BA1FE8B2 CRC64;

Query Match 78.5%; Score 124; DB 1; Length 352;
Best Local Similarity 65.5%; Pred. No. 5.3e-10;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 VTEVIAFLHCCNLNPLYAFVIGKFRNYFL 29
    ||| | |||:||||:||||:|||||
Db 281 VTETLGTHCCINPIIYAFVGEKFRNYLL 309

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Best Local Similarity 65.5%; Pred. No. 5.3e-10;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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RESULT 11
CKR5_PONPY
ID CKR5_PONPY STANDARD; PRT; 352 AA.
AC O97881;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKR5.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y.-W., Zhang Y.-P.;
RT "Sequence evolution of chemokine receptor CCR5 gene in primates.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF075446; AAD19858.1;
CC InterPro: IPR000248;
CC InterPro: IPR000276;
CC InterPro: IPR000355;
CC InterPro: IPR002236;
CC InterPro: IPR002237;
CC InterPro: IPR002240;
CC Pfam: PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PRINTS; PR00241; ANGIOTENSINR.
CC PRINTS; PR00657; CCHEMOKINER.
CC PRINTS; PR01106; CHEMOKINER1.
CC PRINTS; PR01107; CHEMOKINER2.
CC PRINTS; PR01110; CHEMOKINER5.
CC PROSITE; PS00237; G_PROTEIN_RECF_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECF_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
CC DOMAIN 1 30
CC TRANSMEM 31 58
CC DOMAIN 59 68
CC TRANSMEM 69 89
CC TRANSMEM 90 102
CC TRANSMEM 103 124
CC TRANSMEM 125 141
CC TRANSMEM 142 166
CC TRANSMEM 167 198
CC TRANSMEM 199 218
CC TRANSMEM 219 235
CC TRANSMEM 236 260
CC TRANSMEM 261 277
CC TRANSMEM 278 301
CC TRANSMEM 302 352
CC BY SIMILARITY.
CC DISULFID 101 178
CC SEQUENCE 352 AA; 40527 MW; F4E2F47135AF658A CRC64;

RESULT 12
CKR5_PYGBI
ID CKR5_PYGBI STANDARD; PRT; 352 AA.
AC O97880;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKR5.
OS Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=61621;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y.-W., Zhang Y.-P.;
RT "Sequence evolution of chemokine receptor CCR5 gene in primates.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF075445; AAD19857.1;
CC InterPro: IPR000248;
CC InterPro: IPR000276;
CC InterPro: IPR000355;
CC InterPro: IPR002236;
CC InterPro: IPR002240;
CC Pfam: PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PRINTS; PR00241; ANGIOTENSINR.
CC PRINTS; PR00657; CCHEMOKINER.
CC PRINTS; PR01106; CHEMOKINER1.
CC PRINTS; PR01110; CHEMOKINER5.
CC PROSITE; PS00237; G_PROTEIN_RECF_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECF_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
CC DOMAIN 1 30
CC TRANSMEM 31 58
CC DOMAIN 59 68
CC TRANSMEM 69 89
CC TRANSMEM 90 102
CC TRANSMEM 103 124
CC TRANSMEM 125 141
CC TRANSMEM 142 166
CC TRANSMEM 167 198
CC TRANSMEM 199 218
CC TRANSMEM 219 235
CC TRANSMEM 236 260
CC TRANSMEM 261 277
CC TRANSMEM 278 301
CC TRANSMEM 302 352

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Query Match 78.5%; Score 124; DB 1; Length 352;

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FT DISULFID 101 178 BY SIMILARITY.
SQ SEQUENCE 352 AA; 40585 MW; 4366F142730F938F CRC64;

Query Match 78.5%; Score 124; DB 1; Length 352;
Best Local Similarity 65.5%; Pred. No. 5.3e-10;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Oy 1 VTEVLAFLHCCLNPLVLYAFVIGKERNYFL 29
    III I IIII:IIII:IIII:IIII I
Db 281 VTETLGMTHCCINPIIYAFVGEKFRNYLL 309

RESULT 13
CKR5_PYGNE
ID CKR5_PYGNE STANDARD; PRT; 352 AA.
AC 097882;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKBR5.
OS Pygathrix nemaeus (Dove langur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=54133;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y.-W., Zhang Y.-P.;
RT "Sequence evolution of chemokine receptor CCR5 gene in primates.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
CC EMBL; AF075448; AAD19860.1;
CC InterPro; IPR000248;
CC InterPro; IPR000276;
CC InterPro; IPR000355;
CC InterPro; IPR002236;
CC InterPro; IPR002237;
CC InterPro; IPR002240;
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHHODOPSIN.
CC PRINTS; PR00241; ANGIOTENSINR.
CC PRINTS; PR00657; CCHEMOKINER.
CC PRINTS; PR01106; CHEMOKINER1.
CC PRINTS; PR01107; CHEMOKINER2.
CC PRINTS; PR01110; CHEMOKINER5.
CC PROSITE; PS00237; G_PROTEIN_RECP_FL_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECP_FL_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
KW DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).

Query Match 78.5%; Score 124; DB 1; Length 352;
Best Local Similarity 65.5%; Pred. No. 5.3e-10;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Oy 1 VTEVLAFLHCCLNPLVLYAFVIGKERNYFL 29
    III I IIII:IIII:IIII:IIII I
Db 281 VTETLGMTHCCINPIIYAFVGEKFRNYLL 309

RESULT 14
CKR5_TRAFR
ID CKR5_TRAFR STANDARD; PRT; 352 AA.
AC 097878;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CC-CKR-5) (CCR5).
GN CCR5 OR CMKBR5.
OS Trachypithecus francoisi (Francois' langur) (Indochinese langur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Trachypithecus.
OX NCBI_TaxID=54180;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y.-W., Zhang Y.-P.;
RT "Sequence evolution of chemokine receptor CCR5 gene in primates.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
CC EMBL; AF075442; AAD19854.1;
CC InterPro; IPR000248;
CC InterPro; IPR000276;
CC InterPro; IPR000355;
CC InterPro; IPR002236;
CC InterPro; IPR002237;
CC InterPro; IPR002240;
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHHODOPSIN.
CC PRINTS; PR00241; ANGIOTENSINR.
CC PRINTS; PR00657; CCHEMOKINER.
CC PRINTS; PR01106; CHEMOKINER1.
CC PRINTS; PR01107; CHEMOKINER2.
CC PRINTS; PR01110; CHEMOKINER5.
CC PROSITE; PS00237; G_PROTEIN_RECP_FL_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECP_FL_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
KW DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
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FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
SQ SEQUENCE 352 AA; 40496 MW; 4366FL48C255938F CRC64;

Query Match 78.5%; Score 124; DB 1; Length 352;
Best Local Similarity 65.5%; Pred. No. 5.3e-10;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCLNPNVLYAFVIGQKFRNYFL 29
||| | |||:||||:||||| |
Db 281 VTETLGMTHCCINPIIYAFVGEKERNYLL 309

RESULT 15
CKR5_TRAPH
ID CKR5_TRAPH STANDARD; PRT; 352 AA.
AC O97879;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKBR5.
OS Trachypithecus phayrei (Phayre's leaf monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Trachypithecus.
OX NBI_TaxID=61618;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y.-W., Zhang Y.-P.;
RT "Sequence evolution of chemokine receptor CKR5 gene in primates.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC !- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
CC !- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC !- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF075443; AAD19855.1; -
DR InterPro; IPR000248; -
DR InterPro; IPR000276; -
DR InterPro; IPR000355; -
DR InterPro; IPR002236; -
DR InterPro; IPR002237; -
DR InterPro; IPR002240; -
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR00241; ANGIOTENSINR.
DR PRINTS; PR00657; CCHEMOKINER.

DR PRINTS; PR01106; CHEMOKINER1.
DR PRINTS; PR01107; CHEMOKINER2.
DR PRINTS; PR01110; CHEMOKINER5.
DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
SQ SEQUENCE 352 AA; 40509 MW; 4366FL48D3A5938F CRC64;

Query Match 78.5%; Score 124; DB 1; Length 352;

Best Local Similarity 65.5%; Pred. No. 5.3e-10;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCLNPNVLYAFVIGQKFRNYFL 29
||| | |||:||||:||||| |
Db 281 VTETLGMTHCCINPIIYAFVGEKERNYLL 309

Search completed: May 23, 2001, 15:36:21
Job time: 652 sec


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O14694
ID O14694 PRELIMINARY; PRT; 333 AA.
AC O14694;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE CCR5 RECEPTOR (FRAGMENT).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA Ho D.D.;
RL AIDS Res. Hum. Retroviruses 0:0-0(1997).
DR EMBL: AF011504; AAB65704.1; -
DR INTERPRO: IPR000190; -
DR INTERPRO: IPR000276; -
DR INTERPRO: IPR000355; -
DR INTERPRO: IPR001277; -
DR INTERPRO: IPR002236; -
DR INTERPRO: IPR002237; -
DR INTERPRO: IPR002238; -
DR INTERPRO: IPR002240; -
DR PFAM: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODOPSN.
DR PRINTS: PR00635; ANGIOTENSINR.
DR PRINTS: PR00645; LCR1ORPHANR.
DR PRINTS: PR00657; CCHEMOKINER.
DR PRINTS: PR01106; CHEMOKINER1.
DR PRINTS: PR01107; CHEMOKINER2.
DR PRINTS: PR01110; CHEMOKINER5.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
FT NON_TER 333
SQ SEQUENCE 333 AA; 38174 MW; AEFBA07A67893AEB CRC64;

Query Match 78.5%; Score 124; DB 4; Length 333;
Best Local Similarity 65.5%; Pred. No. 3.5e-11;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCCLNPLVYAFIQKFRNYFL 29
   ||| | |||:||||:||||:|||||
Db 262 VTETLGMTHCCINPIIYAFVGEKFRNYLL 290

RESULT 3
ID Q9TU07 PRELIMINARY; PRT; 334 AA.
AC Q9TU07;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN CCR5.
OS Erythrocybus patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Erythrocybus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF162049; AAD47804.1; -
DR INTERPRO: IPR000248; -
DR INTERPRO: IPR000276; -

QY 1 VTEVLAFLHCCLNPLVYAFIQKFRNYFL 29
   ||| | |||:||||:||||:|||||
Db 262 VTETLGMTHCCINPIIYAFVGEKFRNYLL 290

RESULT 3
ID Q9TU07 PRELIMINARY; PRT; 334 AA.
AC Q9TU07;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN CCR5.
OS Erythrocybus patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Erythrocybus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF162049; AAD47804.1; -
DR INTERPRO: IPR000248; -
DR INTERPRO: IPR000276; -

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DR INTERPRO: IPR000355; -
DR INTERPRO: IPR001277; -
DR INTERPRO: IPR002236; -
DR INTERPRO: IPR002237; -
DR INTERPRO: IPR002240; -
DR PFAM: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODOPSN.
DR PRINTS: PR00241; ANGIOTENSINR.
DR PRINTS: PR00645; LCR1ORPHANR.
DR PRINTS: PR00657; CCHEMOKINER.
DR PRINTS: PR01106; CHEMOKINER1.
DR PRINTS: PR01107; CHEMOKINER2.
DR PRINTS: PR01110; CHEMOKINER5.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 334
SQ SEQUENCE 334 AA; 38460 MW; B19DOCEC667B69F0 CRC64;

Query Match 78.5%; Score 124; DB 6; Length 334;
Best Local Similarity 65.5%; Pred. No. 3.5e-11;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCCLNPLVYAFIQKFRNYFL 29
   ||| | |||:||||:||||:|||||
Db 269 VTETLGMTHCCINPIIYAFVGEKFRNYLL 297

RESULT 4
ID Q9UN28 PRELIMINARY; PRT; 339 AA.
AC Q9UN28;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF161913; AAD47670.1; -
DR INTERPRO: IPR000190; -
DR INTERPRO: IPR000248; -
DR INTERPRO: IPR000276; -
DR INTERPRO: IPR000355; -
DR INTERPRO: IPR001277; -
DR INTERPRO: IPR002236; -
DR INTERPRO: IPR002237; -
DR INTERPRO: IPR002240; -
DR PFAM: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODOPSN.
DR PRINTS: PR00241; ANGIOTENSINR.
DR PRINTS: PR00635; ANGIOTENSINR.
DR PRINTS: PR00645; LCR1ORPHANR.
DR PRINTS: PR00657; CCHEMOKINER.
DR PRINTS: PR01106; CHEMOKINER1.
DR PRINTS: PR01107; CHEMOKINER2.
DR PRINTS: PR01110; CHEMOKINER5.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 339
SQ SEQUENCE 339 AA; 39183 MW; 56C819F92D6DB1A6 CRC64;

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Query Match 78.5%; Score 124; DB 4; Length 339;
 Best Local Similarity 65.5%; Pred. No. 3.6e-11;
 Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCLNPVLYAFVIGKFRNYFL 29
 III I III:III:III:III:III I
 Db 274 VTETLGMTHCCINPIIYAFVGEKFRNYLL 302

RESULT 5

Q9UN27 ID Q9UN27 PRELIMINARY; PRT; 339 AA.
 AC Q9UN27;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
 GN CCR5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 species";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161914; AAD47671.1; -
 DR INTERPRO; IPR000190; -
 DR INTERPRO; IPR000248; -
 DR INTERPRO; IPR000276; -
 DR INTERPRO; IPR000355; -
 DR INTERPRO; IPR001277; -
 DR INTERPRO; IPR002236; -
 DR INTERPRO; IPR002237; -
 DR INTERPRO; IPR002240; -
 DR PFAM; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00241; ANGIOTENSINR.
 DR PRINTS; PR00635; ANGIOTENSINR.
 DR PRINTS; PR00645; LCRIORPHANR.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01106; CHEMOKINER1.
 DR PRINTS; PR01107; CHEMOKINER2.
 DR PRINTS; PR01110; CHEMOKINER5.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 KW Receptor.
 FT NON_TER 1
 FT NON_TER 339
 SQ SEQUENCE 339 AA; 39086 MW; 88AD8B44E2CB4EC2 CRC64;

Query Match 78.5%; Score 124; DB 4; Length 339;
 Best Local Similarity 65.5%; Pred. No. 3.6e-11;
 Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCLNPVLYAFVIGKFRNYFL 29
 III I III:III:III:III:III I
 Db 274 VTETLGMTHCCINPIIYAFVGEKFRNYLL 302

RESULT 6

Q9UN26 ID Q9UN26 PRELIMINARY; PRT; 339 AA.
 AC Q9UN26;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
 GN CCR5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 species";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161914; AAD47671.1; -
 DR INTERPRO; IPR000190; -
 DR INTERPRO; IPR000248; -
 DR INTERPRO; IPR000276; -
 DR INTERPRO; IPR000355; -
 DR INTERPRO; IPR001277; -
 DR INTERPRO; IPR002236; -
 DR INTERPRO; IPR002237; -
 DR INTERPRO; IPR002240; -
 DR PFAM; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00241; ANGIOTENSINR.
 DR PRINTS; PR00635; ANGIOTENSINR.
 DR PRINTS; PR00645; LCRIORPHANR.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01106; CHEMOKINER1.
 DR PRINTS; PR01107; CHEMOKINER2.
 DR PRINTS; PR01110; CHEMOKINER5.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 KW Receptor.
 FT NON_TER 1
 FT NON_TER 339
 SQ SEQUENCE 339 AA; 39086 MW; 88AD8B44E2CB4EC2 CRC64;

Query Match 78.5%; Score 124; DB 4; Length 339;
 Best Local Similarity 65.5%; Pred. No. 3.6e-11;
 Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCLNPVLYAFVIGKFRNYFL 29
 III I III:III:III:III:III I
 Db 274 VTETLGMTHCCINPIIYAFVGEKFRNYLL 302

RESULT 7

Q9UN25 ID Q9UN25 PRELIMINARY; PRT; 339 AA.
 AC Q9UN25;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
 GN CCR5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 species";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161914; AAD47671.1; -
 DR INTERPRO; IPR000190; -
 DR INTERPRO; IPR000248; -
 DR INTERPRO; IPR000276; -
 DR INTERPRO; IPR000355; -
 DR INTERPRO; IPR001277; -
 DR INTERPRO; IPR002236; -
 DR INTERPRO; IPR002237; -

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 species";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161914; AAD47671.1; -
 DR INTERPRO; IPR000190; -
 DR INTERPRO; IPR000248; -
 DR INTERPRO; IPR000276; -
 DR INTERPRO; IPR000355; -
 DR INTERPRO; IPR001277; -
 DR INTERPRO; IPR002236; -
 DR INTERPRO; IPR002237; -
 DR INTERPRO; IPR002240; -
 DR PFAM; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00241; ANGIOTENSINR.
 DR PRINTS; PR00635; ANGIOTENSINR.
 DR PRINTS; PR00645; LCRIORPHANR.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01106; CHEMOKINER1.
 DR PRINTS; PR01107; CHEMOKINER2.
 DR PRINTS; PR01110; CHEMOKINER5.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 KW Receptor.
 FT NON_TER 1
 FT NON_TER 339
 SQ SEQUENCE 339 AA; 39162 MW; A56369FE0529F4AB CRC64;

Query Match 78.5%; Score 124; DB 4; Length 339;
 Best Local Similarity 65.5%; Pred. No. 3.6e-11;
 Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCLNPVLYAFVIGKFRNYFL 29
 III I III:III:III:III:III I
 Db 274 VTETLGMTHCCINPIIYAFVGEKFRNYLL 302

RESULT 7

Q9UN25 ID Q9UN25 PRELIMINARY; PRT; 339 AA.
 AC Q9UN25;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
 GN CCR5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 species";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161914; AAD47671.1; -
 DR INTERPRO; IPR000190; -
 DR INTERPRO; IPR000248; -
 DR INTERPRO; IPR000276; -
 DR INTERPRO; IPR000355; -
 DR INTERPRO; IPR001277; -
 DR INTERPRO; IPR002236; -
 DR INTERPRO; IPR002237; -
 DR INTERPRO; IPR002240; -
 DR PFAM; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00241; ANGIOTENSINR.
 DR PRINTS; PR00635; ANGIOTENSINR.
 DR PRINTS; PR00645; LCRIORPHANR.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01106; CHEMOKINER1.
 DR PRINTS; PR01107; CHEMOKINER2.
 DR PRINTS; PR01110; CHEMOKINER5.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 KW Receptor.
 FT NON_TER 1
 FT NON_TER 339
 SQ SEQUENCE 339 AA; 39162 MW; A56369FE0529F4AB CRC64;

Query Match 78.5%; Score 124; DB 4; Length 339;
 Best Local Similarity 65.5%; Pred. No. 3.6e-11;
 Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCLNPVLYAFVIGKFRNYFL 29
 III I III:III:III:III:III I
 Db 274 VTETLGMTHCCINPIIYAFVGEKFRNYLL 302

RESULT 7

Q9UN25 ID Q9UN25 PRELIMINARY; PRT; 339 AA.
 AC Q9UN25;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
 GN CCR5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 species";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161914; AAD47671.1; -
 DR INTERPRO; IPR000190; -
 DR INTERPRO; IPR000248; -
 DR INTERPRO; IPR000276; -
 DR INTERPRO; IPR000355; -
 DR INTERPRO; IPR001277; -
 DR INTERPRO; IPR002236; -
 DR INTERPRO; IPR002237; -

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DR INTERPRO: IPR002240; -.
DR PFAM: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PRINTS: PR00241; ANGIOTENSINR.
DR PRINTS: PR00635; ANGIOTENSINR.
DR PRINTS: PR00645; LCRIORPHANR.
DR PRINTS: PR00657; CCHEMOKINER.
DR PRINTS: PR01106; CHEMOKINER1.
DR PRINTS: PR01107; CHEMOKINER2.
DR PRINTS: PR01110; CHEMOKINER5.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39146 MW; 10FE05FES371D4B3 CRC64;

Query Match 78.5%; Score 124; DB 4; Length 339;
Best Local Similarity 65.5%; Pred. No. 3.6e-11;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCLNPLVLYAFVIGQKFRNYFL 29
   ||| | |||:||||:||||:|
Db 274 VTETLGMTHCCINPIIYAFVGEKFRNYLL 302

RESULT 8
QYUN24 ID Q9UN24 PRELIMINARY; PRT; 339 AA.
AC Q9UN24;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF161919; AAD47676.1; -.
DR INTERPRO: IPR000190; -.
DR Q9UN24;
DR INTERPRO: IPR000248; -.
DR 01-MAY-2000 (TREMBLrel. 13, Created)
DR 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF161919; AAD47676.1; -.
DR INTERPRO: IPR000190; -.
DR INTERPRO: IPR000248; -.
DR INTERPRO: IPR000276; -.
DR INTERPRO: IPR000355; -.
DR INTERPRO: IPR001277; -.
DR INTERPRO: IPR002236; -.
DR INTERPRO: IPR002237; -.
DR INTERPRO: IPR002240; -.
DR PFAM: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PRINTS: PR00241; ANGIOTENSINR.
DR PRINTS: PR00635; ANGIOTENSINR.
DR PRINTS: PR00645; LCRIORPHANR.
DR PRINTS: PR00657; CCHEMOKINER.
DR PRINTS: PR01106; CHEMOKINER1.
DR PRINTS: PR01107; CHEMOKINER2.
DR PRINTS: PR01110; CHEMOKINER5.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39066 MW; 8BAF02E19423BF79 CRC64;

Query Match 78.5%; Score 124; DB 4; Length 339;
Best Local Similarity 65.5%; Pred. No. 3.6e-11;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCLNPLVLYAFVIGQKFRNYFL 29
   ||| | |||:||||:||||:|
Db 274 VTETLGMTHCCINPIIYAFVGEKFRNYLL 302

RESULT 9
QYUN23 ID Q9UN23 PRELIMINARY; PRT; 339 AA.
AC Q9UN23;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF161920; AAD47677.1; -.
DR INTERPRO: IPR000190; -.
DR INTERPRO: IPR000248; -.
DR INTERPRO: IPR000276; -.
DR INTERPRO: IPR000355; -.
DR INTERPRO: IPR001277; -.
DR INTERPRO: IPR002236; -.
DR INTERPRO: IPR002237; -.
DR INTERPRO: IPR002240; -.
DR PFAM: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PRINTS: PR00241; ANGIOTENSINR.
DR PRINTS: PR00635; ANGIOTENSINR.
DR PRINTS: PR00645; LCRIORPHANR.
DR PRINTS: PR00657; CCHEMOKINER.
DR PRINTS: PR01106; CHEMOKINER1.
DR PRINTS: PR01107; CHEMOKINER2.
DR PRINTS: PR01110; CHEMOKINER5.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39115 MW; 3C6369F922C91AA7 CRC64;

Query Match 78.5%; Score 124; DB 4; Length 339;
Best Local Similarity 65.5%; Pred. No. 3.6e-11;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCLNPLVLYAFVIGQKFRNYFL 29
   ||| | |||:||||:||||:|
Db 274 VTETLGMTHCCINPIIYAFVGEKFRNYLL 302

RESULT 10
QYUN29 ID Q9UBT9 PRELIMINARY; PRT; 339 AA.
AC Q9UBT9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
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OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA  Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT  "Sequences of the CCR5 genes from diverse simian and prosimian
RT  species.";
RL  Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
DR  EMBL; AF161915; AAD47672.1; -
DR  EMBL; AF161909; AAD47666.1; -
DR  EMBL; AF161910; AAD47667.1; -
DR  EMBL; AF161911; AAD47668.1; -
DR  EMBL; AF161912; AAD47669.1; -
DR  INTERPRO; IPR000190; -
DR  INTERPRO; IPR000248; -
DR  INTERPRO; IPR000276; -
DR  INTERPRO; IPR000355; -
DR  INTERPRO; IPR001277; -
DR  INTERPRO; IPR002236; -
DR  INTERPRO; IPR002237; -
DR  INTERPRO; IPR002240; -
DR  PFAM; PF00001; 7tm_1; 1.
DR  PRINTS; PR00237; GPCRHHODOPS.
DR  PRINTS; PR00241; ANGIOTENSINR.
DR  PRINTS; PR00635; ANGIOTENSINR.
DR  PRINTS; PR00645; LCR1ORPHANR.
DR  PRINTS; PR00657; CCHEMOKINER.
DR  PRINTS; PR01106; CHEMOKINER1.
DR  PRINTS; PR01107; CHEMOKINER2.
DR  PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW  Receptor.
FT  NON_TER 1 339
FT  NON_TER 339 339
SQ  SEQUENCE 339 AA; 39114 MW; 3C6369F92C29F47A7A CRC64;

Query Match 78.5%; Score 124; DB 4; Length 339;
Best Local Similarity 65.5%; Pred. No. 3.6e-11;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCLNPLVYAFVIGOKFRNYFL 29
   ||| | |||:||||:||||:|||||
Db 274 VTETLGTHCCINPIIYAFVGEKFRNYLL 302

RESULT 11
Q9UBJ7 PRELIMINARY; PRT; 339 AA.
ID Q9UBJ7
AC Q9UBJ7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF161921; AAD47678.1; -
DR EMBL; AF161917; AAD47674.1; -
DR INTERPRO; IPR000190; -
DR INTERPRO; IPR000248; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR000355; -
DR INTERPRO; IPR001277; -
DR INTERPRO; IPR002236; -
DR INTERPRO; IPR002237; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PRINTS; PR00241; ANGIOTENSINR.
DR PRINTS; PR00635; ANGIOTENSINR.
DR PRINTS; PR00645; LCR1ORPHANR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01106; CHEMOKINER1.
DR PRINTS; PR01107; CHEMOKINER2.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39075 MW; 09257FBFB834C4AE CRC64;

Query Match 78.5%; Score 124; DB 4; Length 339;
Best Local Similarity 65.5%; Pred. No. 3.6e-11;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCLNPLVYAFVIGOKFRNYFL 29
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Db 274 VTETLGTHCCINPIIYAFVGEKFRNYLL 302

RESULT 12
Q9TUX1 PRELIMINARY; PRT; 339 AA.
ID Q9TUX1
AC Q9TUX1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF161887; AAD47644.1; -
DR INTERPRO; IPR000190; -
DR INTERPRO; IPR000248; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR000355; -
DR INTERPRO; IPR001277; -
DR INTERPRO; IPR002236; -
DR INTERPRO; IPR002237; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PRINTS; PR00241; ANGIOTENSINR.
DR PRINTS; PR00635; ANGIOTENSINR.
DR PRINTS; PR00645; LCR1ORPHANR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01106; CHEMOKINER1.
DR PRINTS; PR01107; CHEMOKINER2.
DR PRINTS; PR01110; CHEMOKINER5.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39075 MW; 09257FBFB834C4AE CRC64;
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RT	species."	Submitted (JUL-1999)	to the EMBL/GenBank/DBJ databases.
DR	EMBL; AF161894; AAD47651.1;	-	-
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DR	INTERPRO; IPR000248;	-	-
DR	INTERPRO; IPR000276;	-	-
DR	INTERPRO; IPR000355;	-	-
DR	INTERPRO; IPR001277;	-	-
DR	INTERPRO; IPR002236;	-	-
DR	INTERPRO; IPR002237;	-	-
DR	INTERPRO; IPR002240;	-	-

DR PFAM; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00241; ANGIOTENSINR.
 DR PRINTS; PR00635; ANGIOTENSINR.
 DR PRINTS; PR00645; LCRORPHANR.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01106; CHEMOKINER1.
 DR PRINTS; PR01107; CHEMOKINER2.
 DR PRINTS; PR01110; CHEMOKINER5.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 KW Receptor.
 FT NON_TER 1 1
 FT NON_TER 339 339
 SQ SEQUENCE 339 AA; 39079 MW; A4A79753DA2F7AAF CRC64;

Query Match 78.5%; Score 124; DB 6; Length 339;
 Best Local Similarity 65.5%; Pred. No. 3.6e-11;
 Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFTHCCLNPVLYAFVIGOKERNYFL 29
 ||| | |||:||||:||||:||||:|
 Db 274 VTEGLWTHCCINPIIYAFVIGKERNVLL 302

Search completed: May 23, 2001, 15:35:18
 Job time: 624 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:28:33 ; Search time 184.73 Seconds
(without alignments)
13.925 Million cell updates/sec

Title: US-08-887-977-10_COPY_320_364

Perfect score: 237

Sequence: 1 KILKDLWCVRKYSKSGFSC.....ENISQTSATDNDNASFT 45

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq_0401.*

- 1: /SIDS6/gcgdata/geneseq/geneseq/AA1980.DAT.*
- 2: /SIDS6/gcgdata/geneseq/geneseq/AA1981.DAT.*
- 3: /SIDS6/gcgdata/geneseq/geneseq/AA1982.DAT.*
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- 11: /SIDS6/gcgdata/geneseq/geneseq/AA1990.DAT.*
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- 14: /SIDS6/gcgdata/geneseq/geneseq/AA1993.DAT.*
- 15: /SIDS6/gcgdata/geneseq/geneseq/AA1994.DAT.*
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- 19: /SIDS6/gcgdata/geneseq/geneseq/AA1998.DAT.*
- 20: /SIDS6/gcgdata/geneseq/geneseq/AA1999.DAT.*
- 21: /SIDS6/gcgdata/geneseq/geneseq/AA2000.DAT.*
- 22: /SIDS6/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	237	100.0	365	19	W48086 Human dendritic ce
2	237	100.0	365	21	Y97077 Primate (human) ch
3	56	23.6	280	21	G25793 Arabidopsis thalia
4	56	23.6	282	21	G25792 Arabidopsis thalia
5	56	23.6	292	21	G25791 Arabidopsis thalia
6	56	23.6	720	20	Y05452 Human heregulin-l1
7	56	23.6	720	20	W97618 Human neuregulin r
8	55	23.2	166	21	B27319 B. napus NIM1 homo
9	55	23.2	461	21	V77450 Leptospira kirschn
10	52	21.9	166	21	B27320 B. napus NIM1 homo
11	52	21.9	476	19	W37241 Heterodera glycine

12	52	21.9	484	19	W43910 Heterodera glycine
13	52	21.9	800	11	R07713 Human low density
14	51.5	21.7	768	20	W98108 Caenorhabditis ele
15	51	21.5	81	20	Y28848 Maize basal endosp
16	51	21.5	246	20	Y37499 Protein which is s
17	51	21.5	512	21	G28030 Arabidopsis thalia
18	51	21.5	545	21	G28029 Arabidopsis thalia
19	51	21.5	606	21	G28028 Arabidopsis thalia
20	51	21.5	860	15	R47157 Sequence of human
21	51	21.5	910	21	G48217 Arabidopsis thalia
22	51	21.5	957	21	G48216 Arabidopsis thalia
23	51	21.5	991	21	G48215 Arabidopsis thalia
24	50	21.1	141	21	G36206 Arabidopsis thalia
25	50	21.1	169	21	G36205 Arabidopsis thalia
26	50	21.1	183	21	G36204 Arabidopsis thalia
27	50	21.1	500	21	B19742 Rat acyl CoA:chole
28	50	21.1	500	21	Y54139 Acyl-CoA:cholester
29	50	21.1	713	20	W97617 Mouse neuregulin r
30	49.5	20.9	89	21	G27687 Arabidopsis thalia
31	49.5	20.9	96	21	G27686 Arabidopsis thalia
32	49.5	20.9	291	21	G13753 Arabidopsis thalia
33	49.5	20.9	291	21	G51750 Arabidopsis thalia
34	49.5	20.9	353	21	G13752 Arabidopsis thalia
35	49.5	20.9	353	21	G51749 Arabidopsis thalia
36	49.5	20.9	456	21	G13751 Arabidopsis thalia
37	49.5	20.9	456	21	G51748 Arabidopsis thalia
38	49	20.7	149	21	G29834 Arabidopsis thalia
39	49	20.7	189	20	Y42390 Alternative readin
40	49	20.7	497	21	Y94523 Mouse diacylglycer
41	49	20.7	498	21	Y44562 Zea mays protein f
42	48.5	20.5	250	21	G35200 HASNPV polypeptide
43	48.5	20.5	272	18	W00925 Streptococcus pneu
44	48	20.3	106	18	W14541 Pinus radiata tran
45	48	20.3	152	21	B33196

ALIGNMENTS

RESULT 1

W48086

ID W48086 standard; Protein; 365 AA.

XX AC W48086;

XX DT 11-JUN-1998 (first entry)

XX DE Human dendritic cell chemokine receptor.

XX KW Human; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta;

XX KW receptor; dendritic cell; macrophage; inflammation; asthma.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

XX FT Misc-difference 193 /note= "encoded by CAN"

XX FT

XX PN W09801557-A2.

XX PD 15-JAN-1998.

XX PF 02-JUL-1997; 97WO-US10819.

XX PR 04-JUN-1997; 97US-0048593.

XX PR 05-JUL-1996; 96US-0675814.

XX PR 11-OCT-1996; 96US-0028329.

XX XX (SCHE) SCHERING CORP.

XX PA Gish KC, Schall TJ, Vicari A, Wang W, Zlotnik A;

XX PI WPI; 1998-101054/09.

XX XX

XX DR

DR N-PSDB; V15418.
XX Novel chemokines, e.g. thymus expressed chemokine - used for
PT treating inflammatory conditions including asthma.
XX
PS Claim 3; Page 94-95; 202pp; English.
XX
CC The present sequence represents human dendritic cell chemokine receptor.
CC Antibodies which bind to the protein can be used in detecting or
CC diagnosing various immunological conditions related to expression
CC of the protein. The nucleic acid can be used for screening and
CC isolating DNA clones for the chemokines, especially from other
CC species. The chemokine can be used in the treatment of conditions
CC associated with abnormal physiology or development, including
CC inflammatory conditions such as asthma.
XX
SQ Sequence 365 AA;

Query Match 100.0%; Score 237; DB 19; Length 365;
Best Local Similarity 100.0%; Pred. NO. 4.3e-26;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KILKDLWCVRVKYKSSGFCAGRYSENISRTSETADNDNASFT 45
Db 320 kilkdwcvrkykssgfcagrysenisrqtsetadndnassft 364
|||||

RESULT 2
Y97077
ID Y97077 standard; Protein; 365 AA.
XX
AC Y97077;
XX
DT 04-DEC-2000 (first entry)
XX
DE Primate (human) chemokine receptor CCR6.
XX
KW MIP-3-alpha; chemokine; CCR6 receptor; ligand; cytostatic; agonist;
KW antagonist; anti-psoriatic; dermatological; immunosuppressive;
KW anti-inflammatory.
XX
OS Homo sapiens.
XX
FT Key Location/Qualifiers
FT Misc-difference 193 /note= "Encoded by CAN#"
FT
XX
PN W0200046248-A1.
XX
PD 10-AUG-2000.
XX
PF 02-FEB-2000; 2000WO-US00511.
XX
PR 03-FEB-1999; 99US-0244281.
XX
PA (SCHE) SCHERING CORP.
XX
PI Oldham ER, Honey B, Dieu-Nosjean M, Caux C, Zlotnik A;
XX
DR WPI; 2000-543477/49.
DR N-PSDB; A51971.
XX
XX Novel methods for modulating the migration of cells within or to the
PT skin using MIP-3-alpha or CCR6 agonists or antagonists, useful for
PT treating skin disorders, e.g. cancer
XX
PS Disclosure; Page 53-54; 61pp; English.
XX
CC The MIP-3-alpha chemokine is expressed in inflamed skin cells. This
CC chemokine is the ligand for the CCR6 receptor. MIP-3-alpha or CCR6
CC agonists or antagonists can be used to modulate the migration of a cell
CC within or to the skin of a mammal. MIP-3-alpha can be used to purify a

CC population of cells expressing a MIP-3-alpha receptor. The methods are
CC useful for treating a mammalian subject with a skin disease or condition,
CC e.g. cancer, metastasis, psoriasis, atopic or contact dermatitis,
CC systemic lupus erythematosus and lichen ruber planus, or for treating
CC skin transplants or grafts.
XX
SQ Sequence 365 AA;

Query Match 100.0%; Score 237; DB 21; Length 365;
Best Local Similarity 100.0%; Pred. NO. 4.3e-26;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KILKDLWCVRVKYKSSGFCAGRYSENISRTSETADNDNASFT 45
Db 320 kilkdwcvrkykssgfcagrysenisrqtsetadndnassft 364
|||||

RESULT 3
G25793
ID G25793 standard; Protein; 280 AA.
XX
AC G25793;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 30000.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
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PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
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PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
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PR 25-MAY-1999; 99US-0136021.

PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 14-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140053.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
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PR 01-JUL-1999; 99US-0141842.
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PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
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PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
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PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.

XX Y05452;
AC 06-JUL-1999 (first entry)
XX Human heregulin-like factor sequence.
XX Human heregulin-like factor; HLF; cell growth regulator; diagnosis;
KW neural system disorder; cancer.
XX Homo sapiens.
OS
XX WO9857989-A1.
PN 23-DEC-1998.
XX 16-JUN-1998; 98WO-US12403.
XX 17-JUN-1997; 97US-0049942.
XX (HUMA-) HUMAN GENOME SCI INC.
PA (GEOU) UNIV GEORGETOWN.
XX Hijazi MM, King CR, Ruben SM, Young P;
XX WPI; 1999-095327/08.
XX New isolated heregulin-like factor - used to develop products for
PT the diagnosis and treatment of disorders involving regulation of
PT cell growth, particularly cancers
XX Disclosure; Page 97-99; 118pp; English.
XX This sequence is the human heregulin-like factor (HLF) of the
CC invention. The HLF is involved in the regulation of cell growth.
CC Detection of different levels of expression of the HLF gene can be used
CC for the diagnosis of disorders, e.g. in the neural system. In
CC particular, detection of different levels of HLF gene expression in cells
CC or body fluid of an individual can be used for diagnosing cancer. The
CC products can also be used in the treatment of disorders involving
CC abnormal levels of HLF activity.
XX Sequence 720 AA;
SQ
Query Match 23.6%; Score 56; DB 20; Length 720;
Best Local Similarity 41.2%; Pred. No. 15;
Matches 14; Conservative 2; Mismatches 14; Indels 4; Gaps 1;
QY 6 LWCVR-----KYKSGFSCAGRYSENISROTSET 35
||||| ||||| ||| :||
Db 542 lwcverpldkyssgiktdrntsinmqlpsret 575
RESULT 7
W97618
ID W97618 standard; Protein; 720 AA.
XX AC W97618;
XX 10-MAY-1999 (first entry)
XX Human heregulin related ligand NRG3.
DE Neuroregulin related ligand; NRG3; hNRG3B1; human; ErbB4 receptor;
XX signal transduction; nervous system disorder; neurodegeneration;
KW neuropathy; therapy; diagnosis.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH 1..360
FT Domain
FT /note= "extracellular domain, specifically claimed"

FT Region 66..91 in Claim 5(a)"
FT /note= "hydrophobic region"
FT 101..284
FT /note= "mucin-like Ser/Thr-rich region, contains
FT sites for O-linked glycosylation"
FT 285..354
FT /note= "EGF-like domain"
FT 356..394
FT /note= "transmembrane domain"
XX WO9902681-A1.
PN 21-JAN-1999.
XX 30-JUN-1998; 98WO-US13411.
XX 24-JUL-1997; 97US-0899437.
XX 09-JUL-1997; 97US-0052019.
XX (GETH) GENENTECH INC.
XX Godowski PJ, Mark MR, Zhang D;
XX WPI; 1999-120882/10.
XX N-PSDB; X06988.
XX New isolated heregulin related ligand-3 - used to develop products
PT for treating nervous system disorders, e.g. stroke, ischaemia,
PT infection, malignancy, Alzheimer's disease or Down's syndrome
XX Claim 5(b); Page 66-69; 101pp; English.
XX This is the amino acid sequence of human heregulin related ligand
CC NRG3, a novel member of the epidermal growth factor (EGF)-like
CC family of protein ligands that binds to the ErbB4 receptor, but not
CC to the ErbB2 or ErbB3 receptor, and which activates ErbB4 receptor
CC tyrosine phosphorylation. The sequence was deduced from the
CC nucleotide sequence of a cDNA clone (see X06988) from a foetal brain
CC library. The EGF-like domain of NRG3 is distinct from those of NRG1
CC or NRG2, and NRG3 displays receptor binding characteristics that are
CC distinct from those of other heregulins. An alternatively spliced
CC form of human NRG3 is provided in W97619. The invention provides
CC human and murine NRG3 polypeptides (see also W97617), expression
CC vectors, host cells and methods for the recombinant production of
CC NRG3s. The NRG3 polypeptides and polynucleotides and can be used to
CC enhance the survival, proliferation or differentiation of cells
CC having the ErbB4 receptor in vivo and in vitro. They can be used to
CC prevent or treat damage to a nerve or damage to other NRG3-expressing
CC or NRG3-responsive cells, e.g. brain, heart, or kidney cells. In
CC particular, they can be used to treat diseases which involve neural
CC cell growth such as demyelination, or damage or loss of glial cells
CC (e.g. multiple sclerosis). They can be used to treat patients whose
CC nervous system has been damaged by e.g. trauma, surgery, stroke,
CC ischaemia, infection, metabolic disease, nutritional deficiency,
CC malignancy, or toxic agents. NRG3 can also be used to treat
CC motor neuron disorders such as amyotrophic lateral sclerosis (Lou
CC Gehrig's disease), Bell's palsy, conditions involving spinal
CC muscular atrophy or paralysis, neurodegenerative disorders such as
CC Alzheimer's disease, Parkinson's disease, epilepsy, multiple
CC sclerosis, Huntington's chorea, Down's syndrome, nerve deafness,
CC and Meniere's disease. They can also be used to treat neuropathies
CC associated with systemic disease including post-polio syndrome,
CC hereditary neuropathies including Charcot-Marie-Tooth disease,
CC Refsum's disease, abetalipoproteinemia, Tangier disease, Krabbe's
CC disease, metachromatic leukodystrophy, Fabry's disease and
CC Dejerine-Sottas syndrome, to treat disease of skeletal muscle of
CC smooth muscle, such as muscular dystrophy or diseases caused by
CC skeletal or smooth muscle wasting. The products can also be used
CC for detection, diagnosis, for the production of transgenic or
CC knockout animals or for drug screening.
XX Sequence 720 AA;
SQ

Query Match 23.6%; Score 56; DB 20; Length 720;
 Best Local Similarity 41.2%; Pred. No. 15;
 Matches 14; Conservative 2; Mismatches 14; Indels 4; Gaps 1;

QY 6 LWCVR-----KYKSGFSCAGRYSENISROTSET 35
 ||||| ||||| :|||
 Db 542 lwcverpidlkysgsglktgrntsinmqlpsret 575

RESULT 8

B27319
 ID B27319 standard; Protein; 166 AA.

XX AC B27319;

DT 25-JAN-2001 (first entry)

DE B. napus NIM1 homologue SEQ ID NO: 52.

XX Systemic acquired resistance; SAR; signal transduction cascade;
 KW disease resistance; tobacco; tomato; canola; sunflower; sugarbeet;
 KW potato.

XX Brassica napus.

XX WO200053762-A2.

XX 14-SEP-2000.

XX 07-MAR-2000; 2000WO-EP01978.

XX 09-MAR-1999; 99US-0265149.

XX (NOVS) NOVARTIS AG.

PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

XX Salmeron JM, Weislo LJ, Willits MG, Mengiste T;

XX WPI: 2000-594322/56.

XX N-PSDB; A97222.

XX Novel plant genes for enhancing systemic acquired resistance gene
 PT expression and broad spectrum disease resistance in plants, are
 PT homologues of Arabidopsis NIM1 gene -

XX Claim 1; Page 120-121; 152pp; English.

XX The present invention is concerned with the isolation of NIM1 homologues
 CC and their coding sequences from Arabidopsis thaliana, Brassica napus,
 CC Nicotiana tabacum, Lycopersicon esculentum, Beta vulgaris, Helianthus
 CC annuus and Solanum tuberosum. NIM1 is one of the proteins involved in the
 CC signal transduction cascade leading to systemic acquired resistance (SAR)
 CC in plants. This gives the plants an increased resistance to disease. The
 CC protein and gene can be used to produce transgenic plants resistant to
 CC diseases caused by viruses, such as tobacco or cucumber mosaic virus,
 CC ringspot virus, pelargonium leaf curl virus, red clover mottle virus,
 CC tomato bushy stunt virus, fungi, including Phytophthora parasitica and
 CC Peronospora tabacina, bacteria such as Pseudomonas syringae and P.
 CC tabaci, insects, including aphids and lepidoptera and nematodes such as
 CC Meloidogyne incognita. In particular they can be used against disease
 CC organisms of maize.

XX Sequence 166 AA;

Query Match 23.2%; Score 55; DB 21; Length 166;
 Best Local Similarity 37.9%; Pred. No. 3.5;
 Matches 11; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 9 VRRKYKSGFSCAGRYSENISROTSETAD 37
 :|||:|||||:|||||:

Db 77 lkranasgftodgrsavnlicrrlrltppkd 105

RESULT 9

Y77450
 ID Y77450 standard; Protein; 461 AA.

XX AC Y77450;

XX 22-MAY-2000 (first entry)

DE Leptospira kirschneri outer membrane protein, LipL46.

XX Outer membrane protein; LipL46; leptospirosis; pathogenic spirochete;
 KW diagnosis; detection; drug screening; recombinant protein; antibody;
 KW antibacterial; vaccine.

XX Leptospira kirschneri serovar. grippotyphosa.

XX WO200005240-A1.

XX 03-FEB-2000.

XX 22-JUL-1999; 99WO-US16627.

XX 23-JUL-1998; 98US-0122210.

XX (REGC) UNIV CALIFORNIA.

XX Haake D;

XX WPI: 2000-195094/17.

XX N-PSDB; Z90316.

XX Novel Leptospira outer membrane lipoprotein, used in vaccines against
 PT spirochete infection and to raise diagnostic antibodies -

XX Claim 1; Fig 1A-C; 57pp; English.

XX This sequence represents an approximately 46 kD outer membrane
 CC protein, LipL46, from Leptospira kirschneri, serovar grippotyphosa,
 CC strain RM52. LipL46 proteins are immunogenic and are associated
 CC with pathogenic strains of Leptospira. Such strains frequently
 CC cause the zoonotic disease leptospirosis, and are capable of infecting
 CC most mammalian species, including humans. In livestock, leptospirosis
 CC causes economic losses due to death, abortion, stillbirth and decreased
 CC milk production. LipL46 proteins may be used in the diagnostic detection
 CC of antibodies against LipL46, for the generation of anti-LipL46
 CC antibodies, in screening for specific binding agents (potential
 CC therapeutic agents), and in vaccines to generate a protective immune
 CC response against spirochetes (specifically Treponema, Borrelia or
 CC Leptospira) in humans or animals. Nucleic acids encoding LipL46 may be
 CC used for recombinant production of the protein and as a source of
 CC diagnostic probes and primers. LipL46 antibodies are used for diagnosing
 CC and monitoring leptospiral infections in immunoassays, including in
 CC vivo imaging, and may also be used for immunotherapy of spirochete
 CC infections, optionally coupled to therapeutic agents.

XX Sequence 461 AA;

Query Match 23.2%; Score 55; DB 21; Length 461;
 Best Local Similarity 31.9%; Pred. No. 12;
 Matches 15; Conservative 6; Mismatches 16; Indels 10; Gaps 1;

QY 9 VRRKYKSGFSCAGRYSENISROTSETADNDNASSET 45
 :|||:|||||:|||||:

Db 267 iahkyptsoggtastdphgfemdgthsggtasatsatnkvlsnft 313

RESULT 10

B27320

ID B27320 standard; Protein; 166 AA.


```

PD 25-FEB-1999.
XX
XX 20-AUG-1998; 98WO-US17272.
XX
XX 20-AUG-1997; 97US-0914999.
XX
XX (UYNE-) UNIV NEW JERSEY.
XX
XX Hait WN, Pavur KS, Ryazanov AG;
XX
XX WPI; 1999-181050/15.
XX
XX N-PSDB; X24907.
XX
XX New isolated protein kinase, eEF-2 - used to develop agents for
XX controlling the amount, or activity of protein kinases, e.g. for
XX treating cancers or other hyperproliferative pathologies
XX
XX Claim 6; Page 128-130; 195pp; English.
XX
XX This protein is Caenorhabditis elegans elongation factor-2 kinase
XX (eEF-2 kinase), a member of a new superfamily of eukaryotic protein
XX kinases that phosphorylate within an alpha-helical domain of a
XX target protein, as opposed to beta-turns as seen in all other
XX protein kinases. eEF-2 kinase is a ubiquitous enzyme involved in
XX the regulation of protein synthesis and the cell cycle. It has no
XX homolog to any other mammalian protein kinase, and is therefore an
XX ideal target in the search for a specific protein kinase inhibitor.
XX Since preliminary evidence suggests that human eEF-2 kinase (see
XX W98106) is upregulated in human cancers, including breast cancer,
XX identification of specific inhibitors of eEF-2 kinase may lead to
XX the development of novel anticancer drugs. Assays have been
XX developed utilising eEF-2 kinase and a phosphorylation target
XX (see W98109) to facilitate high-throughput screening for compounds
XX that can specifically inhibit eEF-2 kinase. Methods of assessing
XX eEF-2 kinase levels for diagnostic purposes, and therapeutic
XX formulations to inhibit eEF-2 kinase activity are also disclosed.
XX Sequences complementary to eEF-2 kinase may have therapeutic
XX efficacy as antisense drugs or be used in gene therapy. A
XX ribozyme that cleaves eEF-2 kinase mRNA is also claimed.
XX
XX Sequence 768 AA;

Query Match 21.7%; Score 51.5; DB 20; Length 768;
Best Local Similarity 40.0%; Pred. No. 72;
Matches 14; Conservative 7; Mismatches 13; Indels 1; Gaps 1;

Qy 5 DLWCVRKRYKSSGFSACGRVSENISROTSETADND 39
|| :||: | | | | | | | | | | :
Db 451 dlnslrqhdsfr-ssvgtysmnsrqrtdtekd 484

RESULT 15
Y28848
ID Y28848 standard; protein; 81 AA.
XX
XX Y28848;
XX
XX 17-JAN-2000 (first entry)
XX
XX Maize basal endosperm transfer cell layer specific protein-3.
XX
XX Maize basal endosperm transfer cell layer-3; BETL-3 specific protein;
XX defensin-like protein; proteinase inhibitor; endosperm; disulphide bond;
XX grain development; hydrophobic region; glycosylation site; herbicide;
XX growth regulator; pesticide; transgenic plant; solute partitioning;
XX disease resistance; endosperm-derived product; cotton quality;
XX aromatic oil.
XX
XX Zea mays.
XX
XX WO9950427-A2.
XX

```

```

PD 07-OCT-1999.
XX
XX 26-MAR-1999; 99WO-EP02063.
XX
XX 27-MAR-1998; 98EP-0105628.
XX
XX (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
XX Thompson RD, Yan G, Salamini F, Hueros G;
XX
XX WPI; 1999-610858/52.
XX
XX N-PSDB; X90966.
XX
XX New nucleic acid encoding three basal endosperm transfer cell layer
XX proteins, used to produce transgenic plants with e.g. increased disease
XX resistance and to identify specific modulators
XX
XX Claim 1; Page 66; 76pp; English.
XX
XX The present sequence is maize basal endosperm transfer cell layer-3
XX specific protein. This shows some homology to defensin-like proteins and
XX proteinase inhibitors. The basal region of endosperm is highly
XX specialised to facilitate uptake of solutes during grain development.
XX Transgenic plants having altered levels of BETL protein expression are
XX used to modify solute partitioning in the endosperm; to confer or improve
XX disease resistance; to improve endosperm-derived products and to express
XX enzymes that modify quality of cotton or aromatic oils. They are
XX potentially useful as growth regulators, herbicides and pesticides.
XX
XX Sequence 81 AA;

Query Match 21.5%; Score 51; DB 20; Length 81;
Best Local Similarity 50.0%; Pred. No. 5.5;
Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 6 LWCVRKRYKSSGFSACAGR 23
| | : | | : | | |
Db 58 lgcihrgykgtsycrgr 75

Search completed: May 23, 2001, 15:28:35
Job time: 412 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:30:09 ; Search time 95.91 Seconds
(without alignments)
9.014 Million cell updates/sec

Title: US-08-887-977-10_COPY_320_364

Perfect score: 237

Sequence: 1 KILKDLWCRVKYKSGFSC.....ENISRQTSVADNDNASSFT 45

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pap.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pap.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pap.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pap.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pap.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	23.6	720	4	US-08-899-437-6
2	55	23.2	461	4	US-09-122-210-2
3	50	21.1	713	4	US-08-899-437-2
4	48.5	20.5	272	4	US-09-029-213B-27
5	48.5	20.5	3177	2	US-08-477-451-4
6	48	20.3	2182	2	US-08-487-826B-16
7	48	20.3	3169	2	US-08-477-451-6
8	47.5	20.0	491	1	US-08-206-176-4
9	47	19.8	345	3	US-08-718-738-2
10	47	19.8	345	5	PCT-US95-03323A-2
11	47	19.8	356	1	US-08-228-162-2
12	47	19.8	860	1	US-08-092-817-4
13	47	19.8	1074	2	US-08-470-058-2
14	47	19.8	1074	3	US-09-037-188-2
15	47	19.8	1410	2	US-08-470-058-4
16	47	19.8	1410	3	US-09-037-188-4
17	46.5	19.6	413	3	US-08-390-333A-7
18	46.5	19.6	426	3	US-08-390-333A-1
19	46	19.4	379	1	US-07-723-002C-4
20	46	19.4	2205	1	US-08-093-453B-2
21	45	19.0	323	3	US-09-041-889-28
22	45	19.0	377	3	US-09-041-889-29
23	45	19.0	541	2	US-08-540-804-16
24	45	19.0	541	2	US-08-218-265-16
25	45	19.0	541	3	US-08-521-872-16
26	44.5	18.8	501	1	US-08-331-394-4
27	44.5	18.8	501	1	US-08-250-858-4

28	44.5	18.8	501	1	US-08-446-915-4
29	44.5	18.8	501	2	US-08-744-139-4
30	44.5	18.8	501	5	PCT-US95-06639-4
31	44.5	18.8	1702	5	PCT-US95-10661A-5
32	44.5	18.8	1848	5	PCT-US95-10661A-6
33	44	18.6	117	1	US-08-274-661B-39
34	44	18.6	119	1	US-08-340-539A-17
35	44	18.6	410	1	US-08-471-033-40
36	44	18.6	410	1	US-08-471-033-43
37	44	18.6	410	2	US-08-471-044-40
38	44	18.6	410	2	US-08-471-044-43
39	44	18.6	410	2	US-08-463-483A-40
40	44	18.6	410	2	US-08-463-483A-43
41	44	18.6	410	2	US-08-471-046A-40
42	44	18.6	410	2	US-08-471-046A-43
43	44	18.6	410	2	US-08-470-566B-40
44	44	18.6	410	2	US-08-470-566B-43
45	44	18.6	410	2	US-08-469-334-40

ALIGNMENTS

RESULT 1

US-08-899-437-6
; Sequence 6, Application US/08899437
; Patent No. 6121415

; GENERAL INFORMATION:

; APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
; TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/899,437

; FILING DATE: 24-Jul-1997

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Conley, Deirdre L.

; REGISTRATION NUMBER: 36,487

; REFERENCE/DOCKET NUMBER: P1084R1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-2066

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 720 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

; FEATURE:

; NAME/KEY: hNRG3B1 amino acid sequence

; LOCATION: 1-720

; IDENTIFICATION METHOD:

; OTHER INFORMATION:

US-08-899-437-6

Query Match 23.6%; Score 56; DB 4; Length 720;
Best Local Similarity 41.2%; Pred. No. 9.7;
Matches 14; Conservative 2; Mismatches 14; Indels 4; Gaps 1;

QY 6 LMCVRR----KYKSSGFSCAGRYSENISRQTSSET 35


```

; REFERENCE/DOCKET NUMBER: NIH121.001CPI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2182 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; US-08-487-826B-16

Query Match 20.3%; Score 48; DB 2; Length 2182;
Best Local Similarity 37.5%; Pred. No. 4.5e+02;
Matches 12; Conservative 3; Mismatches 9; Indels 8; Gaps 1;

QY 2 ILKDLWCVRKRYKSGFSCAGRYSENISROPTS 33
|||:||||:|||||
Db 1102 IAKDIW-----NAMVCALTYKENDARGTS 1125

RESULT 7
US-08-477-451-6
; Sequence 6, Application US/08477451
; Patent No. 5928865
; GENERAL INFORMATION:
; APPLICANT: Covacci, Antonello
; TITLE OF INVENTION: Helicobacter Pylori Cagi Region
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,451
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McClung, Barbara G.
; REGISTRATION NUMBER: 33,113
; REFERENCE/DOCKET NUMBER: 0335.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-601-2708
; TELEFAX: 510-655-3542
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3169 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-477-451-6

Query Match 20.3%; Score 48; DB 2; Length 3169;
Best Local Similarity 37.1%; Pred. No. 6.9e+02;
Matches 13; Conservative 7; Mismatches 13; Indels 2; Gaps 1;

QY 3 LKDLWCVRKRYKSGF--SCAGRYSENISROTSET 35
|||:|||||:||||:|||||

```


; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
PCT-US95-03323A-2

Query Match 19.8%; Score 47; DB 5; Length 345;
Best Local Similarity 31.4%; Pred. No. 71;
Matches 11; Conservative 5; Mismatches 17; Indels 2; Gaps 1;

QY 7 WCVRRYKSSGFSC--AGRYSENISROTSETADND 39
| : ||||| : | : : | : : |
Db 44 WPEKPKSGFGRCHIGEXVDPVIEQASKESGLD 78

RESULT 11
US-08-228-162-2
; Sequence 2, Application US/08228162
; Patent No. 5521071
; GENERAL INFORMATION:
; APPLICANT: Attie, Alan D
; APPLICANT: Sturley, Stephen L
; APPLICANT: Gretch, Daniel G
; TITLE OF INVENTION: Soluble LDL Receptor and Gene
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nicholas J. Seay, Quarles & Brady
; STREET: P.O. Box 2113
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/228,162
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/925,403
; FILING DATE: 03-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J
; REGISTRATION NUMBER: 27,386
; REFERENCE/DOCKET NUMBER: 9629692026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608)251-5000
; TELEFAX: (608)251-9166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 356 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-228-162-2

Query Match 19.8%; Score 47; DB 1; Length 356;
Best Local Similarity 35.1%; Pred. No. 74;
Matches 13; Conservative 4; Mismatches 18; Indels 2; Gaps 1;

QY 8 CVRRYKSSGFSCAGRYSENISR--QTSETADNDNAS 42
| : ||||| : | : : | : : |
Db 63 CLSVTKSGDFSCGGRVNRCPQFWRCDGQVDCDNGS 99

RESULT 12
US-08-092-817-4
; Sequence 4, Application US/08092817
; Patent No. 5496926
; GENERAL INFORMATION:

; APPLICANT: RUBINSTEIN, Menachem
; APPLICANT: NOVICK, Daniela
; APPLICANT: TAL, Nathan
; TITLE OF INVENTION: SOLUBLE LDL RECEPTOR, ITS PRODUCTION AND
; TITLE OF INVENTION: USE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/092,817
; FILING DATE: 19-JUL-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 100696
; FILING DATE: 19-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 102915
; FILING DATE: 23-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: TOWNSEND, G. Kevin
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: RUBINSTEIN-5A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 860 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-092-817-4

Query Match 19.8%; Score 47; DB 1; Length 860;
Best Local Similarity 35.1%; Pred. No. 2.1e+02;
Matches 13; Conservative 4; Mismatches 18; Indels 2; Gaps 1;

QY 8 CVRRYKSSGFSCAGRYSENISR--QTSETADNDNAS 42
| : ||||| : | : : | : : |
Db 63 CLSVTKSGDFSCGGRVNRCPQFWRCDGQVDCDNGS 99

RESULT 13
US-08-470-058-2
; Sequence 2, Application US/08470058
; Patent No. 5817789
; GENERAL INFORMATION:
; APPLICANT: Heartlein, Michael W.
; APPLICANT: Lemontt, Jeffrey F.
; TITLE OF INVENTION: Chimeric Proteins For Use in Transport
; TITLE OF INVENTION: of a Selected Substance Into Cells
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Milltia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/470,058
;; FILING DATE: 06-JUN-1995
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Granahan, Patricia
;; REGISTRATION NUMBER: 32,227
;; REFERENCE/DOCKET NUMBER: TKT93-01
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-861-6240
;; TELEFAX: 617-861-9540
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1074 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
US-08-470-058-2

Query Match 19.8%; Score 47; DB 2; Length 1074;
Best Local Similarity 35.1%; Pred. No. 2.7e+02;
Matches 13; Conservative 4; Mismatches 18; Indels 2; Gaps 1;

QY 8 CVRRKYSKSGFSCAGRYSENISR--QTSETADNDNAS 42
I: || ||| || : : : |||
Db 63 CLSVTCKSGDFSCGGRVNRNCIPQFWRCDGQVDCDNGS 99

RESULT 14
US-09-037-188-2
;; Sequence 2, Application US/09037188
;; Patent No. 6027921
;; GENERAL INFORMATION:
;; APPLICANT: Heartlein, Michael W.
;; APPLICANT: Lemontt, Jeffrey F.
;; APPLICANT: Concino, Michael F.
;; TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
;; IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
;; NUMBER OF SEQUENCES: 12
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fish & Richardson P.C.
;; STREET: 225 Franklin Street
;; CITY: Boston
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02110-2804
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: Windows95
;; SOFTWARE: FASTSEQ for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/037,188
;; FILING DATE: 02-MAR-1998
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE: 06-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Fraser, Ph.D., J.D., Janis K.
;; REGISTRATION NUMBER: 34,819
;; REFERENCE/DOCKET NUMBER: 07236/009002
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617/542-5070
;; TELEFAX: 617/542-8906
;; TELEX: 200154
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1074 amino acids

;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
US-09-037-188-2

Query Match 19.8%; Score 47; DB 3; Length 1074;
Best Local Similarity 35.1%; Pred. No. 2.7e+02;
Matches 13; Conservative 4; Mismatches 18; Indels 2; Gaps 1;

QY 8 CVRRKYSKSGFSCAGRYSENISR--QTSETADNDNAS 42
I: || ||| || : : : |||
Db 63 CLSVTCKSGDFSCGGRVNRNCIPQFWRCDGQVDCDNGS 99

RESULT 15
US-08-470-058-4
;; Sequence 4, Application US/08470058
;; Patent No. 5817789
;; GENERAL INFORMATION:
;; APPLICANT: Heartlein, Michael W.
;; APPLICANT: Lemontt, Jeffrey F.
;; TITLE OF INVENTION: Chimeric Proteins For Use in Transport
;; OF a Selected Substance Into Cells
;; NUMBER OF SEQUENCES: 12
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
;; STREET: Two Militia Drive
;; CITY: Lexington
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02173
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/470,058
;; FILING DATE: 06-JUN-1995
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Granahan, Patricia
;; REGISTRATION NUMBER: 32,227
;; REFERENCE/DOCKET NUMBER: TKT93-01
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-861-6240
;; TELEFAX: 617-861-9540
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1410 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
US-08-470-058-4

Query Match 19.8%; Score 47; DB 2; Length 1410;
Best Local Similarity 35.1%; Pred. No. 3.7e+02;
Matches 13; Conservative 4; Mismatches 18; Indels 2; Gaps 1;

QY 8 CVRRKYSKSGFSCAGRYSENISR--QTSETADNDNAS 42
I: || ||| || : : : |||
Db 63 CLSVTCKSGDFSCGGRVNRNCIPQFWRCDGQVDCDNGS 99

Search completed: May 23, 2001, 15:30:10
Job time: 417 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 23, 2001, 15:32:03 ; Search time 110.15 Seconds
(without alignments)
28.076 Million cell updates/sec

Title: US-08-887-977-10_COPY_320_364

Perfect score: 237

Sequence: 1 KILKDLWCVRKRYKSGFSC.....ENISQTSADNDNASFT 45

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_67:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	237	100.0	369	JC5068	G protein-coupled
2	64	27.0	1025	T10259	RNA-directed DNA p
3	63	26.6	245	T41291	conserved hypothet
4	59	24.9	515	T45644	hypothetical prote
5	57.5	24.3	959	S61155	hypothetical prote
6	56	23.6	1237	GNFF42	retrovirus-related
7	56	23.6	1500	A42210	alpha-1-macroglobu
8	54.5	23.0	1459	T24088	hypothetical prote
9	54	22.8	409	A47527	transcription fact
10	54	22.8	1671	S71628	sensory transducti
11	53.5	22.6	978	T16948	hypothetical prote
12	53	22.4	412	XNCHDC	aspartate transami
13	52.5	22.2	933	T33621	hypothetical prote
14	52.5	22.2	957	T10633	hypothetical prote
15	52	21.9	160	A82733	conserved hypothet
16	52	21.9	355	T29251	hypothetical prote
17	52	21.9	369	S70847	outer membrane por
18	52	21.9	791	T41573	hypothetical prote
19	51.5	21.7	127	D82479	hypothetical prote
20	51.5	21.7	383	T37171	hypothetical prote
21	51.5	21.7	2222	A36028	DNA-directed DNA p
22	51	21.5	152	T41310	hypothetical prote
23	51	21.5	173	C71484	hypothetical prote
24	51	21.5	1188	T05324	hypothetical prote
25	50.5	21.3	614	T47749	hypothetical prote
26	50.5	21.3	1135	T30561	Scythe protein - A
27	50.5	21.3	1392	T01908	hypothetical prote
28	50.5	21.3	1515	T04204	hypothetical prote
29	50	21.1	142	T41313	hypothetical prote

30 50 21.1 152 2 I41311
31 50 21.1 152 2 I41312
32 50 21.1 210 2 T21120
33 50 21.1 713 2 T44447
34 49.5 20.9 479 2 T01922
35 49.5 20.9 730 2 T46074
36 49.5 20.9 1040 2 T08190
37 49 20.7 129 1 L2OVE
38 49 20.7 178 2 S74871
39 49 20.7 257 2 T31609
40 49 20.7 262 2 T02115
41 49 20.7 711 2 T30107
42 49 20.7 746 2 S62365
43 49 20.7 786 2 T18469
44 49 20.7 1414 2 T33236
45 48.5 20.5 351 1 JSBYPI

hypothetical prote
hypothetical prote
hypothetical prote
neuregulin-3 limpo
hypothetical prote
hypothetical prote
lysozyme (EC 3.2.1
transposase slr124
hypothetical prote
hypothetical prote
SNF1-related prote
hypothetical prote
hypothetical prote
centromere-binding

ALIGNMENTS

RESULT 1

JC5068

G protein-coupled receptor CKR-L3 - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000

C:Accession: JC5068

R:Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.

Biochem. Biophys. Res. Commun. 227, 846-853, 1996

A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-like

A:Reference number: JC5067; MUID:97040707

A:Accession: JC5068

A:Molecule type: DNA

A:Residues: 1-369 <ZAB>

A:Cross-references: EMBL:Z79784; NID:gl668737; PIDN:CAB02144.1; PID:gl668738

C:Comment: This protein belongs to the family of alpha chemokine receptors.

C:Genetics:

A:Gene: GDB:CMKBR6; STRL22; GPR29; CCR6; CKR-L3; GPR-CY4

A:Cross-references: GDB:5370639; OMIM:601835

A:Map position: 6q27-6q27

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

F:42-68/Domain: transmembrane #status predicted <TM1>

F:79-99/Domain: transmembrane #status predicted <TM2>

F:115-136/Domain: transmembrane #status predicted <TM3>

F:160-180/Domain: transmembrane #status predicted <TM4>

F:212-233/Domain: transmembrane #status predicted <TM5>

F:250-271/Domain: transmembrane #status predicted <TM6>

F:292-315/Domain: transmembrane #status predicted <TM7>

Query Match 100.0%; Score 237; DB 2; Length 369;

Best Local Similarity 100.0%; Pred. No. 1.1e-23;

Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KILKDLWCVRKRYKSGSCAGRYSENISRQTSADNDNASFT 45

Db 324 KILKDLWCVRKRYKSGSCAGRYSENISRQTSADNDNASFT 368

RESULT 2

T10259

RNA-directed DNA polymerase (EC 2.7.7.49) - pteromalid wasp (Nasonia vitripennis) ret

C:Species: Nasonia vitripennis

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000

C:Accession: T10259; I44490

R:Burke, W.D.; Malik, H.S.; Lathe III, W.C.; Eickbush, T.H.

Nature 392, 141-142, 1998

A:Title: Are retrotransposons long-term hitchhikers?

A:Reference number: Z17001; MUID:98175715

A:Accession: T10259

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1025 <BUR>
A:Cross-references: EMBL:L00950; NID:g3559783; PIDN:AAC34927.1; PID:g2317818
R:Burke, W.D.; Eickbush, D.G.; Xiong, Y.; Jakubczak, J.; Eickbush, T.H.
Mol. Biol. Evol. 10, 163-185, 1993
A:Title: Sequence relationship of retrotransposable elements R1 and R2 within and between
A:Reference number: A4490; MUID:93196484
A:Contents: retrotransposable element R2
A:Accession: T44490
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 314-956, 'Q', 'A', '971', 'AA' <BU2>
A:Note: sequence extracted from NCBI backbone (NCBIP:127243)
C:Genetics:
A:Mobile element: retrotransposon R2
C:Keywords: nucleotidyltransferase

Query Match 27.08; Score 64; DB 2; Length 1025;
Best Local Similarity 43.98; Pred. No. 2.3;
Matches 18; Conservative 6; Mismatches 11; Indels 6; Gaps 2;

Qy 8 CVRR--KYKSGFSCAGRYSENISROTSETADNDNAS 42
Db 125 CLRQKQKKTTRVARRNRAENRETELRLTETADDPAS 165

RESULT 3
T41291
conserved hypothetical protein SPCC31H12.03c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T41291
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.
submitted to the EMBL Data Library, September 1998
A:Reference number: Z21985
A:Accession: T41291
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-245 <WOO>
A:Cross-references: EMBL:AL031824; PIDN:CAA21220.1; GSPDB:GNO00068; SPDB:SPCC31H12.03c
A:Experimental source: strain 972h-; cosmid c31H12
C:Genetics:
A:Gene: SPDB:SPCC31H12.03c
A:Map position: 3

Query Match 26.68; Score 63; DB 2; Length 245;
Best Local Similarity 40.08; Pred. No. 0.71;
Matches 14; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 9 VRRYKSGFSCAGRYSENISROTSETADNDNAS 43
Db 12 LREKLAEGSLTAGNKAEVLSRLTAATESNDENTS 46

RESULT 4
T45644
hypothetical protein Fl3112.130 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C:Accession: T45644
R:Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sa
submitted to the Protein Sequence Database, November 1999
A:Reference number: Z23010
A:Accession: T45644
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-515 <CHO>
A:Cross-references: EMBL:AL133292
A:Experimental source: cultivar Columbia; BAC clone Fl3112
C:Genetics:
A:Map position: 3
A:Introns: 434/2

A:Note: FL3112.130

Query Match 24.9%; Score 59; DB 2; Length 515;
Best Local Similarity 35.9%; Pred. No. 5.1;
Matches 14; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

Qy 5 DLWCVRKRYKSGFSCAGRYSENISROTSETADNDNAS 43
Db 112 EAFSVKMQELASQFRNAGDEEEENKQKSEAVDNDNSN 150

RESULT 5
S61155
hypothetical protein YDR359c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein D9476.11
C:Species: Saccharomyces cerevisiae
C:Date: 23-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 29-Oct-1999
C:Accession: S61155
R:Du, Z.
submitted to the EMBL Data Library, June 1995
A:Description: The sequence of S. cerevisiae cosmid 9476.
A:Reference number: S61146
A:Accession: S61155
A:Molecule type: DNA
A:Residues: 1-959 <DUZ>
A:Cross-references: EMBL:U28372; NID:g849170; PID:g849181; GSPDB:GNO0004; MIPS:YDR359
C:Genetics:
A:Gene: MIPS:YDR359c
A:Map position: 4R

Query Match 24.3%; Score 57.5; DB 2; Length 959;
Best Local Similarity 37.5%; Pred. No. 15;
Matches 18; Conservative 7; Mismatches 12; Indels 11; Gaps 3;

Qy 3 LKDLW-----CVRRKY----KSSGFSCAGRYSENISROTSETADNDN 40
Db 391 IKDYWTYGETCCVKRKTLLPGKENKLSDDGRISEK-SGRPSDTSRNS 437

RESULT 6
GNFF42
retrovirus-related pol polyprotein - fruit fly (Drosophila melanogaster) retrotranspo
N:Contains: retropepsin (EC 3.4.23.16)
C:Species: Drosophila melanogaster
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 16-Jun-2000
C:Accession: D29349
R:Yuki, S.; Inouye, S.; Ishimaru, S.; Saigo, K.
Eur. J. Biochem. 158, 403-410, 1986
A:Title: Nucleotide sequence characterization of a Drosophila retrotransposon, 412.
A:Reference number: A91171; MUID:86274717
A:Accession: D29349
A:Molecule type: DNA
A:Residues: 1-1237 <YUK>
A:Cross-references: GB:X04132; GB:X03733; NID:g8500; PIDN:CAA27750.1; PID:g1335652
A:Note: the authors translated the codon CAA for residue 21 as Lys
C:Genetics:
A:Gene: FlyBase:412
A:Cross-references: FlyBase:FBgn0000006
C:Superfamily: pol polyprotein
C:Keywords: aspartic proteinase; hydrolase; polypeptide; reverse transcriptase
F:39-133/Product: retropepsin #status predicted <RTP>
F:63/Active site: Asp (shared with dimeric partner) #status predicted

Query Match 23.6%; Score 56; DB 1; Length 1237;
Best Local Similarity 34.1%; Pred. No. 32;
Matches 15; Conservative 8; Mismatches 17; Indels 4; Gaps 1;

Qy 1 KILKD-----LWCVRKRYKSGFSCAGRYSENISROTSETADNDN 40
Db 738 KELKDITGNILKWTTRFQSRQKSCAGKQLDLQKQKTEASEPN 781

RESULT 9
A47527
transcription factor HNF-3 beta - zebra fish

```

Query Match      22.8%; Score 54; DB 2; Length 1671;
Best Local Similarity 32.1%; Pred. NO. 80;
Matches 17; Conservative 8; Mismatches 18; Indels 10; Gaps 2;

QY   1 KILKDLWCVRKKYS-----SGFCAGRYSENI--SRQTSETADNDNASS 43
    || : ||| ||||
Db   499 KVLVSNFLRROOYKSRATIKPPDPDGICIFEXETENLNLYOOPTSLINDRINS 551

```

RESULT 11


```

Query Match      21.9%; Score 52; DB 2; Length 160;
Best Local Similarity 24.3%; Pred. No. 13;
Matches 9; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 1 KILKDLWCVRKRYKSSGFCAGRYSENISRQTSQETAD 37
   : : | | : : : : : : : : : : : : : : : :
db 81 RLARGCWIIQRPYRGFTFLTPAGKALAAASRCHQIVE 117

```

Search completed: May 23, 2001, 15:32:04
Job time: 511 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:36:21 ; Search time 62.39 seconds
(without alignments)

24.707 Million cell updates/sec

Title: US-08-887-977-10_COPY_320_364

Perfect score: 237

Sequence: 1 KILDKLWCVRRKSSGFSC.....ENISQTSFADNDNASFT 45

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	237	100.0	374	1	CKR6_HUMAN
2	164.5	69.4	367	1	O54689 mus musculus
3	64	27.0	1025	1	P021 NASVI
4	56	23.6	720	1	NRG3_HUMAN
5	56	23.6	1237	1	P0L4 DROME
6	54.5	23.0	1459	1	YFIM CAEEL
7	54	22.8	409	1	AXIA BRARE
8	53.5	22.6	978	1	YSX7 CAEEL
9	53	22.4	411	1	AATC CHICK
10	52	21.9	369	1	OMPF XENNE
11	51.5	21.7	768	1	EF2K CAEEL
12	51.5	21.7	2222	1	DPOE YEAST
13	50	21.1	152	1	T200 SALTY
14	50	21.1	638	1	HS70 CERCA
15	50	21.1	713	1	NRG3 MOUSE
16	49	20.7	129	1	LYC ORTVE
17	49	20.7	835	1	AXN1 BRARE
18	48	20.3	282	1	OMPD SALTY
19	48	20.3	363	1	TOBI MOUSE
20	48	20.3	412	1	AATC MOUSE
21	48	20.3	442	1	UL17 HSV6U
22	48	20.3	826	1	CRAA BACUH
23	48	20.3	893	1	AXN1 RAT
24	48	20.3	992	1	AXN1 MOUSE
25	47.5	20.0	100	1	YD79 METJA
26	47.5	20.0	267	1	KORB ARCFU
27	47.5	20.0	477	1	YEK9 YEAST
28	47.5	20.0	491	1	FIBB HUMAN
29	47.5	20.0	527	1	ESR2 SHEEP
30	47.5	20.0	1018	1	DPOG SCHPO
31	47	19.8	72	1	VF06 VARV
32	47	19.8	233	1	RNS4 ANTHI
33	47	19.8	296	1	CYCG RHOSH

34 47 19.8 345 1 TOB1_HUMAN P50616 homo sapien
35 47 19.8 412 1 AATC_BOVIN P33097 bos taurus
36 47 19.8 412 1 AATC_PIG P00503 sus scrofa
37 47 19.8 616 1 Y396_HELPJ Q92kf3 helicobacte
38 47 19.8 619 1 NBL4_BRARE O57457 brachydanio
39 47 19.8 860 1 LDLR_HUMAN P01130 homo sapien
40 46.5 19.6 415 1 B2AR_MACMU Q28509 macaca mula
41 46.5 19.6 615 1 YG10_METJA Q59005 methanococc
42 46.5 19.6 804 1 CADD_STAAU P37386 staphylococ
43 46.5 19.6 961 1 LIN2_CAEEL P54936 caenorhabdi
44 46.5 19.6 1271 1 BCR_HUMAN P11274 homo sapien
45 46 19.4 95 1 NCCY_ALCXX Q44581 alcaligenes

ALIGNMENTS

RESULT 1
CKR6_HUMAN STANDARD; PRT; 374 AA.
AC CKR6_HUMAN Q92846; P78553;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CCR-6) (LARC
DE RECEPTOR) (GPR-CY4) (GPCY4) (CHEMOKINE RECEPTOR-LIKE 3) (CKR-L3)
DE (DRY6).
GN CCR6 OR CMKBR6 OR STRL22 OR GPR29 OR CKRL3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A., AND FUNCTION.
RX MEDLINE=97313465; PubMed=9169459;
RA Baba M., Imai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K.,
RA Nomiya H., Yoshie O.;
RT Identification of CCR6, the specific receptor for a novel
RT lymphocyte-directed CC chemokine LARC.*;
RL J. Biol. Chem. 272:14893-14898(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Lautens L.L., Modi W., Bonner T.J.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97040707; PubMed=8886020;
RA Zaballous A., Varona R., Gutierrez J., Lind P., Marquez G.;
RT Molecular cloning and RNA expression of two new human chemokine
RT receptor-like genes.*;
RL Biochem. Biophys. Res. Commun. 227:846-853(1996).
RN [4]
RP SEQUENCE FROM N.A.
RA McCoy R., Perlmutter D.H.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=97224503; PubMed=9070937;
RA Liao F., Lee H.-H., Farber J.M.;
RT Cloning of STRL22, a new human gene encoding a G-protein-coupled
RT receptor related to chemokine receptors and located on chromosome
RT 6q27.*;
RL Genomics 40:175-180(1997).
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-
CC ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE
CC INTRACELLULAR CALCIUM IONS LEVELS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: SPLEEN, LYMPH NODES, APPENDIX, AND FETAL
CC LIVER. EXPRESSED IN LYMPHOCYTES, T CELLS AND B CELLS BUT NOT IN
CC NATURAL KILLER CELLS, MONOCYTES, OR GRANULOCYTES.
CC -!- INDUCTION: INTERLEUKIN-2.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-6 IS THE INITIATOR.


```

RESULT 3
PO21_NASVI
ID PO21_NASVI STANDARD; PRT; 1025 AA.
AC Q03278;
DT 01-JUN-1994 (Rel. 29, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE RETROVIRUS-RELATED POL. POLYPROTEIN FROM TYPE I RETROTRANSPOSABLE
DE ELEMENT R2 [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49);
DE ENDONUCLEASE] (FRAGMENT).
OS Nasonia vitripennis (Parasitic wasp).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Chalcidoidea; Pteromalidae; Nasonia.
OX NCBI_TaxID=7425;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93196484; PubMed=8383793;
RA Burke W.D., Eickbush D.G., Xiong Y., Jakubczak J.L., Eickbush T.H.;
RT "Sequence relationship of retrotransposable elements R1 and R2 within
RT and between divergent insect species.";
RL Mol. Biol. Evol. 10:163-185(1993).
RN [2]
RP REVISIONS.
RA Burke W.D., Eickbush D.G., Xiong Y., Jakubczak J.L., Eickbush T.H.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE =
CC N PYROPHOSPHATE + DNA(N).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L00950; AAC34927.1; --
CC FIR: I44490; I44490.
CC InterPro: IPR000477; --
CC Pfam: PF00078; rvt; 1.
CC Pfam: PF00096; zf-C2H2; 1.
CC PROSITE: PS00028; ZINC_FINGER_C2H2_1; 1.
CC PROSITE: PS0157; ZINC_FINGER_C2H2_2; 1.
CC Transferase: RNA-directed DNA polymerase; Transposable element;
KW Hydrolyase; Nuclease; Endonuclease.
FT NON_TER 1 1
FT DOMAIN <1 754 REVERSE TRANSCRIPTASE.
FT DOMAIN 755 1025 NUCLEIC ACID-BINDING ENDONUCLEASE.
FT ZN_FING 46 69 C2H2-TYPE.
FT ZN_FING 1025 AA; 115884 MW; 387BDE63BCF5C518 CRC64;
SQ SEQUENCE 1025 AA; 115884 MW; 387BDE63BCF5C518 CRC64;

Query Match 27.0%; Score 64; DB 1; Length 1025;
Best Local Similarity 43.9%; Pred. No. 1.1;
Matches 18; Conservative 6; Mismatches 11; Indels 6; Gaps 2;

QY 8 CVRR--KYKSGFGSCAGRYSENISROTSET-----ETADNDNAS 42
|:|: |||: | | | | | | | | | | | | | | | |
Db 125 CLAKQKQKYKTIRVARRRNRARETETRLTETADDPAS 165

RESULT 4
NRG3_HUMAN
ID NRG3_HUMAN STANDARD; PRT; 720 AA.
AC P56975;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PRO-NEUREGULIN-3 PRECURSOR (PRO-NRG3) [CONTAINS: NEUREGULIN-3 (NRG-
DE 3)].
CN NRG3.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97420720; PubMed=9275162;
RA Zhang D., Sliwkowski M.X., Mark M., Frantz G., Akita R., Sun Y.,
RA Hillan K., Crowley C., Brush J., Godowski P.J.;
RT "Neuregulin-3 (NRG3): a novel neural tissue-enriched protein that
RT binds and activates ErbB4.";
RT Proc. Natl. Acad. Sci. U.S.A. 94:9562-9567(1997).
CC -1- FUNCTION: DIRECT LIGAND FOR THE ERBB4 TYROSINE KINASE RECEPTOR.
CC BINDING RESULTS IN LIGAND-STIMULATED TYROSINE PHOSPHORYLATION AND
CC ACTIVATION OF THE RECEPTOR. DOES NOT BIND TO THE EGF RECEPTOR,
CC ERBB2 OR ERBB3 RECEPTORS.
CC -1- SUBCELLULAR LOCATION: EXISTS AS AN TYPE I MEMBRANE PROTEIN AND AS
CC A PROTEOLYTICALLY RELEASED SOLUBLE GROWTH FACTOR FORM. THE
CC MEMBRANE-BOUND FORM DOES NOT SEEM TO BE ACTIVE (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN MOST REGIONS OF THE BRAIN
CC WITH THE EXCEPTION OF CORPUS CALLOSUM. EXPRESSED AT LOWER LEVEL IN
CC MUSCLE, KIDNEY, PANCREAS, SPLEEN, THYMUS, PROSTATE, OVARY, SMALL
CC INTESTINE, COLON AND PERIPHERAL BLOOD LEUKOCYTES.
CC -1- DOMAIN: THE CYTOPLASMIC DOMAIN MAY BE INVOLVED IN THE REGULATION
CC OF TRAFFICKING AND PROTEOLYTIC PROCESSING. REGULATION OF THE
CC PROTEOLYTIC PROCESSING INVOLVES INITIAL INTRACELLULAR DOMAIN
CC DIMERIZATION (BY SIMILARITY).
CC -1- DOMAIN: ERBB RECEPTOR BINDING IS ELICITED ENTIRELY BY THE EGF-LIKE
CC DOMAIN (BY SIMILARITY).
CC -1- PTM: PROTEOLYTIC CLEAVAGE CLOSE TO THE PLASMA MEMBRANE ON THE
CC EXTERNAL FACE LEADS TO THE RELEASE OF THE SOLUBLE GROWTH FACTOR
CC FORM (BY SIMILARITY).
CC -1- PTM: EXTENSIVE GLYCOSYLATION PRECEDES THE PROTEOLYTIC CLEAVAGE (BY
CC SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE NEUREGULIN FAMILY.
CC InterPro: IPR000561; --
CC Pfam: PF00008; EGF; 1.
CC PROSITE: PS00022; EGF_1; 1.
CC PROSITE: PS01186; EGF_2; 1.
CC Growth factor; EGF-like domain; Transmembrane; Multigene family.
FT CHAIN 1 720 PRO-NEUREGULIN-3, MEMBRANE-BOUND FORM.
FT CHAIN 1 359 NEUREGULIN-3.
FT DOMAIN 1 360 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 361 381 INTERNAL SIGNAL SEQUENCE (POTENTIAL).
FT DOMAIN 382 720 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 105 285 SER/THR-RICH.
FT DOMAIN 286 329 EGF-LIKE.
FT DOMAIN 5 8 POLY-ALA.
FT DOMAIN 13 21 POLY-ALA.
FT DOMAIN 26 34 POLY-ALA.
FT DOMAIN 127 135 POLY-THR.
FT DOMAIN 252 260 POLY-SER.
FT DOMAIN 262 265 POLY-THR.
FT DISULFID 290 304 BY SIMILARITY.
FT DISULFID 298 317 BY SIMILARITY.
FT DISULFID 319 328 BY SIMILARITY.
SQ SEQUENCE 720 AA; 77900 MW; A4D6F10DD895A693 CRC64;

Query Match 23.6%; Score 56; DB 1; Length 720;
Best Local Similarity 41.2%; Pred. No. 8.7;
Matches 14; Conservative 2; Mismatches 14; Indels 4; Gaps 1;

QY 6 LWCVRR-----KYKSGFGSCAGRYSENISROTSET 35
| | | | | | | | | | | | | | | |
Db 542 LWCVERPLDLKYSYSSGLKTRNTSINQLPSRET 575

RESULT 5
POLA_DROME

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ID POL4_DROME STANDARD; PRT: 1237 AA.
AC P10394;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE RETROVIRUS-RELATED POL POLYPROTEIN FROM TRANSPOSON 412 [CONTAINS:
DE PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49);
DE ENONUCLEASE].
GN POL.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86274717; PubMed=2426108;
RA Yuki S., Inouye S., Ishimaru S., Saigo K.;
RT "Nucleotide sequence characterization of a Drosophila
retrotransposon, 412.";
RL Eur. J. Biochem. 158:403-410(1986).
CC -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY U22.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X04132; CAA27750.1; -
DR PIR; D29349; GNPF42.
DR HSSP; P03366; LHG.
DR FlyBase; FBgn000006; 412.
DR InterPro; IPR000477; -
DR InterPro; IPR001969; -
DR InterPro; IPR001995; -
DR Pfam; PF00077; tvp; 1.
DR Pfam; PF00078; tvt; 1.
DR PROSITE; PS00141; ASP_PROTEASE; 1.
DR PROSITE; PS00175; ASP_PROT_RETROV; 1.
KW Hydrolase; Aspartyl protease; RNA-directed DNA polymerase;
KW Endonuclease; Transferase; Polyprotein; Transposable element.
FT ACT_SITE 63
FT ACT_SITE 63 PROTEASE (BY SIMILARITY).
SQ SEQUENCE 1237 AA; 143041 MW; AC57F1C159D14B65 CRC64;

Query Match 23.6%; Score 56; DB 1; Length 1237;
Best Local Similarity 34.1%; Pred. No. 16;
Matches 15; Conservative 8; Mismatches 17; Indels 4; Gaps 1;

QY 1 KILKD----LNCVRRKYSKSGFCAGRYSENISROTSETADNDN 40
Db 738 KELKDITNLIKVTTFOSQKSCAGKEOLDLQKQTKETIAEPPN 781

RESULT 6
VF1M_CAEEL
ID VF1M_CAEEL STANDARD; PRT: 1459 AA.
AC Q21874;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE HYPOTHETICAL 166.0 KDA PROTEIN R09E10.5 IN CHROMOSOME IV.
GN R09E10.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;

Matthews L.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: STRONG, TO C.ELEGANS F54D1.6.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z70287; CAA94300.1; -
DR WormPep; R09E10.5; CE06287.
KW Hypothetical protein; Transmembrane.
SQ SEQUENCE 1459 AA; 165994 MW; 769014C5599513C4 CRC64;

Query Match 23.0%; Score 54.5; DB 1; Length 1459;
Best Local Similarity 40.6%; Pred. No. 30;
Matches 13; Conservative 4; Mismatches 12; Indels 3; Gaps 2;

QY 7 WCVRRK--YKSSGFCAGRYSEN-ISROTSET 35
Db 1370 WCIRKKLQESRNYSGTAAYSNNAFQNTYET 1401

RESULT 7
AXIA_BRARE
ID AXIA_BRARE STANDARD; PRT: 409 AA.
AC Q07342;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE AXIAL PROTEIN.
GN AXIAL.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=93321871; PubMed=7687227;
RA Straehle U., Blader P., Henrique D., Ingham P.W.;
RT "Axial, a zebrafish gene expressed along the developing body axis,
RT shows altered expression in cyclops mutant embryos.";
RL Genes Dev. 7:1436-1446(1993).
CC -!- FUNCTION: MAY PLAY A CRUCIAL ROLE IN SPECIFICATION OF BOTH THE
CC AXIAL MESENODERM AND THE VENTRAL NERVOUS SYSTEM.
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED JUST BEFORE GASTRULATION IN A
CC NARROW REGION ON THE DORSAL SIDE OF THE EMBRYO. EXPRESSION CAN BE
CC DETECTED IN THE INVOLUTED CELLS COMPRISING THE MESENODERM OF THE
CC DEVELOPING AXIS. AT THE END OF GASTRULATION EXPRESSION IS TURNED
CC ON IN THE VENTRAL NEURAL PLATE IN CELLS ADJACENT TO THE AXIAL-
CC EXPRESSING MESENODERMAL CELLS.
CC -!- INDUCTION: BY MESENODERM-INDUCING FACTOR ACTIVIN A.
CC -!- SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z22762; CAA80443.1; -
DR ZFIN; ZDB-GENE-980526-404; axial.
DR InterPro; IPR001766; -
DR Pfam; PF00250; Fork_head; 1.

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DR PRINTS; PR00053; FORKHEAD.
DR DR PROSITE; PS00657; FORK_HEAD_1; 1.
DR DR PROSITE; PS00658; FORK_HEAD_2; 1.
DR DR PROSITE; PS00039; FORK_HEAD_3; 1.
KW DNA-binding; Developmental protein; Nuclear protein.
FT DNA_BIND 150 241
SQ SEQUENCE 409 AA; 45075 MW; 3ABB5B1D7B37071A CRC64;

Query Match      22.8%; Score 54; DB 1; Length 409;
Best Local Similarity 36.1%; Pred. No. 8.6;
Matches 13; Conservative 7; Mismatches 14; Indels 2; Gaps 1;

QY 8 CVRRKYSKGFSCAGRYSENISROTSETADNDNASS 43
   | | | | | | | | | | | | | | | | | | |
DB 239 CYLRQKR--FKCDKKLSKDPKRKTSEGGSSSSSES 272

RESULT 8
YSX7_CAEEL
ID YSX7_CAEEL STANDARD; PRT; 978 AA.
AC Q10025;
DC 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL 113.1 KDA PROTEIN T28D9.7 IN CHROMOSOME II.
GN T28D9.7
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: SOME, TO THE AMILORIDE-SENSITIVE SODIUM CHANNELS
CC FAMILY
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U28738; AAA68309.1; -
DR WormPep; T28D9.7; CE02889.
DR InterPro; IPR001873; -
DR Pfam; PF00858; ASC; 1.
DR Hypothetical protein; Transmembrane.
FT TRANSMEM 32 52 POTENTIAL.
SQ SEQUENCE 978 AA; 113116 MW; B3B5C48ABF2607B9 CRC64;

Query Match      22.6%; Score 53.5; DB 1; Length 978;
Best Local Similarity 32.7%; Pred. No. 26;
Matches 17; Conservative 9; Mismatches 13; Indels 13; Gaps 4;

QY 3 LKDLWCV-RRK-----YKSGFSCAGRY-----SENISRQTS--ETADNDNA 41
   | | | | | | | | | | | | | | | | | | |
DB 819 VKLLWCLDRKSRDRDIGNFKNCQGVRFVNFENFEKNNDETEDSDNS 870

RESULT 9
AATC_CHICK
ID AATC_CHICK STANDARD; PRT; 411 AA.
AC P00504;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (EC 2.6.1.1) (TRANSAMINASE A)

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DE (GLUTAMATE OXALOACETATE TRANSAMINASE-1).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89335814; PubMed=2503046;
RA Mattes U., Jaussi R., Ziak M., Juretic N., Lindenmann J.-M.,
RA Christen P.;
RT "Structure of cDNA of cytosolic aspartate aminotransferase of chicken
RT and its expression in E. coli.";
RL Biochimie 71:411-416(1989).
RN [2]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=80047259; PubMed=499525;
RA Shlyapnikov S.V., Myasnikov A.N., Severin E.S., Myagkova M.A.,
RA Torchinsky Y.M., Braunstein A.E.;
RT "Primary structure of cytoplasmic aspartate aminotransferase from
RT chicken heart and its homology with pig heart isoenzymes.";
RL FEBS Lett. 106:385-388(1979).
RN [3]
RP SEQUENCE.
RC TISSUE=Heart;
RA Shlyapnikov S.V., Myasnikov A.N., Severin E.S., Myagkova M.A.,
RA Demidkina T.V., Torchinsky Y.M., Braunstein A.E.;
RT "Primary structure of cytoplasmic aspartate aminotransferase from
RT chicken heart IV. Structure of cyanogen bromide peptides and the
RT complete amino acid sequence of the protein.";
RL Bioorg. Khim. 6:876-884(1980).
RN [4]
RP GENE STRUCTURE.
RC STRAIN=WHITE LEGHORN;
RX MEDLINE=90382432; PubMed=2401287;
RA Juretic N., Mattes U., Ziak M., Christen P., Jaussi R.;
RT "Structure of the genes of two homologous intracellularly heterotopic
RT isoenzymes. Cytosolic and mitochondrial aspartate aminotransferase of
RT chicken.";
RL Eur. J. Biochem. 192:119-126(1990).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS).
RX MEDLINE=82165126; PubMed=7067826;
RA Harutyunyan E.G., Malashkevich V.N., Tersyan S.S., Kochkina V.M.,
RA Torchinsky Y.M., Braunstein A.E.;
RT "Three-dimensional structure at 3.2-A resolution of the complex of
RT cytosolic aspartate aminotransferase from chicken heart with 2-
RT oxoglutarate.";
RL FEBS Lett. 138:113-116(1982).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).
RX MEDLINE=80143195; PubMed=7360247;
RA Borisov V.V., Borisova S.N., Sosfenov N.I., Vainshtein B.K.;
RT "Electron density map of chicken heart cytosol aspartate transaminase
RT at 3.5-A resolution.";
RL Nature 284:189-190(1980).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=95205406; PubMed=7897655;
RA Malashkevich V.N., Strokopytov B.V., Borisov V.V., Dauter Z.,
RA Wilson K.S., Torchinsky Y.M.;
RT "Crystal structure of the closed form of chicken cytosolic aspartate
RT aminotransferase at 1.9-A resolution.";
RL J. Mol. Biol. 247:111-124(1995).
CC -!- CATALYTIC ACTIVITY: L-ASPARTATE + 2-OXOGLUTARATE = OXALOACETATE +
CC L-GLUTAMATE.
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -!- SUBUNIT: HOMODIMER.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- MISCELLANEOUS: IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC
CC ONE AND A MITOCHONDRIAL ONE.
CC -!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT

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Pfam: PF00012; HSP70; 1.
DR PRINTS; PRO0301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock.
SQ SEQUENCE 538 AA; 70068 MW; EE86A60E861C36D7 CRC64;

Query Match 21.1%; Score 50; DB 1; Length 638;
Best Local Similarity 41.7%; Pred. No. 47;
Matches 10; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 21 AGRYSENISQTSETADNDNASFF 44
||||| :||:: | :| :
Db 520 AGRYAEEDQRNKIAARNLESY 543

RESULT 15
NRG3_MOUSE STANDARD; PRT; 713 AA.
ID NRG3_MOUSE C35181;
AC O35181;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PRO-NEUREGULIN-3 PRECURSOR (PRO-NRG3) [CONTAINS: NEUREGULIN-3 (NRG-3)].
DE 3)].
GN NRG3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97420720; PubMed=9275162;
RA Zhang D., Sliwkowski M.X., Mark W., Frantz G., Akita R., Sun Y.,
RA Hillan K., Crowley C., Brush J., Godowski P.J.;
RT "Neuregulin-3 (NRG3): a novel neural tissue-enriched protein that binds and activates ErbB4.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:9562-9567(1997).
CC -! FUNCTION: DIRECT LIGAND FOR THE ERBB4 TYROSINE KINASE RECEPTOR.
CC BINDING RESULTS IN LIGAND-STIMULATED TYROSINE PHOSPHORYLATION AND
CC ACTIVATION OF THE RECEPTOR. DOES NOT BIND TO THE EGF RECEPTOR,
CC ERBB2 OR ERBB3 RECEPTORS.
CC -! SUBCELLULAR LOCATION: EXISTS AS AN TYPE I MEMBRANE PROTEIN AND AS
CC A PROTEOLYTICALLY RELEASED SOLUBLE GROWTH FACTOR FORM. THE
CC MEMBRANE-BOUND FORM DOES NOT SEEM TO BE ACTIVE (BY SIMILARITY).
CC -! TISSUE SPECIFICITY: EXPRESSED IN SYMPATHETIC, MOTOR, AND SENSORY
CC NEURONS.
CC -! DEVELOPMENTAL STAGE: DETECTED AS EARLY AS E11. IN E13 EMBRYOS,
CC DETECTED MAINLY IN THE NERVOUS SYSTEM. IN E16 EMBRYOS, DETECTED IN
CC THE BRAIN, SPINAL CORD, TRIGEMINAL, VESTIBULAR-COCHLEAR, AND
CC SPINAL GANGLIA. IN ADULTS, EXPRESSED IN SPINAL CORD, AND NUMEROUS
CC BRAIN REGIONS.
CC -! DOMAIN: THE CYTOPLASMIC DOMAIN MAY BE INVOLVED IN THE REGULATION
CC OF TRAFFICKING AND PROTEOLYTIC PROCESSING. REGULATION OF THE
CC PROTEOLYTIC PROCESSING INVOLVES INITIAL INTRACELLULAR DOMAIN
CC DIMERIZATION (BY SIMILARITY).
CC -! DOMAIN: ERBB RECEPTOR BINDING IS ELICITED ENTIRELY BY THE EGF-LIKE
CC DOMAIN (BY SIMILARITY).
CC -! PTM: PROTEOLYTIC CLEAVAGE CLOSE TO THE PLASMA MEMBRANE ON THE
CC EXTERNAL FACE LEADS TO THE RELEASE OF THE SOLUBLE GROWTH FACTOR
CC FORM (BY SIMILARITY).
CC -! PTM: EXTENSIVE GLYCOSYLATION PRECEDES THE PROTEOLYTIC CLEAVAGE (BY
CC SIMILARITY).
CC -! SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -! SIMILARITY: BELONGS TO THE NEUREGULIN FAMILY.

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CC -----

DR EMBL; AF010130; AAB70914.1; -
DR MGD; MGI:1097165; Nf93.
DR InterPro; IPR000561; -
DR Pfam; PF00008; EGF; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
KW Growth factor; EGF-like domain; Transmembrane; Multigene family.
FT CHAIN 1 713 PRO-NEUREGULIN-3, MEMBRANE-BOUND FORM.
FT CHAIN 1 361 NEUREGULIN-3.
FT DOMAIN 1 362 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 363 383 INTERNAL SIGNAL SEQUENCE (POTENTIAL).
FT DOMAIN 384 713 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 105 287 SER/THR-RICH.
FT DOMAIN 288 331 EGF-LIKE.
FT DOMAIN 13 21 POLY-ALA.
FT DOMAIN 26 34 POLY-ALA.
FT DOMAIN 127 135 POLY-THR.
FT DOMAIN 250 253 POLY-ALA.
FT DOMAIN 254 263 POLY-SER.
FT DOMAIN 264 267 POLY-THR.
FT DISULFID 292 306 BY SIMILARITY.
FT DISULFID 300 319 BY SIMILARITY.
FT DISULFID 321 330 BY SIMILARITY.
SQ SEQUENCE 713 AA; 77369 MW; 9F7D1D5E7FC8DCF0 CRC64;

Query Match 21.1%; Score 50; DB 1; Length 713;
Best Local Similarity 38.2%; Pred No. 53;
Matches 13; Conservative 3; Mismatches 14; Indels 4; Gaps 1;
QY 6 LWCVR-----KYKSGFCAGRYSENISQTSRET 35
||||| ||||| :||
Db 535 LWCVERPLDKYVNSGLRTQQNASINMQLPSRET 568

Search completed: May 23, 2001, 15:36:22
Job time: 653 sec


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DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE HYPOTHEtical 58.2 KDA PROTEIN.
GN F13I12.130.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsids.
NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Choinsne N., Robert C., Brottier P., Wincker P., Cattolico L.,
RA Artiguenave F., Saurin W., Weissbach J., Mewes H.W., Lemcke K.,
RA Mayer K.F.X., Quetier F., Salanoubat M.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
[2]
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; ALJ33292; CAB61954.1; -
DR INTERPRO; IPR001440; -
KW Hypothetical protein.
SQ SEQUENCE 515 AA; 58190 MW; 7C9638ED679362C3 CRC64;

Query Match          24.9%; Score 59; DB 10; Length 515;
Best Local Similarity 35.9%; Pred. No. 5.9;
Matches 14; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 5 DLWVRKRYKSGSCAGRYSENISROTSETADNDNASS 43
      : : : : | : | | | : : | | | | | :
Db 112 EAFVKMQELASQFRNAGDEEEENKKQSEAVDNDNSN 150

RESULT 5
Q9JB41 ID Q9JB41 PRELIMINARY; PRT; 113 AA.
AC Q9JB41;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE ORF96.
OS Spodoptera exigua nucleopolyhedrovirus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=10454;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20036646; PubMed=10567663;
RA Ikkel W.F., van Strien E.A., Heldens J.G., Broer R., Zuidema D.,
RA Goldbach R.W., Vlask J.M.;
RA "Sequence and organization of the spodoptera exigua multicapsid
RT nucleopolyhedrovirus genome.";
RL J. Gen. Virol. 80:3289-3304(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Ikkel W.F.J., van Strien E.A., Heldens J.G.M., Broer R., Zuidema D.,
RA Goldbach R.W., Vlask J.M.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF169823; AAF33625.1; -
SQ SEQUENCE 113 AA; 12673 MW; 74C916B80B08075 CRC64;

Query Match          24.7%; Score 58.5; DB 14; Length 113;
Best Local Similarity 46.4%; Pred. No. 1.5;
Matches 13; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

QY 18 FSCAGRYSENISROTSETADNDNASSET 45
      : |||| : | | : ||||::||
Db 20 YFCAGRCNNN-SSSGSGGDNDNSNLFT 46

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RA Tonelli C., Paz-Ares J., Weisshaar B.:
RT "Towards functional characterisation of the members of the R2R3-MYB
RL gene family from Arabidopsis thaliana."
RL Plant J. 16:263-276(1998).
DR EMBL: AF062886; AAC83608.1; -.
DR HSP: P01103; IPOM.
DR INTERPRO: IPR001005; -.
DR PRAM: PF00249; myb_DNA-binding; 1.
DR PROSITE: PS00334; MYB_2; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 240 AA; 26684 MW; 9B789F7CC61AB823 CRC64;

Query Match 23.6%; Score 56; DB 10; Length 240;
Best Local Similarity 26.1%; Pred. No. 6.9;
Matches 12; Conservative 15; Mismatches 15; Indels 4; Gaps

Qy 3 LKDLW--CVRRKKYSSGFS-CAGRYSENISRQTSADNDNASSFT 45
:|:| |:::| | : : :|:|:|:|:|
Db 30 IKLWNLCIKKLMKKGIDPITHKPLSEVGKETNR-SDNNSTSF 74

RESULT 8
Q63041 PRELIMINARY; PRT; 1500 AA.
ID Q63041 PRELIMINARY; PRT; 1500 AA.
AC Q63041;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE ALPHA-1-MACROGLOBULIN.
GN ALPHAI M.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Eggerlsen G., Hudson G., Shields B., Reed D., Lonberg-Holm K.,
RA Fey G.H.;
EL Mol. Biol. Med. 0:0-0(0).
DR EMBL: M77183; AAA40723.1; -.
DR HSP: P01023; IBV8.
DR INTERPRO: IPR001599; -.
DR INTERPRO: IPR002890; -.
DR PRAM: PF00207; A2M; 1.
DR PRAM: PF01835; A2M_N; 1.
DR PROSITE: PS00477; ALPHA_2-MACROGLOBULIN; 1.
SQ SEQUENCE 1500 AA; 167124 MW; 8ABB810985795AB2 CRC64;

Query Match 23.6%; Score 56; DB 11; Length 1500;
Best Local Similarity 41.4%; Pred. No. 45;
Matches 12; Conservative 7; Mismatches 10; Indels 0; Gaps

Qy 9 VRRKYSGFSCAGRYSENISRQTSAD 37
| | | | | : | : | : | : | : |
Db 266 VCRKYTSYGNCHGQHSKICEFESKQAD 294

RESULT 9
Q63332 PRELIMINARY; PRT; 1500 AA.
ID Q63332 PRELIMINARY; PRT; 1500 AA.
AC Q63332;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE ALPHA-1-MACROGLOBULIN PRECURSOR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN-SPRAGUE-DAWLEY; TISSUE=LIVER;
RX MEDLINE=92172859; PubMed=1371696;
RA Waernegard B., Martin N., Johansson S.E.;
RT "cDNA cloning and sequencing of rat alpha 1-macroglobulin.";
RL Biochemistry 31:2346-2352(1992).
DR EMBL: M84000; AAA41591.1; -.
DR HSP: P01023; I1V8.
DR INTERPRO: IPR001599; -.
DR INTERPRO: IPR002890; -.
DR PFAM: PF00207; A2M; 1.
DR PFAM: PF01835; A2M_N; 1.
DR PROSITE: PS00477; ALPHA_2_MACROGLOBULIN; 1.
KW Signal.
FT SIGNAL
FT CHAIN
SQ SEQUENCE 1500 AA; 167158 MW; 2FCDD66CF3A617C6 CRC64;

Query Match 23.6%; Score 56; DB 11; Length 1500;
Best Local Similarity 41.4%; Pred. No. 45;
Matches 12; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy 9 VRRYKSSGFSCAGRYSENISROTSETAD 37
Db 266 VCRYTOSYNSCHGQHSKICEEFSKOAD 294

RESULT 10
Q9MQU4
ID Q9MQU4 PRELIMINARY; PRT; 251 AA.
AC Q9MQU4;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE GP18.
OS Bacteriophage HK022.
OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae;
OC Lambda phage group.
OX NCBI_TaxID=10742;
RN [1]
RP SEQUENCE FROM N.A.
RA Juhala R., Ford M.E., Duda R.L., Youlton A., Hatfull G.F.,
RA Hendrix R.W.;
RT "Genomic sequences of bacteriophages HK97 and HK022: pervasive genetic
RT mosaicism in the lambdaoid bacteriophages.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF069308; AAF30369.1; -.
SQ SEQUENCE 251 AA; 27535 MW; 5116519A0998FFFF CRC64;

Query Match 23.2%; Score 55; DB 9; Length 251;
Best Local Similarity 40.0%; Pred. No. 9.9;
Matches 12; Conservative 6; Mismatches 10; Indels 2; Gaps 2;

Qy 7 WCVRRYKKS-SGFSCAG-RYSENISROTSE 34
Db 186 WCIRKYRTGDCDYAGTRYFDKNNQVSD 215

RESULT 11
Q23901
ID Q23901 PRELIMINARY; PRT; 1670 AA.
AC Q23901;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE HISTIDINE KINASE.
GN DOKA.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Dictyostellida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
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RC STRAIN-AX2;
RX MEDLINE=96324396; PubMed=8670893;
RA Schuster S.C., Noegel A.A., Oehme F., Gerisch G., Simon M.I.;
RT "The hybrid histidine kinase Doka is part of the osmotic response
RT system of Dictyostelium.";
RL EMBO J. 15:3880-3889(1996).
DR EMBL: X96869; CAA65612.1; -.
DR INTERPRO: IPR000410; -.
DR INTERPRO: IPR001789; -.
DR PFAM: PF00072; response_reg; 1.
DR PFAM: PF00512; signal; 1.
SQ SEQUENCE 1670 AA; 186391 MW; 85C76DE847276B5 CRC64;

Query Match 22.8%; Score 54; DB 5; Length 1670;
Best Local Similarity 32.1%; Pred. No. 94;
Matches 17; Conservative 8; Mismatches 18; Indels 10; Gaps 2;

Qy 1 KILKDLWCVRRYKKS-----SGFSCAGRYSENI--SRQTSATADNDNASS 43
Db 498 KVLNLFIRQYKSRATIKPPDPGICIFEYIENILNYQPPTSLNDRINS 550

RESULT 12
Q9IWR9
ID Q9IWR9 PRELIMINARY; PRT; 170 AA.
AC Q9IWR9;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE ENV GLYCOPROTEIN (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=85CD334;
RA Yang C., Dash B., Hanna S.L., Frances H.S., Nzilambi N.,
RA Colebunders R.C., St Louis M., Quinn T.C., Folks T.M., Lal R.B.;
RT "Predominance of HIV-1 subtype G among commercial sex-workers from
RT Kinshasa, Democratic Republic of Congo.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF260457; AAF1605.1; -.
FT NON_TER 1
FT NON_TER 170
SQ SEQUENCE 170 AA; 19430 MW; 3E068F04B1A71F12 CRC64;

Query Match 22.6%; Score 53.5; DB 14; Length 170;
Best Local Similarity 32.8%; Pred. No. 11;
Matches 19; Conservative 4; Mismatches 10; Indels 25; Gaps 3;

Qy 11 RKY-----KSSG-----FSCAGRYSE-----NISROTSETADNDNASS 43
Db 86 RKYFONKTNFTKSSGGDLITHTSFNCAGFEFFYCNLTGFLNSSFNTENDTASNDTVSS 143

RESULT 13
Q9V4Y0
ID Q9V4Y0 PRELIMINARY; PRT; 1482 AA.
AC Q9V4Y0; Q9V4Y1; Q9V4Y2; Q9V4Y3; Q9V4Y4; Q9V4Y5; Q9V4Y6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE SNS PROTEIN.
GN SNS.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
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Dd 329 IRMAYRTS-----GRLSNIIYFTTAEAGDN 353

RESULT 14

ID Q9X9G7 PRELIMINARY; PRT; 152 AA.

AC Q9X9G7;

DT 01-NOV-1999 (TREMBLrel. 12, Created)

DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)

DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)

DE TRANSPOSASE.

GN TNP.

OS Versinia enterocolitica.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC versinia.

OX NCBI_TaxID=630;

RN [1]

RP SEQUENCE FROM N.A.

RA Simonet M., Devalckenaere A., Odaert M., Trieu-Cuot P.;

RT "Characterization of IS1541-like elements in Yersinia enterocolitica
RT and Versinia pseudotuberculosis.";

RL EMBL; AJ238016; CAB46592.1; -

DR INTERPRO: IPR002686; -

DR PFAM: PF01797; Transposase_17; 1.

SQ SEQUENCE 152 AA; 17909 MW; 9D3CEC0C5332E014 CRC64;

Query Match 22.4%; Score 53; DB 2; Length 152;
Best Local Similarity 34.6%; Pred. No. 11;
Matches 9; Conservative 6; Mismatches 11; Indels 0; Gaps

Qy 12 KYKSGFSCAGRYSENISROTSETAD 37
 |::| | | : : : | | : |
Db 99 KYRNEFWCRGYVDVTGKNFSKIRD 124

RESULT 15

ID Q38746 PRELIMINARY; PRT; 224 AA.

AC Q38746;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)

DE OSMOTIN-LIKE PROTEIN.

GN YPR5 OR PA9.

OS Atriplex nummularia.

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales;

OC Caryophyllales; Chenopodiaceae; Atriplex.

OX NCBI_TaxID=3553;

RN [1]

RP SEQUENCE FROM N.A.

RA Casas A.M., Nelson D.E., Raghothama K.G., D'Urzo M., Singh N.K.,

RA Bressan R.A., Hasegawa P.M.;

RL Plant Physiol. 0:0-0(0).

EMBL; M84468; AAA332909.1; -

HSSP: P33679; 1DU5.

DR MENDEL; 11513; Atnru; Ypr5; 11513.

DR INTERPRO: IPR001938; -

DR PFAM: PF00314; thaumatin; 1.

DR PRODOM: PD001321; -; 1.

SQ SEQUENCE 224 AA; 23823 MW; C7A76CA42B69BC9 CRC64;

Query Match 22.4%; Score 53; DB 10; Length 224;
Best Local Similarity 26.1%; Pred. No. 16;
Matches 12; Conservative 8; Mismatches 14; Indels 12; Gaps

Qy 12 KYKSGFSCAGRYSEN-----ISRQTSTADNDNASST 45
 |::| | | : : : | | : |
Db 166 KYSTDVCRCQQPKNPNNKYSMIFKGLCPQAYSXAKDDQSSTFT 211

Search completed: May 23, 2001, 15:35:19
Job time: 625 sec
